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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:35:42; Search time 44.9 Seconds
(without alignments)
950.215 Million cell updates/sec
Perfect score: 779
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Perfect score: 779
Sequence: 1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Aab3634	Aab3634	Aar7462	സ	S	3	Aab3635	Aab3634	Aab3635	Aab3635	33	Aab3635	Aab3634	27	S	Aab3634	ø	9	Ø	Aab3631	33	3	3	Aab3633	33
	ID	AAB36346	AAB36347	AAR74625	AAB36341	AAW23570	AAB36352	AAB36353	AAB36349	535	33	335	AAB36355	AAB36348	AAR62761	AAW23569	AAB36343	ABR82651	AAR52664	AAR52663	AAB36316	AAB36318	AAB36321	AAB36326	AAB36338	AAB36325
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de	Query Match Le						84.1		78.7	78.4				74.5								16.9				
	Score	779	969	69	695	069	655	614	613	611	605	604	603	580	560	260	520	515	485	413	237	132	123	123	123	115
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Salmonell	Salmonell	E. coli c	Salmonell	Salmonell	Salmonell	Salmonell	Drosophil	Drosophil	E. coli c	E. coli c	Protein e	Candida a	Plectreur	Escherich	Human tru	Truncated	Human tru	Truncated	Human tan
Aab36339	Aab36320	Abr82644	Aab36340	Aab36324	Aab36319	Aab36342	Abb65764	Abb62708	Abr82645	Abr82647	Abu36649	Abp74039	Aae36890	Aab36331	Aay44403	Aau79538	Aay44404	Aau 79539	Aay44402
AAB36339	AAB36320	ABR82644	AAB36340	AAB36324	AAB36319	AAB36342	ABB65764	ABB62708	ABR82645	ABR82647	ABU36649	ABP74039	AAE36890	AAB36331	AAY44403	AAU79538	AAY44404	AAU79539	AAY44402
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115	115	113	109	109	109	100.5	98.5	98.5	86	95		94.5	93	92	92	92	92	9.	92
26	27	28	5 2	30	31	32	33	34	35	36	37	38	39	40	4.	42	43	44	45

ALIGNMENTS

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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of Stains of Salmonella. Bscheritchia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into back into the chromosome of the hamologous species, replacing the native
                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                      AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                            vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison SK,
                               AAB36346 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                         99US-0127888P.
                                                                                                      (first entry)
                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
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                                                                                                                                                                                                                                              Escherichia coli
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                                                                                                      26-FEB-2001
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                                                                                                                                                                                                                                                                 Synthetic.
                                                                    AAB36346;
RESULT 1
AAB36346
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copy of that gene, and (4) eliciting an immune response in an animal, compy of that gene, and (4) eliciting an immune acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coll or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for the expression of recombinant Agfa protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36347 standard; protein; 151 AA.
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Matches 151; Conservative
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                   Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA ceguence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbried (SPEP1/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Entertabacteriaceae for the production of fimbriae comprising recombinant of Entertabacteriaceae for the production of fimbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant of the comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments or segments of sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expensive the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers of the vaccine, the carrier fimbrial submit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention recombinated in present are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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26-JUN-1995
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Best Local Similarity
Matches 136; Conserv
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29-SEP-1997
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                                                                                                                                                                                                                                                                              09
                                                                                                                   The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                          Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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                                                                                                                                                                                                       Score 695; DB 2; Length 151;
Pred. No. 2.2e-58;
                                                                                                                                                                                                                               Indels
 Doran JL;
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; Mismatches
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| NNAALVNOTASDSSVMVRQVGFGNNATANQY
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 Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 135; 139pp; English
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                                                                                              7B; 95pp; English.
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                                                                                                                                                                                                     Query Match
Best Local Similarity 90.1%;
Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
 Collinson SK,
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N-PSDB; AAC64617.
                         WPI; 1994-358275/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA;
                                      N-PSDB; AAQ87467
                                                                                                                                                                                  Sequence 151 AA;
                                                                                                Disclosure; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 695; DB 3; Length 151;
Pred. No. 2.2e-58;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbried (SET)/TAP? nucleation depended assembly system of strains of Salmonella. Escherichia coli and streates for the production of fimbried compisiang recombinant CC Enterobacterizace for the production of fimbried compisiang recombinant CC directing recombination of a recombinant gene into the chromosome of the composous species; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the main colliciting an immune response in an animal. In a fimbrial presentation eliciting an immune response in an animal. In a fimbrial presentation containing acernal segment for an efficient live immunogenicity and adhesion properties relevant for an efficient live immunogenes, which may be immortant for directing an immune response in an animal are usually strong immunogenes.
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protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
84.1%; Score 655; DB 3; L
Best Local Similarity 79.8%; Pred. No. 1.4e-54;
Matches 134; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                               Page 138; 139pp; English.
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                                               Disclosure;
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                                                                                                                                                                                                            The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 2765-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probacteria of the nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from greater than 99% of Salmonella acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                           Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
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Pred. No. 6.5e-58;
4; Mismatches 12
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                                                                                                                                                                     Example 2; Fig 7; 85pp; English
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ilarity 89.4%;
Conservative
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Escherichia coli.
Synthetic.
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                     WPI; 1997-309886/28
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N-PSDB; AAC64628.
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Best Local Similarity
                                               N-PSDB; AAT74142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
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Length 151;

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbries (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the chromosome of the chromosome of the composition of a recombinant gene into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation containing are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbriae ne usually strong immunogens, which may be important for an efficient live the animal process and adhesion properties relevant for an efficient live the animal process and adhesion properties relevant for an efficient live the animal process and adhesion properties relevant for an employed immunogens, which may be important for directing an immune response adjants the innerted epitope, and hybrid fimbride are easy and immunostation the animal process and an invention of the animal process are easy and the animal process and adhesion process and animal a
                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                    Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 138; 139pp; English.
                                                                                                                    Collison SK,
99US-0127888P.
                                                       (UYVI-) UNIV VICTORIA.
                                                                                                                    Doran JL,
                                                                                                                                                                              2000-672631/65
05-APR-1999;
                                                                                                                    White AP,
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Sequence 151 AA;

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                                                                                                                           LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYOYGSANAALYDO 60
                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                            Gaps
                            .;
0
    Length 151;
                            Indels
Score 614; DB 3;
Pred. No. 1.2e-50;
6; Mismatches 23;
                                                                                                                                                           NNAALVNYDQEVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                          |||||||
| NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                 AAB36349 standard; protein; 151 AA.
 78.8%;
80.8%;
                            Conservative
               Similarity
                                                                                                                                                                                                                                                                                                    26-FEB-2001
                          122;
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 Query Match
                Local
                        Matches
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Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.

AgfA::PT3#4 amino acid sequence SEQ ID NO:18.

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEP1/7PAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterioraceae for the production of fimbriae comprising recombinant of directing recombination of a recombinant gene chorologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant and animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign animo acid polymer comprising a replacement segment or segments of foreign amino acid polymer comprising a replacement segment or segments of foreign amino acid polymer of sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expense in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 100,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immunogens, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.7%; Score 613; DB 3; Length 151; 80.8%; Pred. No. 1.5e-50;
                                                                                                                                                                                                                                                                                                                                                        Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 136; 139pp; English.
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                                                                                                                                                                                                                05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                             99US-0127888P
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Matches 122, Conservative
                      Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672631/65.
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                                                                                                                   WO200060102-A2
                                                                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                          White AP,
                                                                        Synthetic.
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEP1/7AR) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of fimbriae comprision grecombinant of a recombinant gene into the chromosome of the homologous species, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or containing a nation acid polymer for the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein gare usually strong immunogenicity and adhesion properties relevant for an efficient live is against the inserted epitope, and hybrid fimbrine are easy and incerting an immune response and intering an immune response and intering an immune response in an animal. The contains are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and adhesion properties relevant contains and intering an immune response and hybrid fimbriae are easy and adhesion properties relevant contains and and an administration in the contains and any and adhesion properties electring an immune response are effected an
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                                                                                                                                                                                                       Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%; Score 611; DB 3; Length 151; 80.8%; Pred. No. 2.3e-50; ive 7; Mismatches 22; Indels
                                                                                                                                                    AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
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                                                                                                                                                                                                                                  vaccine; immune response; immunogen.
AAB36350 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356.
                                                                                                   26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA.
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Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                 WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                   AAB36350;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment with the morodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SERI) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterior accambination of finbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an emino acid polymer response in an animal, protein containing a replacing an immune response in an animal, protein containing a replacement segment or segments of foreign amino acid polymer into the animal in conjunction with a carrier or diluent. (I) is call sequence or sequences grown on a Salmonella, E. Coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin proteins protein possesses both the immunogens, which may be important for directing an immune response confine, the carrier fimbrial subunit proteins are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                     SDARKYDOLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
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| NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                  NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 138; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
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Salmonella enteri
Escherichia coli.
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                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                       SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                     .,
                                              Length 151,
                                           , DB 3; Length 15
8.5e-50;
ches 25; Indels
                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#6 amino acid sequence SEQ ID NO:22.
the exemplification of the present invention
                                                                                                                                                                                   151
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                                            Score 605; DB
Pred. No. 8.5e-
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                              AAB36351 standard; protein; 151
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                                            77.7%;
80.1%;
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                                                                                                                                                                                                                                                                                                            (first entry)
                                           Query Match
Best Local Similarity 80.1
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
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                       AA;
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Synthetic.
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copiess/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 604; DB 3;
Pred. No. 1.1e-49;
6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.5%;
80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromosovaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 80.8
les 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enteritidis.
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N-PSDB; AAC64631.
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cc assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and comparable case for the production of fimbriae comprising recombinant.

Agfa, CsgA and Agfa-homologue fimbrin subunits, respectively, (2) directing recombination of a recombination of a recombinant gene into the chromosome of the homologues species, replacing the native comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising a replacement sequent or sequence or sequences grown on a Salmonella, E. coli or comprising an amino acid sequence or sequences grown on a Salmonella, E. coli or contenting a replacement sequent or sequence or sequences grown on a Salmonella, E. coli or contenting an immune response in an animal. In a fimbrial presentation collotting an immune response in an animal. In a fimbrial presentation system the heterologues antigens are presented in high numbers (up to colotes/cell), the hybrid fimbrin protein sequence is given in mannogens, which may be important for directing an immune response contents in the inserted epitope, and hybrid fimbriae are easy and given in contents in the inserted epitope, and hybrid fimbriae are easy and contents in the expensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
                                                                                                                                                                                                                                                                                                                                                        Query Match

77.4%; Score 603; DB 3;
Best Local Similarity 80.8%; Pred. No. 1.3e-49;
Matches 122; Conservative 6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA concerning the encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbrise (SETIJ/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coll and concerning recombinate comprising recombinant comprising recombinant gene of the composition of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a namino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coll or acid sequence or sequences grown on a Salmonella, E. coll or containing an immune response in an animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful conjunction with a carrier or diluent. (I) is useful for the expression of recombinant for an efficient live vaccine, the carrier fimbrial submit protein sequence is given in against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.5%; Score 580; DB 3;
80.1%; Pred. No. 2.1e-47;
iive 7; Mismatches 23
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                                                                                                                                                                                              Disclosure, Page 136; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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hes 121; Conserv
N-PSDB; AAC64624.
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26-JUN-1995
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Matches
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ID AAR6
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10-NOV-1994

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1 VVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                                                                                                                                             VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                  Sequence 120 AA;
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                                                                                                                                                                                          Query Match
Best Local &
                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                            The sequence represents the Salmonella enteritis 27655-3b InphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                     VVPQWGGGGGNHWGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                                                                  using attenuated Salmonella g. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                 22 VVPQWGGCGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                                                                                                                                                                               71.9%; Score 560; DB 2; Length 120; 100.0%; Pred. No. 1.2e-45; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated Salmonella gene agfA - used for diagnosis of Enteropathogenic bacteria of the Enterobacteria family
                                                                                                   Doran JL;
                                                                                                                                                                Eliciting an immune response to Salmonella - us strains, vector constructs, or compsns. contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                            (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                   Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW23569 standard; protein; 120 AA
                                                                                                                                                                                                       Disclosure; Fig 7A; 95pp; English.
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            94WO-IB000207
                                    93US-00054452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WW.
                                                                                                   Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis
                                                                                                                         WPI; 1994-358275/44.
N-PSDB; AAQ73066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-309886/28.
N-PSDB; AAT74141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay
                                                                                                                                                                                                                                                                                                                        Sequence 120 AA;
                                                                         KING/) KING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1994;
            26-APR-1994;
                                   26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5635617-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW23569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                   Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW23569
à
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The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 93% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
Example 2; Fig 7; 85pp; English.
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Gaps 0 71.9%; Score 560; DB 2; Length 120; 100.0%; Pred. No. 1.2e-45; ive 0; Mismatches 0; Indels al Similarity 100. 106; Conservative 81

2, 2004, 14:48:24 completed: August e : 45.9 secs

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August 2, 2004, 14:40:48 ; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                             US-09-543-407-12
779
1 MKLLKVAAFAAIVVSGSALA.......VTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                1: /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                 389414 segs, 51625971 residues
                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                              Title:
Perfect score:
                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                            87.5
87.5
82.5
81.5
81.5
                                      OM protein
                                                                                                                                                                 Searched:
                                                                                                                    Sequence:
                                                         Run on:
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9, Appli 10, Appl	2, Appli	4, Appli	1, Appli	22119, A	4, Appli	3401, Ap	280, App	8, Appli	39, Appl	5434, Ap	2, Appli	2, Appli	13002, A	7, Appli
Sequence Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
US-09-336-447A-9 US-08-968-685A-10	US-08-254-573-2	US-08-687-379-4	US-08-172-332-1	US-U8-216-328-2 US-09-252-991A-22119	US-09-841-786-4	US-09-540-236-3401	US-09-025-769B-280	US-09-490-291-8	US-09-595-684B-39	US-09-543-681A-5434	US-08-856-253-2	US-09-382-276-2	US-09-489-039A-13002	US-09-336-447A-7
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941	900	906	906	702	714	878	415	528	1690	2315	159	186	605	624
10.1	10.0	10.0	10.0	0.6	9	9.0	9.9	9.9	6.6	6.6	9.8	9.6	9.6	9.7
78:5	78	7 0 0	7.8	77.5	77.5	77.5	77	77	77	77	76.5	76.5	76.5	75.5
77 77 70 88 70 88	30	32	33	ա տ 4 ռ	391	37	38	39	40	41	42	43		45

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
COUNTY: Seattle
STATE: Washington
COUNTY: Seattle
STATE: Washington
COUNTY: Seattle
STATE: Washington
CONFUTER FLOOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Tloppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 18M PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: 26-ARR-1994
COMPUTER: SEATTLON NUMBER: 35,570
REPERBENCE/ADGRET INFORMATION:
NAME: King, Joshua
REGISTATION NUMBER: 35,570
REPERBENCE/ADGRET INFORMATION:
TELLEFAX: (206) 62-631
TELLEFAX: (206) 62-631
TELLEFAX: (206) 62-631
TELLEFAX: (206) 62-631
TELLEFAX: (206) 68-2-631
INFORMATION FOR SEQ ID NO: 59:
SEDGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

88.6%; Score 690; DB 1; Length 151;
Best Local Similarity 89.4%; Pred. No. 7.1e-62;
Matches 135; Conservative 4; Mismatches 12; Indels
RESULT 1
US-08-233-788A-59
Sequence 59, Application US/08233788A
Patent No. 5635617
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 151 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-233-788A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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9 1 MXLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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6 VAAFAAI-VVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFTILIANT: SMALL, CASAL
AFTILIANT: SMALL, CASAL
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
NUMBER OF SEQUENCES: 12
NUMBER OF SEQUENCES: 13
NUMBER OF SEQUENCES: ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack
ADRESSEE: Klauber & Jackson
STREET: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: OFf01
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                              A PROTEIN THAT BINDS TO TRF1 AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.8%; Score 92; DB 3; Length 673; ilarity 30.4%; Pred. No. 0.6; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING APPLICATION:
PRIOR APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson BSG., 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFERK: 20.1341-684
                                                                                                                                                                                                                                   ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Smith, Susan
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTE
TITLE OF INVENTION: OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 8EQUENCE CHARACTERISTICS: LENGTH: 673 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-196-387-8
                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                      New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 35; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-841-835-8
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                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Doran, James L.
APPLICANT: Clauthinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.9%; Score 560; DB 1; Length 120; Best Local Similarity 100.0%; Pred. No. 6e-49; Matches 106; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGRY INFORMATION:
NAME: King, Joshus
REGISTRATION NUMBER: 35,570
REFRENCE/DOCKET NUMBER: 35,570
TELECOMMUNICATION INVERE: 35,570
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (206) 622-6930
                                                                                                                                                                                                                                           121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                         121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 57, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
US-09-196-387-8
; Sequence 8, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
TELEX: 3728.86 SEBDANBERRY
INFERMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOHN TOPOLOGY: 1:- OLECTION ACIDS AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Co
CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-233-788A-57
                                                                                      61
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8

157

8; Gaps

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TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
TYPE: amino acid
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Best Local Similarity 30.44
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-09-841-835-10
                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-09-196-387-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-841-835-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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Sequence 10, Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:
APPLICANT: Gaith, Susan
TITLE OF INVENTION: OF USE THEREOF
TITLE OF INVENTION: OF USE THEREOF

TITLE OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 92; DB 4; Length 673; 30.4%; Pred. No. 0.6; tive 15; Mismatches 57; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                          APPLICATION
TO A STREAM OF THE STREAM OF THE
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMINICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 30.49
Matches 35; Conservative
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TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                               COUNTRY: U
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPFISS-SSSSPSSPGSSIAESPEAA 157
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                                                       65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                                                                                                                                                                                              APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 1327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
FILING DATE:
CLASSIFICATION 1000 10, 1998
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 92; DB 2
30.4%; Pred. No. 1.5;
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FP: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REPERCHS/DOCKET NUMBER: 600-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                        Sequence 2, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
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Matches 35; Conservative
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NO
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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USA
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STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
HYPOTHETICAL: NO
                                                                                                                                                                          US-09-196-387-2
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Sequence 2, Application US/09841835; Patent No. 6506587; GENERAL INFORMATION:

RESULT 8 US-09-841-835-2

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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
WINBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 1327;
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APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OP INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERBINCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMPUTICATION INFORMATION:
TELEPHONE: 201-487-5800
TELERAX: 201.343-1684
ITELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 92; DB 4
; Pred. No. 1.5;
15; Mismatches
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09972115A Patent No. 6599728 GENERAL INFORMATION APPLICANT: Geron Corporation APPLICANT: Gregg, Morin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.4%;
Matches 35; Conservative 15
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ADDRESSEE:
STREET: IS
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                                                                                                                                                                                                                                                         STATE: Mi
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 G-----ADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVT 137
                                                                                                                                                                                                                                            99 VAAAPVVPANSTSSAAGVAPNPAGSGSNNSPSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                               158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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Patent No. 6576244
GENERAL INFORMATION;
APPLICANT: Weltzin, Richard A.
APPLICANT: Weltzin, Richard A.
TITLE OF INVENTION: LT and CT in Parenteral Immunization;
TITLE OF INVENTION: Methods Against Helicobacter Infection;
TILE REFERENCE: 06132/05502
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 09/100,258
PRIOR APPLICATION NUMBER: US 09/100,258
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                       DB 4; Length 1327;
                                                                                                                                                                           57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 90.5; DB 20.8%; Pred. No. 0.97; rative 28; Mismatches
                                                                                                                                     11.8%; Score 92; DB 4
30.4%; Pred. No. 1.5;
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 721
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-115C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-864-038A-3
; Sequence 3, Application US/08864038A
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Helicobacter pylori
                                                                                                                                                                             35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Conservative
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                                                                          ; ORGANISM: Homo sapiens
US-09-972-115A-8
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1) ... (20)
                                                                                                                                     Query Match
Best Local Similarity
Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SIGNAL
                                      1327
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US-09-336-115C-6
                                                           TYPE: PRT
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LENGTH: 74
                                        LENGTH:
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TREAT
GENERAL INFORMATION:
APPLICANT: KUNIO NAKASHIMA et al.
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA BNCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: DILLON, COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GGGAGALA-
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                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 LLKSSASASASASASAG-----GGGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89.5; DB 3;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: Îrôm 1 to 738
IDENTIFICATION METHOD: E (by experiment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLAINS: IDEN COMPAGELLE CONTRACTOR CONTRACTS: Word Perfect 6.1
CURRENT, APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6.184459
FILING DATE: 15-U1y-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AALAAAGAGGLGGGGG 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 ARKSETTITQSGYGNGADVGQG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REPERENCE/DOCKET NUMBER: F-56
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-2340
TELEPHX: (212)953-7733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%;
35.4%;
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                                                                                                                                                                                                                                                                                                          Mie-prefecture: Japan
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                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                        Isshinden
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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DB 4; Length 943;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRINT APPLICATION DUATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLEASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C9
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEFORMUNICATION INFORMATION:
TELEFAM: (206) 622-4900
TELEFAM: (206) 622-4900
TELEFAM: (206) 622-6031
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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11.4%; Score 89; DB 4
Best Local Similarity 25.6%; Pred. No. 1.9;
Matches 33; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQ ID NO 131
LENGTH: 943
TYPE: PRT
CRGANISM: Mycobacterium tuberculosis
US-09-477-135A-131
                                                                                                                                                                                                                                                                                                                            : 943 amino acids amino acids
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Best Local Similarity
Matches 33; Conserv
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US-09-477-135A-131
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US-09-072-596-199
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Dillon, Davin C.
Campos-Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
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11.4%; Score 89; DB 4; Length 943;
Best Local Similarity 25.6%; Pred, No. 1.9;
Matches 33; Conservative 15; Mismatches 55; Indels
                                                                                                           COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSITCATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J. 392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEPEX: (205) 622-4900
TELEPKS: (205) 622-4900
TELEPKS: C105) 622-4900
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TWVDF: Amino acids
        5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6468366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GGNNAALVN 127
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APPLICANT: Campos-Ne
APPLICANT: Campos-Ne
APPLICANT: Houghton,
APPLICANT: Twardzik,
APPLICANT: Lodes, Mi
APPLICANT: Hendricks
APPLICANT: Hendricks
THILE OF INVENTION:
                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                     STATE: Washingto
COUNTRY: USA
ZIP: 98104-7092
                                                   Seattle
           ADDRESSEE:
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| Sequence 13. Application US/09477135A
| Patent No. 652865
| GENERAL INFORMATION:
| APPLICAMT: Nano, Francis
| TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
| TITLE OF INVENTION: immunostimulatory Peptides
| PRIOR FILING DATE: 1996-06-14
| PRIOR FILING DATE: 1996-06-15
| NUMBER OF SEQ ID NOS: 169
| SOFTHARE: FatentIn Ver: 2.0
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                                                   69 IITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQY---
11.4%; Score 89; DB 4; Length 943; 25.6%; Pred. No. 1.9; cive 15; Mismatches 55; Indels
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Job time : 13 secs

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206 NSYNTGFGNSGDANTGFFNSGIANTGVONAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNG 265
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313 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGOYNTGYLNS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels 26; Gaps
                                                                                                                                               Sequence 204, Application US/09072967

Sequence 204, Application US/09072967

Patent No. 6592877

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Object Antonio

APPLICANT: Object Antonio

APPLICANT: Towas S.

APPLICANT: Wedvick, Thomas S.

APPLICANT: Wedvick, Thomas S.

APPLICANT: Houghton, Raymond

APPLICANT: Houghton, Raymond

APPLICANT: Hondrickson, Romald C.

APPLICANT: Hendrickson, Romald C.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 355

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
11.4%; Score 89; DB 4; Length 943;
Best Local Similarity 25.6%; Pred. No. 1.9;
Matches 33; Conservative 15; Mismatches 55; Indels
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                                   119 GGNNAALVN 127
                                                                     373 GNYNTGLAN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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US-09-072-967-204
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Search completed: August 2, 2004, 14:58:31

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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB_pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NBW_PUB_pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NBW_PUB_pep:*

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8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB_pep:*

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18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB_pep:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Sequence 49960, A	Sequence 64573, A	Seguence 7876, Ap	Sequence 147343,	Sequence 8, Appli	Sequence 10, Appl	Sequence 2, Appli	Seguence 8, Appli	Sequence 4, Appli	Sequence 203823,
SUMMARIES	ΔI	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-425-114-49960	US-10-282-122A-64573	US-10-032-585-7876	US-10-437-963-147343	US-09-841-835-8	US-09-841-835-10	US-09-841-835-2	US-09-972-115A-8	US-10-199-937-4	US-10-437-963-203823
	DB	12	12	12	12	15	12	12	14	16	6	6	6	10	14	16
	.% Query Match Length DB	151	151	131	131	445	263	678	688	271	673	949	1327	1327	1327	705
	% Query Match	66.4	66.4	56.4	56.4	12.8	12.5	12.1	12.1	11.9	11,8	11.8	11.8	11.8	11.8	11.7
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ALIGNMENTS

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US-90-741-856-4
US-90-741-856-4
US-90-741-856-4
Sequence 4, Application US/09741873B
Sequence 4, Application No. US20020081722A1
Sequence 4, Application No. US20020081722A1
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation
FILE REPERBENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT APPLICATION NUMBER: US 8801723-1
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-06
PRIOR PELING DATE: 1997-11-06
PRIOR FILING DATE: 1992-11-06
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARRE: Patentin Version 3.0
SOFTWARRE: Patentin Version 3.0
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Best Local Similarity 66.2'
Matches 100; Conservative
RESULT 1
US-09-741-873B-4
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56.4%; Score 439;
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ORGANISM: Escherichia coli
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GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012899-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 1998-05-06
FRIOR PELING DATE: 1998-05-06
FRIOR PELING DATE: 1998-05-06
FRIOR PELING DATE: 1998-05-06
FRIOR PELING DATE: 1999-11-06
FRIOR PELING DATE: 1999-11-06
FRIOR PELING DATE: 1991-11-06
FRIOR PELING DATE: 1991-11-06
FRIOR PELING DATE: 1991-11-06
FRIOR PELING DATE: 1991-11-06
FRIOR PELING DATE: 1994-10-05
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR PELING DATE: 1994-10-05
FRIOR PELING DATE: 1994-10
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                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                              61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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Publication No. US20020081722A1
GENERAL INFORMATION
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENITON: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-088
CURRENT APPLICANION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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                                                                                                                                                                                                                                                                                  121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09741873B Publication No. US20040096965A9 GENERAL INFORMATION:
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US-09-741-873B-2
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81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEM 140
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PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PLILING DATE: 1991-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
NUMBER: OF SEQ ID NOS: 10
SOFWARE: PATCHTING DATE: 1994-10-05
NUMBER: PRIOR PLILING DATE: 1994-10-05
SOFWARE: PATCHTING DATE: 1994-10-05
SEQ ID NOS: 10
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Length 131;

DB 12;

0

9 80

Gaps

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APPLICANT: Xu, H.

APPLICANT: Xu, H.

ITILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFRENCE: ELITRA.034A
CURRENT PLILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,846
PRIOR PRIOR PLILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PRIOR APPLICATION NUMBER: 60/220,347
PRIOR PRIOR DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PRILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-- 74
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NUMBER OF SEQ ID NOS: 78614
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 49960 LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Indels
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12.5%; Score 97.5; DB 12;
Best Local Similarity 26.6%; Pred. No. 0.17;
Matches 34; Conservative 18; Mismatches 53;
                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: 700071884_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64573, Application US/10282122A publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari
Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Porsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 GAAGAPSY 204
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-282-122A-64573
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Publication No. US2003023675A1

GENERAL INFORMATION:

APPLICANT: Garacy Yorden

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS

FILE REFERENCE: 80-10(5.0.5.2)

PRICE REPRESSION NUMBER: US 60/360,039

PRICE FILING DATE: 2002-02-21

NUMBER: OF SEQ ID NOS: 47374
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US-10-425-114-49960
US-10-425-114-49960
S-10-425-114-49960

S-204cence 49960
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Lau, Jingdong
APPLICANT: Abou, Yihua
APPLICANT: Rovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Babaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELIQNGFRNNATIDQWNAKN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GNSNSV-----GRDIQGKÖSGAGNSAAIFÖEGTGSDVELQÓTGTSNGAVPSGWNWTN 129
                                                                                                                                                                                                                                   81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEM 140
                                                                                                                                                                                                                                                                   61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AAFAADSNITVYINQIGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 77
                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----SDITVGQYGGNNAALVNYDQLVTRVVTHEMAHANNATA-NQ 150
                                                                                                                                                         21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                      0; Gaps
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Best Local Similarity 26.6%; Pred. No. 0.18;
Matches 47; Conservative 20; Mismatches 56; Indels 5.
                                                      Indels
                                                      28;
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COTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
                                                      Mismatches
                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rhodopseudomonas palustris
62.6%; Fig. N
                         Best Local Similarity 62.6%
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                          141 AHANNATANOY 151
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US-10-369-493-20638
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Query Match
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                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7876, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION

APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REPERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1

SEQ ID NO 7876
LENGTH: 688
                                                                                                                                                                                                                                                                  73 SGYGNGADVGQGADNS-----TIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                                                                       90 IELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ--SDARKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                       Length 678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                Indels
                                                                                                                                                12.1%; Score 94.5; DB 12; ilarity 25.7%; Pred. No. 1.1; Conservative 24; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%; Score 94.5; DB 14; 25.8%; Pred. No. 1.1; tive 24; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                              123 AALVNYDOLVTRVVTHEM-----AHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LVTGSMGLFNSGHTNTGSFN 511
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US-10-437-963-147343
i Sequence 147343, Application US/10437963
i Sequence 147343, Application US/10437963
i Publication No. US20040123343A1
i GENERAL INFORMATION:
APPLICANT: La Rosa J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                  ORGANISM: Mycobacterium tuberculosis
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64573
LENGTH: 678
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US-10-032-585-7876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.8<sup>§</sup>
Matches 31; Conservative
                                                                                                                                                  Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                         US-10-282-122A-64573
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59 GGEGGGSESGGGLGRQR------YWNSRLSTERQRLVDHVFKNSDVVCDVF 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VVGRAAAAYPEVGSGDGGESGGGGGGGGGG------GGDGSVAAVNPEAGSGDGDRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09841835
Patent No. US/0020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                           11.9%; Score 93; DB 16; Length 271; 22.2%; Pred. No. 0.49; ive 18; Mismatches 59; Indels
                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT MRT4530 47881C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 SGVGPIAIS----AARKVKYVYANDLNPTAVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 SGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 GGNNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147343
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 201-487-58
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                        US-10-437-963-147343
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US-09-841-835-8
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RESULT 13
US-09-972-115A-8
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                                                                                                          99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                            Gaps
                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09841835
; Patent No. US20020076795A1
; GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
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ch 11.8%; Score 92; DB 9; Length 673; Similarity 30.4%; Pred. No. 1.9; 35; Conservative 15; Mismatches 57; Indels
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11.8%; Score 92; DB 9; Length 949;
Best Local Similarity 30.4%; Pred. No. 2.9;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
TELEPHONE: 20.742
TELEPHONE: 20.742
TELEPHONE: 20.742
TELEPHONE: 20.745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 949 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-841-835-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
TELEFAX: 20
TELEX: 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                  RESULT 11
US-09-841-835-10
  Query Match
Best Local (
                                         Matches
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RESULT 12

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Patente 2, Aggrance 2, Aggranc
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                                                                                                                                                                                                                                                                                                                                                     99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                          6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               65 KSETTIT----QSGYGNGADVGQGADNSTIELTONG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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Best Local Similarity 30.4%; Pred. No. 4.4;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                     DB 10; Length 1327;
                                                                                                                                                                                                                                                                                 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Christenson, Erik
APPLICANT: Christenson, Erik
APPLICANT: Defaagio, Anthony J.
APPLICANT: Defaagio, Anthony J.
APPLICANT: Defaagio, Anthony J.
APPLICANT: McBiligott, David L.
TITLE OF INVENTION: TANKRASEZ MATERIALS AND METHODS
FILE REFERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/207-28
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-66-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1327
                                                                                                                                                                                                                                                              ; Pred. No. 4.4;
15; Mismatches
                                                                                                                                                                                                                                          11.8%; Score 92; 30.4%; Pred. No.
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PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
SEQ ID NO 8
LENGTH: 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10199937
Publication No. US20030190739A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.4%
Matches 35; Conservative
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; ORGANISM: Homo sapiens
US-10-199-937-4
                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                                                                                                              US-09-972-115A-8
                                                                                                                                                       TYPE: PRT
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APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 138-21 (33221)8

CURRENT APPLICATION NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 203823

LENGTH: 705

TYPF: ---

TYPF: ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 IVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYG---SANAALALQSDARKSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - ADVGQGADNSTIELTQNGFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NEWYKK-----GHYG---EALRHYDQAVALCPDSAACRSNRAAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 705;
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US-10-437-963-203823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match. 11.7%; Score 91.5; DB 16; Best Local Similarity 24.7%; Pred. No. 2.3; Matches 42; Conservative 19; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 2, 2004, 15:36:09 Job time : 37.8 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 TITQSG---YGNG--
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
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sequence 6, Appli
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 20638, A
Sequence 20638, A
Sequence 358, App
Sequence 358, App
Sequence 9317, App
Sequence 24084, A
                                                                                                                                                                                                                                                                  Sequence 36, Appl Sequence 16, Appl Sequence 7, Appl Sequence 7, Appl Sequence 2, Appl Sequence 2, Appl Sequence 5834, Appl Sequence 5834, Appl Sequence 2, Appl Sequence 34, Appl Sequence 37, Appl Sequence 37, Appl Sequence 35, Appl Sequence 5833, Appl Seq
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                            Sequence 14, 2
Sequence 5, 35
Sequence 24, 2
Sequence 26, 3
Sequence 18, 3
Sequence 20, 3
Sequence 20, 3
Sequence 21, 3
Sequence 22, 3
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GENERAL INFORMATION:
APPLICANT: Wither, Aaron P.
APPLICANT: Wither, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: Sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
19 US-09-543-407-12

US-09-543-407-12

US-09-543-407-14

US-09-543-407-16

US-09-543-407-24

US-09-543-407-26

US-09-543-407-20

US-09-543-407-30

US-09-614-1150-24084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-614-150A-24084
US-60-191-637-24179
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       RESULT 1
US-09-543-407-12
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24735
100237
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                                                                                                                                                                                                                                                             US-09-543-407-12
779
1 MKLLKVAAFAAIVVSGSALA......VIRVVTHEMAHANNATANQY
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1: /cgn2 6/ptodata/2/paa/BCTUS CONB.pep:*

2: /cgn2 6/ptodata/2/paa/USO6 GONB.pep:*

3: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

5: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

6: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

6: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

7: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

8: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

10: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

10: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

10: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

11: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

12: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

13: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

14: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

15: /cgn2 6/ptodata/2/paa/USO8 GONB.pep:*

16: /cgn2 6/ptodata/2/paa/USO9 GONB.pep:*

17: /cgn2 6/ptodata/2/paa/USO9 GONB.pep:*

18: /cgn2 6/ptodata/2/paa/USO9 GONB.pep:*

19: /cgn2 6/ptodata/2/paa/USO9 GONB.pep:*

19: /cgn2 6/ptodata/2/paa/USO9 GONB.pep:*

10: /cgn2 6/ptodata/2/paa/USO9 GONB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6019581
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                         6019581 segs, 976053577 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                         Perfect score:
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Maximum DB
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No.
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Query Match

88.6%; Score 690; DB 6; L.
Best Local Similarity 89.4%; Pred. No. 8.6e-65;
Matches 135; Conservative 4; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
       NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSEQ for W.
SEQ ID NO 5
LENGTH: 151
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                  1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Exp. William, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT FILING DATE: 2000-04-05
SOFTWAREN FILING DATE: 2000-04-05
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran: James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION WHERE: US/09/543,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                       ô
                                         Length 151;
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Best Local Similarity 87.6%; Pred. No. 2e-65;
Matches 141; Conservative 0; Mismatches 0; Indels 20
                                                                                       Indels
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100.0%; Pred. No. 2.9e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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US-09-543-407-14

Sequence 14, Application US/09543407

GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                      Query Match
Best Local Similarity 100.
Matches 151; Conservative
US-09-543-407-12
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US-09-543-407-5
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                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KAY, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Coluthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             Length 151;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION UMABER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 42*
ATTORNEY/ARRAIN: 42*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seed and Berry 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                             Score 695; DB 19;
Pred. No. 2.5e-65;
4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                        Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Application US/08233642A GENERAL INFORMATION:
                                                                                                                              ) ORGANISM: Salmonella enteritidis US-09-543-407-5
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REGISTRATION NUMBER: 35,570
2000-04-05
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ilarity 90.1%;
Conservative
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: BACTERIAL FOR

TITLE OF INVENTION OF HETEROLOGOUS PEPTIDE SEQUENCES

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE FASTSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 151
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Doird, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILE OF BOOKS: 2000-04-05
SOFTWARE: FRSESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNYDQLVTRVVTHEMAHA--------NNATANQY 151
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ORGANISM: Artificial Sequence
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Best Local Similarity 79.8
Matches 134; Conservative
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US-09-543-407-26
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US-09-543-407-24
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US-09-543-407-24
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LENGTH: 151
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                                       OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA orther INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-26
                                                                                                                                                   Length 151;
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80.8%; Pred. No. 1.4e-56;
iive 7; Mismatches 22;
                                                                                                                                              Score 614; DB 19;
Pred. No. 1.1e-56;
6; Mismatches 23;
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| 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Sequence 18, Application US/09543407
GENERAL INPORMATION:
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Ray, William W.
TITLE OF INVENTION: BRCTERIAL FUMBRIAL SYSTE
TITLE OF INVENTION: BACTERIAL FUBBRIAL SYSTE
TITLE FEFRENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-543-407-20
; Sequence 20, Application US/09543407
; GENERAL INFORMATION:
                                                                                                                                              78.8%;
80.8%;
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 80.8
Matches 122; Conservative
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Matches 122; Conservative
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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hes 122;
                                                  JS-09-543-407-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Callinson, S. Karen
APPLICANT: CAL WIlliam W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 59
SOFWRARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
EMPORT: 131
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASISEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.4%; Score 611; DB 19; Length 1: Best Local Similarity 80.8%; Pred. No. 2.2e-56; Matches 122; Conservative 7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
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Pred. No. 3.9e-56;
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; Sequence 31, Application US/09543407
; GENERAL INFORMATION:
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                                                                                                                                                                                                                 SEQ ID NO 20
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 88.5%;
Matches 116; Conservative
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Callinson, S. Karen
APPLICANT: RAY, William W.
ITLE OF INVENTION: BACTERIAL PIMBRIAL SYSTEM FOR
ITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151

LENGTH: 151
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                                                   APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Colling.
S. Karen
APPLICANT: Colling.
S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 220043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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larity 80.8%; Pred. No. 1.2e-55;
Conservative 6; Mismatches 23; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.7%; Score 605; DB 19; I Best Local Similarity 80.1%; Pred. No. 9.8e-56; Matches 121; Conservative 5; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNYDQLVTRVVTHEMAHANNATANQY
Sequence 28, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 28
LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Sequence
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US-08-233-642A-55
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                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                             61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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1 MKLIKVAAPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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US-09-543-407-16
Sequence 16, Application US/09543407
Sequence 16, Application US/09543407
Sequence 16, Application US/09543407
Sequence 16, Application US/09543407
Setel CANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: RAPLICANT: BACTERIAL FINBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: White, Aaron P. APPLICANT: White, Aaron P. APPLICANT: Doran, James L. APPLICANT: Collinson, S. Karen APPLICANT: Collinson, S. Karen APPLICANT: Kay, William W. TITLE OF INVENTION: BATTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: EastSEQ for Windows Version 4.0
LENGTH: 151
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US-09-543-407-30
; Sequence 30, Application US/09543407
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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FEATURE:
COTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
CHER INFORMATION: sequence containing the replacement fragment
CHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-16
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: MATHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS: -
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                              Query Match
Best Local Similarity 80.1%; Pred. No. 4.5e-53;
Matches 121; Conservative 7; Mismatches 23; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.9%; Score 560; DB 6; Length 120; Best Local Similarity 100.0%; Pred. No. 4.5e-51; Matches 106; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-233-642A-55
Gequence 55, Application US/08233642A,
George INFORMATION:
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ATTORNEY AGENT INFORMATION:
RAGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92004
TELECOMPUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 632-6031
TELEFAX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 120 amino acids
amino acid
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STATE: Washington
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1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                                                                     RESULT 15
US-09-543-407-7
SQUENCE 7, Application US/09543407
SQUENCE 7, Application US/09543407
SQUENCE 7, Application US/09543407
APPLICANT: Minte, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: AAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE REFERENCE: 20043.406
CURRENT PAPLICATION NUMBER: USO,09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ FOR WINGOWS VERSION 4.0
ILENGTH: 151
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                                                                                         61 GOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGGNNAALVN 106
                                                82 GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
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ORGANISM: Escherichia coli
US-09-543-407-7
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Sequence 4, Appli
Sequence 3.0390,
Sequence 310468,
Sequence 3751, A
Sequence 741, Appl
Sequence 7608, Appl
Sequence 7906, Appl
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                                                                        August 2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151
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2: /cgn2_6/ptodata/2/paa/USG6 NEW COMB.pep:*
4: /cgn2_6/ptodata/2/paa/USG7_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USG8_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/USG8_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/USG8_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/USG8_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/USG8_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-741-873C-2
US-10-425-115-312468
US-09-248-796A-17559
US-110-205B-741-
US-110-205B-751-
US-110-205B-751-
US-110-205B-751-
US-110-205B-751-
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Listing first 45 summaries
                                                 protein search, using sw model
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US-99-441-836-4

Sequence 4, Application US/09741873C

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Olsen, Arne

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REPRENCE: 012889-084

CURRENT FILING DATE: 2000-12-22

CURRENT FILING DATE: 2000-12-22

CURRENT FILING DATE: 1999-08-06

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR PRILING DATE: 1991-11-06

PRIOR PRILING DATE: 1991-11-06

PRIOR PRILING DATE: 1994-10-28

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/318,519

PRIOR PLILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Version 3.0
                                                                                      Sequence 10326, A Sequence 10327, A Sequence 100, App Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 285216, Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 11109, A Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 11109, A Sequence 1110
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                         Sequence 13, Appl
Sequence 13, Appl
Sequence 254240,
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Best Local Similarity 66.2%; Pred. No. 1.1e-36;
Matches 100; Conservative 22; Mismatches 29; Indels
121 NNAALVNYDQLVTRVVTHEMAHANNATANOY 151
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ORGANISM: Escherichia coli
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GENERAL INFORMATION:
GENERAL I
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Experiment of the control of the control
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                                                                                  12.5%; Score 97.5; DB 6; Length 258; 26.6%; Pred. No. 0.86;
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US-10-425-115-312468
                                                                                                                                                                         Mismatches
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Best Local Similarity 29.7'
Matches 38; Conservative
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                                                                                                                           Local Similarity
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ORGANISM: Zea mays
US-10-425-115-300390
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US-10-425-115-312468
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US-09-248-796A-17559
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                                                                                  Query Match
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Acvaltc, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Co, Yonguei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: 1053223 BCURRENT 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 258
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                                                                                                                                APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
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OTHER INFORMATION: Clone ID: WRT4577_37025C.1.pep
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LOCATION: (1)..(258)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 26 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR PELING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1992-11-03
PRIOR PILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-10-05
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: PATCHING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATCHIN VERSION 3.0
                                                                Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-873C-2
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| 121 GFGNNATAHQY 131
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Best Local Similarity
Matches 82; Conserv
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ORGANISM: Zea mays
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FORGURANCE AND ADDICATION PC/TUS0402338
GENERAL INFORMATION:
APPLICANT! EXETIXIS. INC.
TITLE OF INVENTION: MAPCASS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF TITLE OF INVENTION: USE
FILE REPERENCE: EXOQ-003-CPC
CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-06-19
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Sequence 301334, Application US/10425115

Sequence 301334 Thomas U.

Sequence 301334

APPLICANT: Lar Rosa, Thomas U.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Application of the molecules and other molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 369326

LENGTH: 256
99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 VALAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                        65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION; Clone ID: MRT4577_37894C.1.pep
US-10-425-115-301334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.8%; Score 92; DB 1;
Best Local Similarity 30.4%; Pred. No. 16;
Matches 35; Conservative 15; Mismatches 5'
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26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: ADAMS, MAR.
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CLOOMS181
CURRENT PAPLICATION NUMBER: US/10/170,205E
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SEQ ID NO 741
LENOTH: 1203
TYPE: RAT
TENOTH: 1203
TYPE: RAT
TORGANISM: Homo sapiens
US-10-170-205E-741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35751, Application US/10170205E
GENERAL INFORMATION:
SPELICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PATENTIN version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 TGLINN---NNSKSPAKSKKKSNFD----NNSNSALNNIDKSKLKINTNEITNISETTSN 615
                                                                                                                                                                                                                                                                                                                                                       519 GNNNGSGNSSGTTNNSNNYNN------KSISKKNE-----IDDGDDLNPTSITNN 562
                                                                                                                                                                                                                                                                                                                                                                                                                                   90 IELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAHANNATAN 149
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                                                                                                                                                                                                                                                                                                                30 GNHNGGGNSSGPDSTLSIYOYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
12.1%; Score 94.5; DB 5; Length 719;
Best Local Similarity 25.8%; Pred. No. 4.9;
Matches 31; Conservative 24; Mismatches 42; Indels 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
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11.8%; Score 92; DB 6;
Best Local Similarity 30.4%; Pred. No. 14;
Matches 35; Conservative 15; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30,4%
Matches 35; Conservative
                                                                            TYPE: PRT Candida albicans US-09-248-796A-17559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-170-205E-35751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-10-170-205E-35751
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LENGTH: 299
                      SEQ ID NO 17559
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   5
                                                                                                                           SSVAG-----GGGGGGGGGGTNGGSGGGGGGGGGTSSTAASGPSSGNYANAEGKGAG 133
                                                                                                                                                                                         73 SGYGNGAD------VGQGADNSTIEL--TQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                  185 GMNPQGAPWGQGG--NGGPPNFCTNTQGAVAQPGYGSVRA----SNQNEGCTNPPPSGS 237
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                                                             17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA----RKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILE OF INVENTION: Human Secreted Proteins
FILE REPERENCE: PS900
CURRENT APPLICATION: Human Secreted Proteins
FILE REPERENCE: PS900
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT PILING DATE: 1097-03-19
FRIOR APPLICATION NUMBER: US 60/040,162
FRIOR APPLICATION NUMBER: US 60/043,576
FRIOR PILING DATE: 1997-03-70-11
FRIOR FILING DATE: 1997-03-23
FRIOR FILING DATE: 1997-03-23
FRIOR FILING DATE: 1997-03-23
FRIOR FILING DATE: 1997-03-23
FRIOR APPLICATION NUMBER: US 60/056,845
FRIOR FILING DATE: 1997-03-23
FRIOR FILING DATE: 1997-04-11
FRIOR FILING DATE: 1997-04-11
FRIOR APPLICATION NUMBER: US 60/056,664
FRIOR PELING DATE: 1997-04-21
FRIOR PELING DATE: 1997-03-23
FRIOR APPLICATION NUMBER: US 60/056,664
FRIOR PELING DATE: 1997-03-23
FRIOR APPLICATION NUMBER: US 60/056,664
FRIOR APPLICATION NUMBER: US 60/056,692
FRIOR APPLICATION NUMBER: US 60/056,892
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   23; Gaps
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   Indels
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52;
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11.7%; Score 91.5; DB 6; I
Best Local Similarity 26.0%; Pred. No. 5.1;
Matches 33; Conservative 18; Mismatches 43;
16; Mismatches
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US-60-565-632-7906
; Sequence 7906, Application US/60565632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7608, Application US/10100683 GENERAL INFORMATION:
Conservative
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US-10-100-683-7608
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33
Matches
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APPLICANT: Monsanto Technology, LLC
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Tichifa R. I.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, James K.
APPLICANT: Canage, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
TITLE REFERENCE: 38-21(53403)8
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT APPLICATION NUMBER: US/60/4-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7906
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APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Along, Bei
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION OF THE COMPOSITION OF THE COMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>о</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 AAQGTDNGAAAENTGNADPAQGNDNGAA----AENSGNENGTAAGNNA---NPD---- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 GNENGTGAENNANADAQTDAAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

NAME/KEY: misc feature

LOCATION: (810)

CHER INFORMATION: Xaa can be any naturally occurring amino acid

18-60-565-632-7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature; LOCATION: (810); COTER INFORMATION: Xaa can be any naturally occurring amino acid v1S-60-579-062-7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 91.5; D
32.6%; Pred. No. 11;
live 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baum, James A
APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Munylkwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Diabrotica virgifera FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 VVTHEMAHAN-NATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.6<sup>§</sup>
Matches 44, Conservative
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347 GGNFGGNNNGGGGFNSGNNFNSPGGVNNFGNNFGSNFGGNGGGGFNNGGNFVSSSGVGNF 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24] GNENGTGAENNANADAQTDVAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 VGQGADNSTI-------ELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 GG--GGNHNGGG-----NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                       79 ADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNY 128
                                                                                                                                                                                                                                                                                                                                                                                                           407 GPIGGGRINNNGNFGNSGF-------GNFGGNNNVGSNF 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                    Query Match
Best Local Similarity 25.5%; Pred. No. 9.5;
Matches 28; Conservative 12; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%; Score 88; DB 7; Length 573; 26.2%; Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 LVNYDQLVTRVVTHEMAHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: August 2, 2004, 15:29:50 Job time : 17.8 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 QVN-----DNGAAAENNGNAD 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7907, Application US/6056532 GENERAL INFORMATION:
APPLICANT Monsanto Technology, LLC
  PRIOR APPLICATION NUMBER: 60/422,377
PRIOR FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 381
SEQ TWARE: Patentin version 3.1
SEQ ID NO 317
LENGTH: 586
                                                                                                                                             ORGANISM: Drosophila melanogaster
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Best Local Similarity
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US-60-565-632-7907
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                                                                                                                         TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Syngente Participations AG
APPLICANT: Stam, Lynn
APPLICANT: Spana, Exic
APPLICANT: Bachmann, Jane
TITLE OF INVENTION: Desential for Viability and Uses Thereof
FILE REFERENCE: 70131WOPCT
CURRENT APPLICATION NUMBER: PCT/US03/24982A
CURRENT FILING DATE: 2003-08-08
                                                                                                                                                                                                                                                                                                                                                                           Sequence 45603, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
LENGTH: 234
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                                                                                                                       269 GNENGTGAENNANADAQTDAAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD 327
                                                                                                                                                                81 VGQGADN-STIELTQN-----GFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTR 134
                                                                                                                                                                                                      328 AAQGTDNGAAAENTGNADPAQGNDNGAA----AENSGNENGTAAGNNA---NPD---- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GXYGEAGGSGXAYAQGGGQGGGGGGQYGGSG-------SGYGSGSGYG 102
                                                                                   GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKSETTITQSGYGNGAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SSGPDSTL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 SIY-------QYGSANAALALQSDARKSETTITQSGYGNGADVG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                            Gaps
                                            48; Indels 31;
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      DB 7; Length 841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVV -- SGSALAGVVPQW --- GGGGNHNGGGN -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C62834_1.pep
US-10-767-701-45603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 QGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.6%; Score 90.5; DB 6;
Best Local Similarity 24.2%; Pred. No. 3;
Matches 39; Conservative 12; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
th 11.7%; Score 91.5; Di Similarity 32.6%; Pred. No. 11; 44; Conservative 12; Mismatches
                                                                                                                                                                                                                                               135 VVTHEMAHAN-NATA 148
                                                                                                                                                                                                                                                                       ORGANISM: Sorghum bicolor
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-767-701-45603
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec

Title:
US-09-543-407-12
Perfect score: 779
Sequence: 1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 283366

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_78:*
1: Dix1:*
2: Dix2:*
3: Dix3:*
4: Dix4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID 695 89.2 151 2 AIC639	+		. * 5			SELVATION	
695 89.2 151 2 JC6039 695 89.2 151 2 JC6039 696 89.2 151 2 JC6039 607 88 6.8 151 2 JC6035 60.4 152 2 JC6039 60.5 64.4 152 2 JC6040 60.5 13.6 1748 2 JC6040 60.5 12.9 151 2 JC6040 60.5 12.9 145 2 JC6040 60.5 12.9 12.9 145 2 JC6040 60.5 12.9 12.9 12.9 12.9 12.9 12.9 12.9 12.9		core	Match	Length	DB	ID	uo
695 89.2 151 2 A10635 major curlin 521 66.8 151 2 S70788 curlin myord 501.5 64.4 152 2 D90806 curlin myord 501.5 64.4 152 2 D90806 curlin myord 501.5 64.4 152 2 D90806 curlin myord 106 13.4 174 2 D55965 curlin myord 100.5 12.9 151 2 D40635 curlin myord protein 100.5 12.9 151 2 D40635 curlin myord better 100.5 12.9 12.1 2 D40635 curlin myord better 100.5 12.9 12.1 2 D40635 curlin myord better 100.5 12.9 12.1 2 D40635 curlin myord better 100.5 12.1 12.2 D40636 curlin myord better 100.5 12.1 12.2 D40638 curlin myord better 100.5 12.1 12.1 12.1 12.1 12.1 12.1 12.1 12		695	89.	15		JC603	in protein a
520 66.8 151 2 570788 curlin prote 501.5 64.4 152 2 B9606 curlin major 501.5 12.6 12.8 2 B9655 curlin protein 100.5 12.9 151 2 A9635 curlin protein 100.5 12.9 151 2 A9634 curlin protein 100.5 12.9 12.8 145 2 A99144 curlin protein 100.5 12.3 12.0 12.3 2 A9626 curlin mucle 100.5 11.7 151 2 G906 curlin mucle 100.5 11.7 151 2 G906 curlin mucle 100.5 11.7 1250 2 B6455 curlin mucle 100.5 11.7 1250 2 B6455 curlin mucle 100.5 11.7 1250 2 B6455 curlin mucle 100.5 11.6 575 2 B6455 curlin kinal 100.5 11.5 343 2 T05221 curlin kinal 100.5		g	٥,	15	N	53	r curlin chai
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101.5 13.0 151 2 AH0635 mücleation (100.5 12.6 12.8 2 A60340 MA-binding 98.5 12.6 1213 2 A56034 MA-binding 98.5 12.6 1213 2 A56034 MA-binding 98.5 12.6 1213 2 A56034 MA-binding 98.5 12.0 123 2 A70762 MA-binding 93.5 12.1 678 2 A70762 MA-binding properties of the control of th		0		217	7	96	hypothetical glyci
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12.6 1028 2 A5638 DNA-binding 5.5 12.6 1028 2 S16356 Covo protein 5.5 12.6 12.3 145 2 H98144 PNA-binding 5.6 12.1 678 2 A70762 Probable PNA-binding 5.7 11.9 573 2 C86266 Curlin minol 6.5 11.7 151 2 G8566 Curlin minol 6.5 11.7 151 2 G8566 Curlin minol 6.5 11.7 1250 2 P1024 PNA-binding 6.6 11.7 1250 2 P1024 PNA-binding 6.6 11.7 1250 2 P1028 PNA-binding 6.6 11.7 1250 2 P1028 PNA-binding 6.6 11.7 1250 2 P1028 PNA-binding 6.6 11.6 575 2 S1327 Probable PNA-binding 6.6 11.5 2 S1327 PNA-binding 7.6 11.5 2 S1327 PNA-binding 7.		00	ď	15	~	4	fimbrin protein ad
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ALIGNMENTS

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	C,Species: Salmonella enteritidis C,Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text change 08-Oct-1999
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	, F.A.; Kay, W.W.
	A,Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A,Reference number: JC6039; MJID:96146512; PMID:8550497
ray Paly	A,Accession: JC6039 A,Molecule Lype: DNA
· N4	A; Kesidues: 1-151 <col/> A; Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714
~ ~	A,Accession: PC6015 A,Molecule type: protein
~ .	A, Residues: 21-52 <co2></co2>
٠, ٨,	A;Experimental source: strain 27655-35 A;Note: the authors translated the codon ACG for residue 44 as Ile
н.	
1 44	A, Title: Purification and characterization of thin, aggregative fimbriae from Salmonell
	A.Reference number: A44898; MUID:91310586; PMID:1677357
	A.Accession: A4898
2	A; Status: preliminary
~. A	A;Molecule type: protein A:Residnes: 21-33 < 03.
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	O.Genetics: B.Gene. acfi
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- FI, F	on: major component of thin aggregative
., O	A,wore: ilmbilae bina to ilbronectin, plasminogen, tissue plasminogen activator C,Keywords: fimbria
<u>и</u> и	F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>
	l.8e-50; nes 11; Indel
	Oy 1 MKLEKVARRAAIVVSGSALAGVVPQMGGGGNHNGGGNSGPDSTLSIXQXGSANAALALQ 60
<u>ы</u>	Db 1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSGPDSTLSIYQYGSANAALALO 60
<i>O</i>	Qy 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
Ц	Db 61 SDARKSETTITQSGYGNGADVGQGADNSTIELIQUGFRNNATIDQWNAKNSDITVGQYGG 120
<i>o</i>	QY 121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151

csg

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Cyclin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C;Species: Escherichia coli (c;Date: 18-011-2001 #sequence_revision 18-011-2001 #text_change 18-011-2001 C;Accession: D90806 F;Accession: D90806 F;Acsions, M.; Kunkino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 F; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A;Accession: D90806 F;Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: major component of wild-type curli; interaction between CsgA and CsgB tr. A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG> F;21-151/Product: curlin #status experimental <MAT>
A, Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A, Reference number: S31202; MUID:93211294; PMID:8459772
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A;Bxperimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS1420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-13, -...
A;Crosi-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
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65.8%; Pred. No. 1.6e-34;
iive 21; Mismatches 30,
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4.7e-36;
                                                                               A,Accession: S11202
A,Molecule type: DNA
A,Residues: 1-6, 'W. Bels! OLS1>
A,Cross-references: EMBL: L04979
A,Accession: S34560
A,Molecule type: protein
A,Residues: 21-42,44-50 oLS2>
R,Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library, October 1992
A,Accession: S34559
A,Accession: S34559
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Best Local Similarity 66.9%;
Matches 101; Conservative 2
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Best Local Similarity
Matches 100; Conserv
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A,Residues: 1-152
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                                                                                                                                                                                                                                      C; Species: Salmonella enterica subsp. enterica servar Typhi
C; Species: Salmonella enterica subsp. enterica servar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-NOv-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A16635
R; Parkhill, J; Dougan, G;; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar, S; Moule, S; O'Gaora, P.
Nature 413, 848-852, 2001
A; Hill: Complete genome sequence of a multiple drug resistant Salmonella enterica servow A; Reference number: AB0502; MUD:21534947; PMID:11677608
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-151 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
C; Genetics:
A; Genetics:
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A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curlin protein csgA precursor - Escherichia coli (strain K-12)
NyAlternate names: csgA protein; major curlin protein
C;Species: Escherichia coli
C;Species: Bacherichia coli
C;Accession: S70788; G64846; S31202; S34560; S34559
E;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1939
A;Title: Expression of two osg operons is required for production of fibronectin- and A;Reference number: S70783; MUID:96414468; PMID:8817489
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A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
B;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                              curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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A, Status: nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 695; DB 2;
Pred. No. 1.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                           NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
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ilarity 90.1%;
Conservative
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Best Local Similarity
Matches 136; Conserv
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C,Accession: E95965 ... 3., Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Frötnan, T.W.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A,Title: The complete sequence of the 1,683-kb pSym8 megaplasmid from the N2-fixing end: A,Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:ALS91985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
B;Calibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, D:; Hyman, R.W.; Jones, T.
Science 39; 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mag
                                                                                                                           290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021)
C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CQSNVQESTTTSSGGWGSSGSGN 1685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT----QSGYGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106; 1
Pred. No. 1;
A,Cross-references: EMBL:X06462
C,Genetics:
A,Gene: cnj8
A,Genetic code: SGC5
A,Introns: 85/3; 136/1; 157/3; 201/2; 290/2; C,Keywords: 2inc finger
F,1164-1450/Region: glyoine-rich
F;1451-1464/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1530-1564/Region: zinc finger CCHC motif
F;1551-1568/Region: zinc finger CCHC motif
F;1551-1592/Region: zinc finger CCHC motif
F;1551-1592/Region: zinc finger CCHC motif
F;1602-1615/Region: zinc finger CCHC motif
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32.1%;
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Best Local Similarity
Matches 35; Conserv
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Best Local Similarity
Matches 35; Conserv
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A;Gene: SMb21548
A;Genome: plasmid
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                                                                                                                                                                                                                                                                           Nypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 Cypate: L6.Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 Cypate: L6.Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 Cypate: L8566 L9.Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew lature 409, 529-533, 2001 Liler, L.; Grotheck, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Accession: H85665 A;Status: preliminary A;Molecule type: DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-152 <STO>
A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z16
A;Cross-references: GB:AE005174; Substrain EDL933
C;Genetics:
A;Gene: csgA
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B/Across-references: Embl.103710; NID:g161751; PID:g161752
B/Aritle: Retroviral-type zinc fingers and glycine-rich repeats in a protein encoded by careference number: S42135; MUID:94051569; PMID:8233798
A/Residue: S42135; MUID:94051569; PMID:8233798
A/Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-7
A/Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-7
A/Residues: Acids Res: 16, 2189-2201, 1988
A/Fitle: Aultiple introns in a conjugation-specific gene from Tetrahymena thermophila. A/Reference number: S03650; MUID:88189811; PMID:3357771
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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65.8%; Pred. No. 1.6e-34;
live 21; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cnjB protein - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #
C;Accession: S42136; 842135; S30450
R;Taylor, F.M.; Martindale, D.W.
Bbmitted to the EMBL Data Library, October 1992
A;Accession: S42136
                                                                                                                              GGNGAAVDQTASNSTVNVTQVGFGNNATAHOY 152
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A,Residues: 236-250,'I',252-255,'N',257-773 <MAR>
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Best Local Similarity 65.8
Matches 100; Conservative
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
C;Accession: As6038
R;Gatchinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
Mol. Cell. Biol. 14, 6809-6818, 1994
A;Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaste
A;Reference number: A56038; MUID:95021209; PMID:7935398
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-1028 cGRR>
A;Cross-references: GB:U11383; NID:9520526; PIDN:AAB60216.1; PID:9520527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S16356
R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
A;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
A;Title: The ovo gene of Drosophila encodes a zinc finger protein required for female generate number: S16356; MUID:91293102; PMID:1712294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ovo protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Feb-1997
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   protein ovo - fruit fly (Drosophila melanogaster)
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12.6%; Score 98.5; DE
Best Local Similarity 24.5%; Pred. No. 2.3;
Matches 46; Conservative 15; Mismatches
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A,Cross-references: FlyBase:FBgn0003028
A,Introns: 931/3; 1152/3
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A;Cross-references: EMBL:X59772
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Best Local Similarity 24.55
Matches 46; Conservative
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DNA-binding
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                     nucleation component of curlin monomers [imported] - Salmonella enterica subsp. enterica scalmonella enterica subsp. enterica serovar Typhi G; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Baccession: AH0635
C; Accession: AH0635
R; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, L, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L; White, N.; Farrar, S; Moule, S; O'Gacra, P.
Nature 413, 848-852, 2001
A; Athitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; R; Ricterence number: AB0502; MUD:21534947; PMID:1167608
A; Reference number: AB0502; MUD:21534947; PMID:1167608
A; Redence number: Cype: DNA
A; Residues: 1-151 < PAR>
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics:
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C,Species: Salmonella enteritidis
C,Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C,Accession: 0.66040
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
A;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A;Reference number: 0.6039; WUID:96146512; PMID:8550497
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A;Residues: 1-151 <COL>
A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A;Gene: agf8
C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Description: minor component of thin aggregative fimbriae
A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
C;Reywords: fimbria
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-151/Product: fimbrin protein agf8 #status predicted <MAT>
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Matches 29; Conserv
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A; Molecule type: DNA
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Accession: A70762
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70762
A;Accession: A70762
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-678 <COL>
A;Cross-references: GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98335.1; PID:e1300075
A;Cross-references: Strain H37Rv
C;Genetics:
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C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AH0038
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MJID:21470413; PMID:11586360
                                                                                                                                                                                                                           61 IVGHQYGRHNLS-AVGQBGHDNYGSTTQNGNRNVAGIGQFGSNHTTLTLQDGNGNIAAGV 119
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A;Cross-references: GB:AL590842; PIDN:CAC89171.1; PID:g15978410; GSPDB:GN00175
                                                                                                                                                                               45 LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATID 104
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                                                                           --QWG----GGGNHNGGGN----SSGPDST
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Best Local Similarity
Matches 39; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I krage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C58, Cered C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Accession: H98144
R, Mullam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
R, Feference number: A97359; MUD:21608551; PMID:11743194
R, Accession: H98144
R, Accession: H9
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Afacession: AFREWARD Afaces (B185021; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187
Afacesides: Afaces (B18508689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187
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-----TVGQ------YGGNNAAL-----VNYDQ-----LVTRVVTHEMAHA 143
                                           LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATID 104
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12.3%; Score 96; DB 2; Length 145;
Best Local Similarity 27.1%; Pred. No. 0.41;
Matches 38; Conservative 23; Mismatches 59; Indels
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33; Mismatches
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Best Local Similarity 27.1%; Pre
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A, Map position: linear chromosome
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	, 6 sı	-P 41	10G 464	GN 77	AT 524	L 125	I 580
.238;	Matches 45; Conservative 19; Mismatches 48; Indels 67; Gaps	SSGP 41	SAFSAITATGHLTABWGQGAMLQTHSSLGDATTLIHFNDITAMSSGISLINBANQG 464	LALQSDARKSETTITQSGYGN 77	465 TSTADITVTGQINVSHGEGITLNALTTDGRTLVNVDVNNIASEYDAIRLYNYNYNDNYAT 524	78 GADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGGNNAAL 125	525 GVDDGTGADNGTSTIDLITRGALVSQQGYGINIETNTADTYVTVGGLVHGGNGTAI
Length 1	; Indels	8	 HFNDITAMS	-LALOSDARK	II III I	NAKNSDITVG	: :
5; DB 2; 7.3;	ches 48	NGGGN	SSLGDATTL		RTLVNVDVN	RNNATIDOM	GINIETR
Query Match 12.0%; Score 93.5; DB 2; Length 1238; Best Local Similarity 25.1%; Pred. No. 7.3;	9; Mismat	7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGN	 	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ITLNALTIDG	TONGE	: ; RGALVSQQGY
12.0%;	ative 1	SALAGVVPO	HLTAE	SANAA	QINVSHGEG	STIEL	GTSTIDLIT
milarity	Conserv	AFAAIVVSG	AFSAITATG	42 DSTLSIYOYGSANAA	STADITVTG	ADVGQGADN	VDDGTGADN
y Match Local Si	hes 45;	4 7	409 S	42 D	465 T	с В	525 G
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Search completed: August 2, 2004, 14:56:21 Job time : 10.4 secs

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GenCore version 5.1.6
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in searc	OM protein - protein search, using sw model	August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec
	ch, usir	, 2004,
	OM protein -	Run on:

US-09-543-407-12 779 1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	225 salmonell	escherich	Ψ	salmonell	salmonell	drosoph	М	_	_	_	P07875 bacteriopha	_	-	neisseri	drosophil	P45508 escherichia	bordetell	streptc	streptomy	drosophil	leishmani	leishmani	leishmani	leishmani	m.		xanthc	Q05925 homo sapien	saccha	oryza sat	drosophil	mycor	sacci
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Oppjyl chlamydia m P42611 mycobacteri P366 escherichia Q50367 mycoplasma P28159 drosophila Q81081 drosophila Q9174 schizosacch Q83172 treponema p P75780 escherichia P27053 campylobact	
PMPC_CHLMU Y442_MYCTU YDBA_ECOLI PDBA_ECOLI FRU_DROME RTU_DROME N189_SCHPO Y136_TREPA PSIL_ECOLI FLAA_CAMCO	NPA3_HUMAN N116_YEAST
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800.5 800.5 800.5 800.7 79.5 79.5	79
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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- PUNCTION: CURLIN IS THE STRUCTURE SUBINIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
'Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                       SEQUENCE OF 21-33.
SPECIES-S.enteritidis; STRAIN=27655-3B;
MEDLINE=91310566; PubMed=1677357;
COllinson S.K., Emcody L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                               SEQUENCE FROM N.A. STRAIN=27655-3B;
SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                            SEQUENCE OF 21-151 FROM N.A.
SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE-94013073; PubMed-8104955;
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
The Structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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SVMVRQVGFGNNATANQY -> DSYTQVAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR, JC6039, JC6039.
Stygene, SG10608, csgA.
Fimbria, Signal, Complete proteome.
                         Bacteriol. 185:2330-2337(2003)
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                                                                                                                      Bacteriol. 178:662-667(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE008749; AAL20074 1; --
EMBL, AL627269; CAD08268 1; --
EMBL, AE016840; AAC69399 1; --
EMBL, U43280; AAC43599.1; --
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Best Local Similarity
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                                                                                                            fimbriae.
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SEQUENCE OF 21-31.

MEDINE=9310586; PubMed=1677357;

Collinson S.K., Emcedy L., Trust T.J., Kay W.W.;

"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritididis.";

J. Bacteriol. 173:4773-4781(1991).

J. PROCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061202; PubMed=8905232;
Oshima T., Abba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Abba H., Baba T., Kujita K., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
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STRAIN=K12 / MG1655;
MDDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                        Last sequence update)
Last annotation update)
151 AA.
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STRAIN-K12 / W3110;
MEDLINE=93211294; PubMed=8459772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.";
Mol. Microbiol. 7:523-536(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Escherichia.
                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                               Major curlin subunit precursor
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                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                       CSĞA OR B1042.
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152 AA;
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[3]
SEQUENCE FROM N.A.
STRAIN=0157:H7 / R
                                                                                                                                                                                                                                                                                                             FIBRONECTIN.
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Blder R.O.;
Whutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.8%; Score 520; DB 1; Length 151; 66.9%; Pred. No. 1.5e-36; ive 21; Mismatches 29; Indels
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C003470D208D395F CRC64;
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    SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                                                                                                                                         EMBL; L04979; AAA23616.1; -.
EMBL; X90764; CAA62282.1; -.
EMBL; AB000205; AAC74126.1; -.
EMBL; D90741; BA35832.1; -.
EMBL; S70748; SA35840.1; -.
PIR; S70788; S70788.
ECOGONE; EG11489; CSGA.
SIGNAL: Signal; Complete proteome.
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebalhia M., Baker S., Basham D., Evoks K., Chillingworth T., Connetton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
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MAJOR CURLIN SUBUNIT.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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EMBL; AE005315; AAG55788.1; -.
EMBL; AP002554; BAB34843.1; -.
PIR; D90806; D90806.
PIR; H85665; H85665.
Finbria; Signal; Complete proteome.
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152 MA.
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CSGB OR STY1180 OR T1777.
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 65.8
Matches 100, Conservative
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[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  fimbriae."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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OVO_DROME
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                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EWBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 IGQVGTDNSA-RVRQEGSKLLSVISQEGENNRAKVDQAGNYRFAYIEQTGNANDASISQS 107
                                                                                                                                                                                                    J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                         SECUENCE FROM N.A.
STRAINE-TY2 / ATCC 700931;
STRAINE-TY2 / ATCC 700931;
Deng W., Liou S.-R., PubMed=12644504;
Burland W., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.typhimurium, STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
TCUTLI fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CI18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
MINOR CURLIN SUBUNIT.
161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 AYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSH 143
                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.2%; Pred. No. 0.071
Matches 29; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE016840; AA069400.1; -. Fimbria; Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL627269; CAD08267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA; 16254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEACEFIGHT. 178:662-667(1996).
- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
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                                                                                                                                                                                      Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES-S. enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neopera, Endoptery, Endoptery, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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MINOR CURLIN SUBUNIT.
; COFC5430E6DD361D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSH 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2003 (Rel. 42, Last annotation update)
0VO protein (Shaven baby protein).
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EMBL; AB008749; AAL20073.1; --
EMBL; UJ2280, AAC43598.1; --
PIR; JC6040; JC6040
StyGene; SG10609; csgB.
Fimbria; Signal; Complete protecome.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
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1028 AA; 110620 MW; D7068BB2BC0F6F77 CRC64;

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PROUBUCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

SEQUENCE PROM N.A.

SEQUENCE PROM N.A.

STRAIN=00e90n-R;

WEDLINE=91233102; PubMed=1712294;

Mevel-Naio M.T.M., Terracol R., Kafatos F.C.;

EMBO J. 10:2259-2256(1991).

LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-1- SUBCELDULAR LOCATION: Naclear (Pocential).

C.-1- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OGGENESIS. STORED IN THE EGG,

BUT IS RAPIDIX LOST IN THE EMBRYOS EXCEST FOR ITS CONTINUED

C. PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.

C. PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
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SEQUENCE FROM N.A.
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PitterPro; PRR07081; Zif C2H2.

Pfam; PF00096; zf-C2H2; 3.

SMART; SM00355; ZnF C2H2; 4.

SMART; PS00128; ZnC_FINGER C2H2_1; 3.

PROSITE; PS00129; ZinC_FINGER C2H2_2; 3.

Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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POLIY-GLY.

POLIY-GLY.

POLIY-GLN.

POLY-GLN.

POLY-GLN.

POLY-GLN.

POLY-GLN.

POLY-ALA.

POLY-ALA.

POLY-ALA.

POLY-ALA.

POLY-ALA.

POLY-ALA.

POLY-ALA.

POLY-ALA.

POLY-ALA.

POLY-GLN.

POLY-GLN.

POLY-GLN.

POLY-GLN.

POLY-GLN.

CZHZ-TYPE 1.

CZHZ-TYPE 3.

CZHZ-TYPE 3.
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EMBL, X59772; CAB36921.1; ALT_SEQ.
PRY, ASCO38, ASCO38.
HSSP, P07248; ZADR.
TRANSFAC; T00669; -.
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DOWAIN 72 77
DOMAIN 72 77
DOMAIN 98 108
DOMAIN 144 152
DOMAIN 144 152
DOMAIN 336 339
DOMAIN 347 353
DOMAIN 410 414
DOMAIN 410 414
DOMAIN 445 453
DOMAIN 445 453
DOMAIN 445 659
DOMAIN 445 659
DOMAIN 639 651
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                                                                                                                                     104
                                                                                                                                                                                                        -----GGNGYINCGGVG-GPNNS---LDGNNLLNFASVSNYNESNSKFHNHHHHQH 152
                                                                                                                                                                                                                                          ----TVGQ-----YGGNNAAL-----VNYDQ-----LVTRVVTHEMAHA 143
                                                                                                                                                                                                                                                                ູ່
                                                                                                                          LLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          006653;
30-MAY-2000 (Rel. 39, Created)
40-MAY-2000 (Rel. 39, Last sequence update)
40-MAY-2010 (Rel. 40, Last annotation update)
50-MAY-2011 (Rel. 40, Last annotation update)
60uter membrane protein B precursor (168 Kba surface-layer protein)
60utface protein annigen) (Cell surface antigen 5) (Sca5) (rômpB)
610-MAT AND B) (Contains: 120 Kba surface-exposed protein (Surface protein antigen) (120 Kba outer membrane protein ompB); 32 Kba beta peptidel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).

-i- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY similarity).

-i- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a £ layer with hexagonal symmetry.

-i- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                         63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uchiyaman,
Uchiyaman,
Uchiyaman,
Uchiyaman,
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
"Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
-!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A WAJOR
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                  . 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettšia japonica.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
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32 kDa BETA PEPTIDE.
POLY-GLY.
                               Length 1028;
                               5; DB 1;
1.1;
                                                                  62;
                      12.6%; SCCL NO. 1.1, 24.5%; Pred. No. 1.1, 4, 4, 5%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           1656 AA.
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InterPro; IPR005315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfan; PF03797; Autotransporter; 1.
TIGREAMS; TIGR01414; autotrans_bar1; 2.
Autigen; S-layer; Cell wall.
CHAIN 1338 1556
DOMAIN 528 533 POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                    46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                    144 NNATANOY 151
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                                   Query Match
Best Local Similarity
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ID OMPB_RICJA
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SEQUENCE
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72

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15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ--SDARKSETTITQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 SGSGNLG----FGNSGNGNIGFFNSG-NNNIGMGNSGNGVGALSVEFGSSAERS----
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Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith S., de Lange T.;
"Cell cycle dependent localization of the telomeric PARP, tankyrase,
to nuclear pore complexes and centrosomes.";
J. Cell Sci. 112:3649-3656(1999).
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Chi N.-W., Lodish H.F.;
Tankyrase is a Golgi-associated mitogen-activated protein kinase
substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMX1. HUMAN C1. Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
12-OCT-2003 (Rel. 42, Last annotation update)
17-OCT-2003 (Rel. 42, Last annotation update)
17-OCT-2003 (Rel. 42, Last annotation update)
17-OCT-2003 (Rel. 41, Last annotation update)
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Mol. Cell. Biol. 22:332-342(2002).
Mol. Cell. Biol. 22:332-342 (2002).
-!- FUNCTION: May regulate vesicle trafficking and modulate the
subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP
activity and can modify TRFI, and thereby contribute to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith S., Giriat I., Schmitt A., de Lange T., "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres."; Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 12.1%; Score 94.5; DB 1; Length 678; Local Similarity 25.7%; Pred. No. 1.5; etc. 39; Conservative 24; Mismatches 48; Indels 4:
                                                                                                                                                                                                          Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                        258 D -> G (IN REF. 2).
66736 MW; 209F1593D52533A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 AALVNYDQLVTRVVTHEM-----AHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LVTGSMGLFNSGHTNTGSFN
Tuberculist, Rv1548c; -.
InterPro; IPR000303; Microbac_PPE.
InterPro; IPR002999; Mycobac_Dentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
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200
258
                                                                                                                                                                                             Hypothetical protein; T
TRANSMEM 14 34
TRANSMEM 180 200
CONFLICT 258 258
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                                                                                                                                                                                                                                                                                                                                                              678 AA;
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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        RACE RACE FEE OS
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-----GAALQSITLANDATK 547
                                                                                                                                                                                                                                                                                                                                                                                               66 SETTITOSG----YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG--QYG 119
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                                                                                                                                                                                                                                   6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK 65
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STRANS-CDC 1551 / Oshkosh;
STRANS-CDC 1551 / Doshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                           12.5%; Score 97; DB 1; Length 1656; 28.3%; Pred. No. 2.6;
1656 AA; 168097 MW; 3132A69C9DD5999F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599.
RV1548C OR MT1599 OR MTCY48.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 VVDASSLTNAQTLİISGİIGİNNITLGÖF 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GNNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                    509 VLAAGAITLDGSATI-----TGDIGNGGG-
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PIR; A70762; A70762.
TIGR; MT1599; -.
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                                                                                                                                                            Conservative
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                                                                                                             Similarity
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Q10778;
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPSSPTSS-SSSPSSPGSSLAESPEAA 157
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                                                           POLY-HIS.
POLY-PRO.
POLY-SER.
POLY-SER.
POLY-SER.
POLY-SER.
FORT -> CHR (in isoform 2).
FTIG-VSP 004539.
Missing (in isoform 2).
FTIG-VSP 004539.
H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.
E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
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STRAIN=K12 / MC4100;
MEDLINE=96414468; Pubmed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Access operons is required for production of fibromectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomira K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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STRAIN=K12 / MG1655;

MRDINES-97426617, PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

"The Complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).
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01-CT-1996 (Rel. 34, Last sequence update)
01-CT-1996 (Rel. 34, Last sequence update)
Minor Curlin subunit precursor.
CSGB OR: B1041 OR Z1675 OR BCS1419.
Escherichia coll, and
Escherichia coll, and
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacterials, Enterobacteria, Enterobacteria, Enterobacteria, Enterobacteria, Callina Coll, and Enterobacteria, Callina Coll, Olson Callina Coll, Olson Callina Coll, Olson Callina Coll, Olson Callina Coll, Olson Callina Coll, Olson Callina Coll, Olson Callina Coll, Olson Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callina Callin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITH A-1184.
1327 AA; 142010 MW; E14DE985C710B957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
SAM.
PARP.
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MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%;
30.4%;
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Best Local Similarity 30.4%
Watches 35; Conservative
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1089
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128
137
641
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                                                                                                                                                                                                                                                                                           644
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CSGB ECOLI
ID CSGB ECOLI
AC P39828;
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGRPFGVGGKIGSDSILS----GSNASL---TDAGTGGTTF-QYGAGNGGNVGAGGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87283911; PubMed=3302276; MEDLINE=87283911; PubMed=3302276; MEDLINE=87283911; PubMed=3302276; Middle 1. Drexhler K., Eschbach M.L., Henning U.; Discherce of genes 38 encoding a receptor-recognizing protein of bacteriophages T2, K3 and of K3 host range mutants."; J. Mol. Biol. 194:31-39(1987).
J. Mol. Biol. 194:31-39(1987).
Lhe phage recognition site for the cellular receptor.
Lhe phage recognition site for the cellular receptor.
-I. MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTR
                                                                                                                                                                                                                                                                                                                                       Viruses, dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
NCBI_TaxID=10664;
        89 NLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=9115668; PubMed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate Nig32 / Nigeria).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0567366918F6C745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-CCT-1966 (Rel. 34, Last annotation update)
Merozoite surface antigen 2 precursor (MSA-2).
                                                                                                                                                                                                          01-AUG-1988 (Rel. 08, Last sequence update) 01-AUG-1990 (Rel. 15, Last annotation update) Receptor recognizing protein (Protein Gp38).
                                                                                                                                        262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 NSTIELTQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------RGWGKNVYTSEGGAAGAAVT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 89.5; 34.1%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X05312; CAA28935.1; -.
PIR; S00275; S00275.
InterPro; IPR07932; Tail_fibre_GP38.
Pfam, PF05268; GP38.1.
Fiber protein; Phage recognition.
SEQUENCE 262 AA; 25801 MW; 056736
                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequ
01-AUG-1990 (Rel. 15, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AS RECEPTORS.
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                                                                                                                                                                                                                                                                                                                         Bacteriophage T2
                                                                                RESULT 11
VG38 BPT2
ID VG38 BPT2
AC P07875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSA2 PLAF2
Q03646;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : | |: | : | : | |: | 33 FAVNELSKSSFNQAAII---GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Armqvist A., Olsen A., Normark S.,
"Sigma S-dependent growth-phase induction of the csgBA promoter in
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coll can be achieved in vivo by sigma 70 in the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CREIN IS THE STRUCTURE SUBUNIT OF THE CURLI. CURLI ARE
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21156231; PubMed=11258796; MEDLINE-21156231; PubMed=11258796; MEDLINE-21156231; PubMed=11258796; MEDLINE-21156231; PubMed=11258796; Maxino K., Ohtsubo E., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Womplete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                           STRAIN=015:H7 | EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 SETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7%; Score 91.5; DB 1; Length 151; 29.1%; Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MINOR CURLIN SUBUNIT.
B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AE000205; AAC74125.1; -...
EMBL, D90741; BAA3831.1; -...
EMBL, AE005315; AAG55787.1; -...
EMBL, AE00254; BAB34842.1; -...
PIR; C50806; C90806.
PIR; G86665; G85665.
PIR; S70787; S70787.
ECGGne; EG12621; CSGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95157246; PubMed=7854117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15882 MW;
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SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 29.1s
These 32; Conservative
                           DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AA;
                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE

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SIGNAL

17; Gaps

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RESULT 14
OMB2_NEIMB
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 ETTITQSGYGNGA--DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                             POTENTIAL.

MEROZOITE SURFACE ANTIGEN 2.

HYDROPHOBIC, REMOVED DURING MATURATION

(BY SIMILARITY).

POLYMORPHIC REGION.

POLYTHR.

N-LINKED (GLCNAC. .) (POTENTIAL).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 AGNGÁVASAGNGAGNGAGNGAGNGAGNGAG------NGAGNGA---GNGÁGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AGNGAGNGAGNGAGNGAGNGAGNGAVASAGNGAGNGAVASAGNGAVAERSSSTPATTTTT
'Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                 -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=M.tuberculosis; STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
                                                            by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
         antigen 2.";
Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: May play a role in the merozoite attachment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Score 89; DB 1; Length 347; 23.4%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Indels
                                                                                                                                                                                                                              InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last and Luberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                  ABCF24BB560BF537 CRC64;
                                                             membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                                                erythrocyte.
-!- SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 TTTNDAEASTSTSSENSNHNNAETN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 LVNYDQLVTRVVTHEMAHANNATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                  33786 MW;
                                                                                                                                                                                                         EMBL; M59765; AAA29691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                           347
                                                                                                                                                                                                                                                                      GPI-anchor; Merozoite
SIGNAL 1
                                                                                                                                                                                                                      PIR; B39112; B39112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                 144
222
222
224
3206
3206
3321
347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                       (Potential).
                                                                                                                                                                                                                                                                                             21
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CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                  DOMAIN
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(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECISE=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Rolson W.C., Unayam L.A., Ermolaeva M., Salzberg S.L., Bishai W., Jacobs W.R. Jr., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 59. Ref.1 sequence has been checked by authors in Ref.1 and they report that no errors have been found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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SPECIES=M.bovis; STRAIN=AF2122/97;
SPECIES=M.bovis; STRAIN=AF2122/97;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100,7877-7882(2003).
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock, K., Babham D., Brown D., Chillingworth T., Connor R., Davies R., Deviin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Hurphy L., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares S., Seeger K., Mhitchead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.3%; Score 88; DB 1; Length 491; 26.8%; Pred. No. 3.6; ive 13; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00334; PE: 1. Probon; PD01223; PE region; 1. Probom; PD01223; PE region; 1. Protectical protein; Complete proteome. CONFLICT 312 G -> GG (IN REF. 1). SEQUENCE 491 AA; 41979 MW; 12CB630C59CA0C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, 273966; CAA98228.1; ALT_FRAMB.
EMBL; AE007065; AAK46440.1; -.
EMBL; BX248341; CAD96978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
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Tuberculist; Rv2098c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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PER_DROWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 NGLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFG--KLRVGRLNSVLKDTGDINPWDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LPVAAMADVTLYGTIKAGV--ETSRSVEHNGGQVVSVETGT-GIVDLGSKIGFKGQEDLG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGS------A 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ward M.J., Lambden P.R., Heckels J.E.; "Sequence analysis and relationships between meningococcal class 3 serotype proteins and other porins from pathogenic and non-pathogenic Neisseria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAJOR OUTER MEMBRANE PROTEIN P.IB.
                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Major outer membrane protein P.IB precursor (Protein IB) (PIB) (Porin) (Class 3 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CU385 / Serogroup B / Serotype 4 / Subtype 15;
MEDLINE=93116587; PubMed=1335540;
Zapata G.A., Vann W.F., Rubinstein Y., Frasch C.E.;
"Identification of variable region differences in Neisseria meningitidis class 3 protein sequences among five group B
                                                                                                                                                                                                                                                      Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 6:3493-3499(1992).
-!- FUNCTION: Serves as a slightly cation selective porin.
-!- SUBGNIT: Homotrimer.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer.
-!- SIMILARITY: Belongs to the Gram-negative porin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSDYLGVNKIAEPEARLISVRYDSPEFAGLSGSVQYALNDNAGKY 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 KNSDITVGQYGGNNAAL--VNYDQLVTRVVTHEMAHANNATANQY 151
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35EA35B7EBD28301 CRC64;
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Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; ECOLNEIPORIN; 1.
PROSITE; PS00186; GRAM_MGE PORIN; 1.
Outer membrane; Porin; Transmembrane; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CCUG 37604 / M981 / Serogroup B / Serotype 4;
MEDLINE-93051225; PubMed=1330818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78;
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25.5%; Pred. No. 2.8;
:ive 23; Mismatches
331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEMS Microbiol. Lett. 73:283-289(1992)
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Best Local Similarity 2000
Loca 42; Conservative 2
                                                                                                                                                                                                                                                                                                                        Neisseriaceae; Neisseria.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S21409; S21409.
PIR; S28441; S28441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=491;
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   OMB2 NEIMB
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   SOLUTION SOLUTION SELECTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
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721 GGGGGGGGGGGGLPLFLDVTHTSS-----SSQNKGPTGVAAGGAGGVGGGG-- 770
                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PAS 1.
PAS 2.
PAC.
POLY-LIXS.
POLY-GLY.
POLY-SER.
POLY-SER.
POLY-ALA.
T -> A (IN STRAIN 0811.4).
G -> V (IN STRAIN 0811.4).
G -> A (IN STRAIN MANAUS 2).
G -> S (IN STRAIN MANAUS 2).
G -> S (IN STRAIN PORTO ALEGRE 3).
MISSING (IN STRAIN PORTO ALEGRE 3).
MISSING (IN STRAIN PORTO ALEGRE 4).
MISSING (IN STRAINS MANAUS 1 AND MANAUS 3).
MISSING (IN STRAINS MANAUS 1 AND MANAUS 3).
MISSING (IN STRAINS MANAUS 1 AND MANAUS 2).
G -> V (IN STRAINS DATE ALEGRE 4).
MISSING (IN STRAINS MANAUS 1 AND MANAUS 2).
G -> V (IN STRAINS MANAUS 4, PORTO ALEGRE 1 AND MUSSING (IN STRAINS MANAUS 2).
MISSING (IN STRAINS MANAUS 4, PORTO MUSSING (IN STRAINS MANAUS 2).
MISSING (IN STRAINS MANAUS 4).
MISSING (IN STRAINS MANAUS 3).
MISSING (IN STRAINS MANAUS 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.0%; Score 86; DB 1; Length 1093;
Best Local Similarity 27.2%; Pred. No. 13;
Matches 25; Conservative 6; Mismatches 45; Indels 16; Gaps
EMBL; U51063; AAB41368.1; -.

REMBL; U51066; AAB41369.1; -.

REMBL; U51066; AAB41370.1; -.

REMBL; U51066; AAB41370.1; -.

REMBL; U51066; AAB41370.1; -.

REMBL; U51069; AAB41370.1; -.

REMBL; U51069; AAB41370.1; -.

REMBL; U51070; AAB41370.1; -.

REMBL; U51070; AAB41370.1; -.

REMBL; U51070; AAB41370.1; -.

REMBL; U51070; AAB41370.1; -.

REMBL; U51070; AAB41370.1; -.

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REMBL; U51080; PAS; 1.

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Search completed: August 2, 2004, 14:49:27 Job time : 6.3 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 2, 2004, 14:39:17; Search time 29.7 Seconds (without alignments)

Title: US-09-543-407-12

Perfect score: 779
Sequence: 1 MKLIKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum Match 10%

Maximum Match 10%

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*
sp_unvirus:*
sp_bacteriap:*
sp_archeap:*

sp_rodent:* sp_virus:*

sp_bacteria:*
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	1155 125 125 125 125 125 125 125 125 125
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	4 4 4 4 4 4 4 2 2 2 2 2 2 3 2 3 2 3 2 3

ALIGNMENTS

RESULT 1 033802 AC 033802 DT 01-JAN-1998 (TrEMBLrel. 05, Created) DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) DT 01-DEC-2000 (TrEMBLrel. 19, Last annotation update) DE AgfA protein (Fragment). DE AgfA protein (Fragment). AGFA. NOS Salmonella typhimurium. OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; CC Bacteria; Proteobacteria; Gammaproteobacteriales; CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; CC Bacteria; Proteobacteria; Gardon J.I., Bian Z., Pfeifer J.D., CC Bacteria; Proteobacteria; Gardon J.I., Bian Z., Pfeifer J.D., CC Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacteria; Bacter	Query Match 88.1%; Score 686; DB 2; Length 152; Best Local Similarity 88.7%; Pred. No. 4.1e-45; Matches 134; Conservative 5; Mismatches 12; Indels 0; Gaps 0;	OY 1 MKLIKVAAFAAIVVSGSALAGVVPOMGGGNINGGGNISSGPDSTLSIYOYGSANAALALO 60 	Oy 61 SDARKSETTITQSGYGNGADVQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG 120
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01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,

Curlin-csgA protein.

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CSGA. Citrobacter

SEQUENCE FROM N.A. STRAIN=Fec2;

Query Match Best Local Similarity Matches 117; Conserv

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Q7X243; Q7X243

RESULT 2 Q7X243

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60 OSDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacee; Escherichia.
VCBI_TaxID=217992;
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WCBI_TaxID=28141;
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63.6%; Score 495.5; DB 16; Length 152;
Best Local Similarity 65.1%; Pred. No. 1.5e-30;
Matches 99; Conservative 21; Mismatches 31; Indels 1;
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SEQUENCE 152 AA,
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
EMBL: AJS15700; CAD56672.15 'SEQUENCE ISO AA, 15016 MW; 1D7141B8D6973DC6 CRC64;
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STRAIN=Fec4;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Fimbriae by Members of the Fami Enterobacteriaceae Isolated from the Human Gastrointestinal Tract. Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515701; CAD56675.1;
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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      121 NNAALVNQTASDSSVMVRQVGFGNNAPANQY 151
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PRELIMINARY;

25, 25, 25,

(TrEMBLrel. (TrEMBLrel.

Citrobacter freundii.

SEQUENCE FROM N.A.

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NCBI_TaxID=546;

Q7X240
Q7X240;
01-OCT-2003 (TEMBLRE)
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CUTIAN-CSGA Protein.

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Gaps

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57 LALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG 116
SEQUENCE FROM N.A.
TRANSPOSON-Insertion sequence IS1;
MEDLINE=99314153; PubMed=10386375;
La Radione R.W., Collighan R.J., Woodward M.J.;
La Radione R.W. Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coll 078:R80 isolates associated with
IS1 inserti on in csgB and reduced persistence in poultry infection.";
FEMS MAIGNOBIOL. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -.
SEQUENCE 29 AA. ~~~~
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MEDLINE=21081879; PubMed=11823852;

MEDLINE=21081879; PubMed=11823852;

Arlat M., Billault A., Artiguenave F., Gouzy J., Mangenot S., Salanoubat M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Chandlar M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Squier P., Thebault P., Whalen M., Wincker P., Levy M., Chonder C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
Burkholderiaceae, Ralstonia.
                                                                                                                                                                                                                                                                                                                       2; Length 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Indels
                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3501 AA; 348421 MW; 290B41C99018A107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%; Score 113.5; DB 16; 28.8%; Pred. No. 8.3; cive 19; Mismatches 43;
                                                                                                                                                                                                                                                                                                                       Score 122; DB 2;
Pred. No. 0.0078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3501 AA
                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08Y106;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequen
01-OCT-2003 (TrEMBLrel. 25, Last annota
Probable hemagglutinin-related protein.
RSC0887 OR RSO6116.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAIAAIVFSGSALAGVVPQYGGG
                                                                                                                                                                                                                                                                                                                       15.7%;
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Best Local Similarity 28.8
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                    26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 QYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
SEQUENCE 3501 A
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                                                                                                                                                                                                                                                                                                                           Query Match
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Q8Y106
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                                                                                                                                                                                                                                                                                                                                                61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                      60 TDARNSVLNISQIGGGGNGADVGQGSDDSSINLTQNGFGNSATLDQWNSKDSVMNVSQYGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                       1 MKFIKVAALAAIVVSGSAMAGMINQ-GGWGHGHGHGGYGGPNSTLNIYQNGGGNSALALQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST
                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                        "Production of Cellulose and Curli Fimbriae by Members of the Fami Enterobacteriaceae Isolated from the Human Gastrointestinal Tract. Infect. Immun. 72:4151-4158(2003).
EMBL, AJ515702. CAD5678.1; -. SEQUENCE 150 AA; 15112 MW; SD8B82D872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SE30;
Cox J.M., Eglezos S., Woolcock J.B.;
Iviulence of Salmonella enteritidis in chickens correlates with colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
BMBL; U53207; AAA98671.1;
NON TER
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Pred. No. 1.9e-22;
0; Mismatches 1; Indels
                                                                                                                                                                          Length
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 AA; 7704 MW; 2FD5411241A7BCB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              098335, CrewBirel 13, Created) 01-MAY-2000 (TrEWBirel 13, Last sequence update) 01-MAY-2001 (TrEWBirel 16, Last annotation update) curlin subunit monomer (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                     Score 427.5; DB 2;
Pred. No. 2.3e-25;
6; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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                                                                                                                                                                        54.9%; Scor
58.3%; Prective 26; 1
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                                                                                                                                                                                          Local Similarity 58.3
les 88; Conservative
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75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                            Query Match
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Q9S3J5
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Q54069
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Shewanella oneidensis.
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SEQUENCE 502 AA; 52
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
[1]
SEQUENCE FROM N.A.
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                                                                                                                                chromosome 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM:

X STRAIN=GMI1000;

X MEDLINE=21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave F., Gauzy J., Mangenot S.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

RA Arlat M., Billault A., Brottier P., Cannac S., Demange N.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schiex T.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schiex T.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schiex T.,

RA Gaspin C., Lavie M., Malen M., Wincker P., Levy M.,

RI "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RI "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RY "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RY "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RY "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RY Nature 415:497-502(2002).

BR EMBL; Alfe46079; CAD17631.1, -

DR GO; GO:00045821; F:endonuclease activity; IEA.

DR GO; GO:000566; F:nucleic acid binding; IEA.

DR GO; GO:0005669; F:nucleic acid binding; IEA.

DR InterPro; IPR008619; Fil haemagg.

BR InterPro; IPR008619; Fil haemagg.

DR InterPro; IPR008619; Fil haemagg.

FilmerPro; IPR008639; Filmemagg.
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OSJNBB0039P10.07G10.
OSJNBB0039P10.07G10.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.8%; Pred. No. 8.4;
Matches 36; Conservative 19; Mismatches 43; Indels 27;
                                                                                                                                                                                                                                                                                                                                        Plasmid megaplasmid.
Bacteria; Proteobacteria, Betaproteobacteria, Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C5432AABE2CCF59C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA---
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                             Probable hemagglutinin-related protein.
RSP0540 OR RS06117.
Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                PRT; 3552 AA.
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Pfam; PF05860; Haemagg act; 1.
PROSTIE; PS01070; NUCLEASE NON SPEC; 1.
Plasmid; Complete protecome.
SEQUENCE 3552 AA; 352934 MW; C5432A
                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                PRELIMINARY;
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2542 DLGGN 2546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2541 DLĞĞN 2545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=305;
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                                                                                                                                                         QBXSD6;
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                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Mayer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAAL 125
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Alteromonadaceae; Shewanella.
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 191;
STRAIN=cv. Nipponbare,
The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
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                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE01101; AAPS4078.1; -.
SEQUENCE 191 AA; 17021 MW; 95A246FBIIDE3AC5 CRC64;
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52441 MW; D08CA23D6C46B62D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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13.9%; Score 108.5; DE
1. Similarity 29.5%; Pred. No. 0.72;
33; Conservative 15; Mismatches
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EMBL; AE015532; AAN53941.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conserved hypothetical protein.
                                                                                                                             Science 300:1566-1569(2003).
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Best Local 33; Conservative
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                                                                                                                                                                                                                                        Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
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Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCB_TaxID=602;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.,
Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.";
Nucleic Acids Res. 16:2189-2201(1988).
                                                                                                                  Q94821 PRELIMINARY, PRT; 1748 AA. Q94821, P92146; P92146; P92147; P92143; P92141; Q94820; O1-FEB-1997 (TERMELrel. O2, Created) O1-FEB-1997 (TERMELrel. O2, Last sequence update) O1-OCT-2003 (TERMELrel. 25, Last annotation update)
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I -> N (IN REF. 1).
dw; OBO3F210104008A3 CRC64;
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Last annotation update)
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Pred. No. 14;
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(TrEMBLrel. 23,
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LTZ.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to the C-terminal region of AIDA, ICSA, subspecies I specific, Peyer's patch colonization and shedding factor.
SHDA ON STWAS13.
Salmonella typhimurium.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STLSIYQYGSANA--------ALALQSDARKS-ETTITQSGYGNGADVG
                                                                                                                                                                                                                                                                                                                                                     "Complete sequence of the xseA-hisS intergenic region of the S. enterica serotype Typhimurium genome and its distribution within the genus Salmonella.";
Salmonella.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFT40550; AAD25110.2; -.
InterPro; IPR005346; Autotransporter.
InterPro; IPR004849; Petractin.
InterPro; IPR00413; PfkB.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03797; Autotransporter; 1.
TICRFAMS; TIGR01414; autotrans_barl; 3.
PROSITE; PS00584; PFKB_KINASES_2; 2.
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to warm blooded
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                                                    Kingsley R.A., van Amsterdam K., Baumler A.J., "The presence of a pathogenicity island specific enterica subspecies I correlates with adaptation
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les 54; Conservative
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SEQUENCE FROM N.A STRAIN=ATCC14028;
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Search completed: August
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"Characterization of the Campylobacter fetus saph promoter: evidence
that the saph promoter is deleted in spontaneous mutant strains.";
J. Bacteriol. 174:5916-5922(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campylobacter fetus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
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"Surface array protein of Campylobacter fetus. Cloning and gene
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                                                                                                                                                            13.5%; Score 105; DB 16; Length 2039; 26.3%; Pred. No. 20; ive 20; Mismatches 61; Indels 70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative high-molecular-weight surface-exposed protein Cf0009
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                                                                                                                                     894E41F8F29339EA CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                      InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR002173; PfkB.
Pfam; PF03297; Autotransporter; 1.
Pfam; PF03212; Pertactin; 1.
TIGRPAMS; TIGR01414; autotrans_barl; 3.
PROSITE; PS00584; PFKB_KINASES_2; 2.
Complete proteome.
SEQUENCE 2039 AA; 207127 MW; 894E41F81
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         EMBL; AE008813; AAL21407.1; -.
InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
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J. Biol. Chem. 265:19372-19372(1990)
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STRAIN=23D;
MEDLINE=90354448; PubMed=2387868;
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MEDLINE=91035477; PubMed=2229082;
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Matches 54; Conservative
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Nature 413:852-856(2001)
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MEDLINE=93348254; PubMed=8346244;
Tummuru M.K., Blaser M.J.;
"Rearrangement of sapA homologs with conserved and variable regions in Campylobacter fetus.";
Proc. Natl. Acad. Sci. U.S.A. 90:7265-7269(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Campylobacter fetus surface layer proteins are transported by a type I secretion system."; J. Bacteriol, 180:6450-6458(1998).
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PubMed=12694614;
Tu Z.C., Wassenaar T.M., Thompson S.A., Blaser M.J.;
"Structure and genotypic plasticity of the Campylobacter fetus sap
                                                                                                                                                                                                                               MEDLINE=55204338; PubMed=7896695; Dworkin J., Tummuru M.K., Blaser M.J.; Dworkin J., Tummuru M.K., Blaser M.J.; Ithe Campylobacter fetus S-layer protein resides within the conserved N terminus of a family of silent and divergent homologs.", J. Bacteriol. 177:1734-1741(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069317; PubMed=9851986;
Thompson S.A., Shedd O.L., Ray K.C., Beins M.H., Jorgensen J.P.,
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EMBL; AY211269; AA064216.1; -.
InterPro; IPRO05546; Autorransporter.

Pfam; PF03797; Autorransporter; 1.

SEQUENCE 1286 AA; 134079 MW; AIFF9CBC34158789 CRC64;
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13.4%; Score 104.5; Best Local Similarity 27.8%; Pred. No. 13;
Matches 44; Conservative 26; Mismatches
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26	27	28			31	32	93	34	35	36	37	38	36	0.4	41	42	43	44	45

ALIGNMENTS

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbriae (SETI/TAF) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-honologue filmbrin subunits, respectively, (2) directing recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope; AgfA::PT3#2 amino acid sequence SEQ ID NO:14. M Kay Disclosure; Page 136; 139pp; English. vaccine; immune response; immunogen. Collison SK, AAB36347 standard; protein; 151 AA. 05-APR-2000; 2000WO-CA000356. 99US-0127888P. (first entry) Salmonella enteritidis. (UYVI-) UNIV VICTORIA. white AP, Doran JL, WPI; 2000-672631/65. Escherichia coli. Synthetic. N-PSDB; AAC64623 WO200060102-A2. 05-APR-1999; 26-FEB-2001 12-OCT-2000. AAB36347; RESULT 1 AAB36347

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copy of that gene; and (4) eliciting an immune response in an animal, compurising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonalia, E. ool or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant Agfa protein which is useful for into the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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for
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100.0%;
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Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA consequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TAP) mucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriacae for the production of finbriae comprising recombinant C. AgfA, CspA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologus species; (3) directing recombination of a recombinant gene comprising separating and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid segment or segments of soli or. Enterobacteriaceae host cell, from the nost cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for clitting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to coliciting an immune response in an animal. In a fimbrial presentation vaccine, the carrier fimbrial submit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogensive to purify in large amount. The present sequence is given in the exemplification of the present invention response to purify in large amount. The present sequence is given in
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Pred. No. 4.3e-61;
0; Mismatches 0;
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Escherichia coli.
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Best Local Similarity
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicepe or antigen. Also described are: (I) use of thin aggregative finbriae (SEP17/TAP) nucleation depended assembly system of strains of Salmonella. Escherichia coli and CE Enterobacteriaceae for the production of finbriae comprising recombinant CE AgfA, CSpA and AgfA-homologue finbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. CC comprising separating an animo acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Comprising recombinant AgfA protein containing a replacement segment or regenets of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Defining an immune response in an animal. In a finite direction of recombinant AgfA protein which is useful for an animal and man and an animal and an animal and an animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal and animal animal and animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animal animanimal animal animal animal animal animal animal animal animal ani
                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Pred. No. 2.4e-59;
0; Mismatches 0; Indels 2
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                        Kay WW;
                                                                                                                                                                                                                                                                               Disclosure; Page 135; 139pp; English.
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                        Collison SK,
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                           Doran JL,
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                                                                              WPI: 2000-672631/65.
                                                                                                               N-PSDB; AAC64622
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                           White AP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                         Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmoneila, agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                 Doran JL;
                                                                                                                                                                                                                                                                                                                                          Score 693; DB 2;
Pred. No. 4.7e-59;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                           UNIV VICTORIA INNOVATION & DEV CORP.
KING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kay WW;
                                                                                                                                 Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36341 standard; protein; 151 AA
                                                                                                                                                                                                                                 Disclosure, Fig 7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888P.
                                             94WO-IB000207
                                                                      93US-00054452
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.7%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis.
                                                                                                                                 Collinson SK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
                                                                                                                                                        WPI; 1994-358275/44.
N-PSDB; AAQ87467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1999;
                                             26-APR-1994;
                                                                     26-APR-1993;
 WO9425598-A2
                       10-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
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                                                                                                                                 Kay WW,
                                                                                             (UYVI-)
                                                                                                         (KING/)
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AAB36341
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The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 2765-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or eneropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probase or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella acid molecules from warm-blooded animals relative to nucleic 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                               Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.3%; Score 692; DB 2; 90.7%; Pred. No. 5.8e-59; iive 3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36355 standard; protein; 151 AA
                                                                                                                                                                                                             VICTORIA INNOVATION
                                                                                                                                                                                                                                                                   Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 7; 85pp; English.
                                                                                                        94US-00233788
                                                                                                                                                        93US-00054452
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                                                                                                                                                                                                                                                                   Kay ww,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                      WPI; 1997-309886/28.
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Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT74142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200060102-A2.
                                                                                                                                                                                                                                                                Collinson SK,
                                                                                                                                                                                                                AIND (-IAAD)
                                                                                                        26-APR-1994;
                                                                                                                                                             26-APR-1993;
  US5635617-A.
                                                     03-JUN-1997
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ID AAB3
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                                                                                                                                                                                          The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA cequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SERI/TAR) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of monologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native compositing secreting recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising recombinant AgfA comprising separating an amino acid polymer comprising recombinant of comprising separating an amino acid polymer comprising recombinant of protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of foreign amino containing a mannel in conjunction with a carrier or diluent. (I) is useful for the animal in conjunction with a carrier or diluent. (I) is useful for the animal in conjunction with a carrier or diluent. (C) coliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to c) immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live the exemplification of the present invention invention in the exemplification of the present invention
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                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.4%; Score 693; DB 3; Best Local Similarity 90.7%; Pred. No. 4.7e-59; Matches 137; Conservative 3; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                           Disclosure; Page 135; 139pp; English.
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Misc-difference 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23570 standard; protein; 151 AA
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(first entry)
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N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
29-SEP-1997
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AAW23570

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Kay WW;

Collison SK,

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA control of the gene has been replaced by a segment of a foreign DNA control of the encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SERIA/TAR) mucleation depended assembly system of strains of Salmonella Escherichia coli and control of the production of fimbriae comprising recombinant of a recombination of a recombination of a recombination of a recombinant gene chomologus species; (3) directing recombination of a recombinant gene into the chromosome of the homologus species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of foreign amino cold sequence or sequences grown on a Salmonella, E. coli or coliciting an immune response in an animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sea usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial submuit proteins are usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial submuit proteins are usually strong aminored the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 139; 139pp; English.
99US-0127888P
                                                   (UYVI-) UNIV VICTORIA.
                                                                                                       Doran JL,
                                                                                                                                                                                          N-PSDB; AAC64631
  05-APR-1999;
                                                                                                          White AP,
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Sequence 151 AA;

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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                 105
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                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT-------YDQ
                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                           Gaps
                                         30;
Score 659; DB 3; Length 151;
Pred. No. 9.1e-56;
0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                      121 LVTRVVTHEMAHA-----SVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                           106 LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
  tch 85.0%; al Similarity 81.9%; 136; Conservative C
                                                                                                                                                             61
        Query Match
                          Best Local
Matches 13
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Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                           AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                       AAB36353 standard; protein; 151 AA.
                                                                      (first entry)
                                                                      26-FEB-2001
                                               AAB36353;
RESULT 8
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbried (SERIJ/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and control of a recombination control of the production of fimbried comprising recombinant GAGA, CSGA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene composition of a recombinant gene copy of that gene; and (4) eliciting an emimologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or copy. The expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to Sou, ono copies/cell), the hybrid fimbrin protein sale usually strong immunogens, which may be important for an efficient live vaccine; the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response consequence is given in the expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                           Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                            99US-0127888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 138; 139pp;
                  Salmonella enteritidis.
                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                Doran JL,
                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-672631/65.
                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC64629
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                                                                                                   WO200060102-A2
                                                                                                                                                                                                                            05-APR-1999;
                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                  White AP,
                                                            Synthetic.
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 0 23; Indels Query Match

79.0%; Score 612; DB 3;
Best Local Similarity 81.5%; Pred. No. 3.2e-51;
Matches 123; Conservative 5; Mismatches 23; 151 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 61 g ò g

Length 151;

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121 NNAALVNOTASDSSVMVRQVGFGNNATANQY

us-09-543-407-14.rag

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AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
                                                                                                                                        Kay WW;
                                                                                                                                                                                       Disclosure; Page 136; 139pp; English.
                                                   vaccine; immune response; immunogen.
    AAB36349 standard; protein; 151 AA.
                                                                                                                                       Collison SK,
                                                                                                        05-APR-2000; 2000WO-CA000356.
                                                                                                                  99US-0127888P
                         (first entry)
                                                             Salmonella enteritidis.
Escherichia coli.
                                                                                                                            (UYVI-) UNIV VICTORIA.
                                                                                                                                       Doran JL,
                                                                                                                                                  WPI; 2000-672631/65.
N-PSDB; AAC64625.
                                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
                                                                                   40200060102-A2.
                                                                                                                  05-APR-1999;
                         26-FEB-2001
                                              Salmonella;
                                                                                             12-OCT-2000
                                                                        Synthetic.
                                                                                                                                       White AP,
              AAB36349;
AAB36349
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collison SK,
                                                                                                                                                                                                                                                                 AAB36350 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64626.
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61
                                                                                                                                                                                                                                                                                                                     AAB36350;
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AAB36350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                           agfA; chromosomal gene replacement; fimbrin; epitope;
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Pred. No. 4e-51;
6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.5%;
Matches 123; Conservative
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of thin aggregative fimbriae (SETI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and cassembly system of strains of Salmonella, Escherichia coli and directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, respectively; (2) dack into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilution of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation constanting are constant for an efficient live the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation consolies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein possesses both the immunogens, which may be important for directing an immunogens, and aminor aminor and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
                                                                                                                        121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                    Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 137; 139pp; English.
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgiA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                          Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-672631/65.
                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC64627
                                                                                                                                                                                                  Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAXNSDITVGQYDQ 120
                                                                                                                                                                                                                SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                     09
                                                                                                                                                       1 MKLLKVAAFFAALVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                             Score 609; DB 3; Length 151;
Pred. No. 6.3e-51;
5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
       of the present invention
                                                                                                                                                                                                                                              121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay WW
                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                   AAB36354 standard; protein; 151 AA
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                                                                78.6%;
81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immune response;
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64630.
      the exemplification
                                                                              Local Similarity
es 123; Conserv
                                     Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella;
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                              MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmoneila; agfA; chromosomal gene replacement; fimbrin; epitope;
   Length 151;
Score 603; DB 3;
Pred. No. 2.4e-50;
4; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgfA::PT3#6 amino acid sequence SEQ ID NO:22
                                                                                                                                                                                                                                                                                                                                                                   LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNOTASDSSVMVRQVGFGNNATANQY
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      77.8%;
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Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                DB 3;
                                                                                                                                                                                               77.7%; Score 602; DB 3
81.5%; Pred. No. 3e-50;
                                                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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5; Mismatches
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                                                                                                                                                                                                                                                                                                                                             AAB36348 standard; protein; 151 AA
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
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Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                 Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbried (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and cassembly system of strains of Salmonella Escherichia coli and fereting recombination of finbriaca comprising recombinant on the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an aminon acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence are host cell, and introducing the coll or the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous antiqens are presented in high numbers (up to 500,000 coples/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens, and hybrid fimbrial an entitie or an interest and protein and protein security and managent and protein and protein secure and an immunogent and protein and protein and protein secure and an immunogent and protein and protein and protein secure and and interest and protein and protein secure and and interest and protein and prote
                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKSETTIIQSGYGNGADVGQGADNSTIELIQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 578; DB 3; Length 15
Pred. No. 6.3e-48;
6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immune response; immunogen.
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Best Local Similarity 80.8%;
Matches 122; Conservative
                    N-PSDB; AAC64624
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cc (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and combidate combacteriacae for the production of fimbriae comprising recombinant of the forbacteriacaes for the production subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement sequent or sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is confusing an immune response in an animal conjunction with a carrier or diluent. (I) is confusioned the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to conjuct) and adhesion properties relevant for an efficient live to vaccine, the carrier fimbrial subunit proteins are usually strong community and adhesion properties relevant for an efficient live conformation. The present sequence is given in confinence in sequence is given in the exemplification of the present invention
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0; Gaps

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protein; immune response; antibacterial; vaccine; gene therapy
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                                                                                                                                                                                                                         Wikstroem M,
                                                                                                                          30-JAN-2003; 2003WO-EP000943.
                                                                                                                                                          31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                          (HANS-) HANSA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 68.2
103; Conservative
                                                                                                                                                                                                                       Bjoerck L, Olsen A,
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Job time : 44.9 secs
                                                                                                                                                                                                                                                       WPI; 2003-646136/61.
                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151 AA;
                                                                                                                                                                                                                                                                      N-PSDB; ACF36153
                                                               WO2003064446-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 kDa protein
                                                                                          07-AUG-2003
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   Plasma
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                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbrine (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Eschericha coli and Enteropacteriaceae for the production of fimbriae comprising recombinant of Enteropacteriaceae for the production of fimbriae comprising recombinant of a recombination of a recombinant on a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement sequent or sequents of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sare usually strong immunogens, which may be important for directing an immune response in an animal incompansive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                               Kay WW;
                                                                                                                                                                                                                                        Disclosure; Page 135; 139pp; English.
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                                                                                               Collison SK,
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 05-APR-2000; 2000WO-CA000356.
                                 99US-0127888P.
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Matches 104; Conservative
                                                               (UYVI-) UNIV VICTORIA
                                                                                               Doran JL,
                                                                                                                              WPI; 2000-672631/65.
                                                                                                                                             N-PSDB; AAC64619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 151 AA;
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                                 05-APR-1999;
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                                                                                               White AP,
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ABR82651
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABREGAG4. ABREGAG4.49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein, to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                              New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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Herwald H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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Matches 137; Conservative
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Sequence 67, Appl
Sequence 8, Appli
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Sequence 3, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 204, Appli
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Sequence 4, Appli
                                                   August 2, 2004, 14:40:48 ; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
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                                                                                      US-09-543-407-14
775
I MKLLKVAAFAAIVVSGSALA.......HASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                Description
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/FGCOMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                       389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   - protein search, using sw model
                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
Sequence:
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No.
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Sequence 33, Appl	Sequence 4, Appli	33,	Sequence 33, Appl	Seguence 47, Appl	Ο.	Sequence 1, Appli	Sequence 5818, Ap	Seguence 257, App	Sequence 280, App	-	Sequence 42, Appl	Sequence 63, Appl	Sequence 21268, A	Sequence 41, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	
US-09-377-155-33	-913-	-669-974-3	US-09-797-862-33	4	US-09-268-347-36	US-09-841-786-1	US-09-107-532A-5818	-453-702B-2	US-09-025-769B-280	US-09-595-684B-39	US-09-495-880A-42	US-09-134-078-63	US-09-252-991A-21268	US-09-919-172-41	US-08-960-780-6	US-09-073-898-6	US-09-850-351A-6	
m	m	4	4	4	4	4	4	4	4	4	4	4	4	4	'n	m	41	
2353	2353	2353	2353	2354	2411	3241	318	3169	415	1690	238	926	1413	645	789	789	789	
10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.0	10.0	6.6	6.6	9.0	9.9	6.6	9.7	7.6	7.6	9.7	
78.5	78:5	78:5	78:5	78:5	78:5	78.5	77.5	77:5	77	77	76.5	76:5	76:5	75:5	75:5	75.5		
28			31			34	35	36	37	38	39	40	41	42	43	44	4.5	

ALIGNMENTS

		Gaps
		0
US-08-233-788A-59 Sequence 59, Application US/08233788A PERENT NO. 55635617 GENERAL INFORMATION: APPLICANT: Doran, James L. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S.	INVENTION: METADOS AND COMPOSITIONS FOR TEXABLE AND COMPOSITIONS FOR SEQUENCES: 61 NDENCE ADDERSS: 63 10 6300 Columbia Center, 701 Fifth Avenue Seatle Washington 11 0.S.A. 12 0.S.A. 13 0.S.A. 14 0.S.A. 15 1 0.S.A. 16 25 0.S.A. 17 PE: Floppy disk Expansion #1.25 18 PALOMINE FORM: 18 PALOMINE FORM: 18 PALOMINE FORM: 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 18 PALOMINE POSS/MS-DOS 19 PARCIATION: 10 PARCATION: 10 PARCATION: 11 PARCATION: 11 PARCATION: 12 PARCATION: 13 72 333 SEEDANBERRY 14 POR SEQ ID NO: 59: 15 AMINO ACIDS: 15 AMINO ACIDS 17 PE: protein 17 PPE: Trotein 18 PERCENTINE 18 PALOMINE POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 19 PARCATION TO SECOND POSS/MS-DOS 10 PARCATION TO SECOND POSS/MS-DOS 11 PARCATION TO SECOND POSS/MS-DOS 11 PARCATION TO SECOND POSS/MS-DOS 11 PARCATION TO SECOND POSS/MS-DOS 12 PARCATION TO SECOND POSS/MS-DOS 15 PARCATION TO SECOND POSS/MS-DOS 16 PARCATION TO SECOND POSS/MS-DOS 17 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION TO SECOND POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18 PARCATION POSS/MS-DOS 18	Query Match 89.3%; Score 692; DB 1; Length 151; Best Local Similarity 90.7%; Pred. No. 3.9e-62; Matches 137; Conservative 3; Mismatches 11; Indels (

9 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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07601
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                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                    Sequence 57, Application US/08233788A

Patent No. 5635617
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
WHERE OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Seed and Berry 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 97
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100.0%; Pred. No. 2.2e-44
iive 0; Mismatches 0
                                                                                                                                                         121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
TELERAX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 97; Conservative
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CITY: Seattle
STATE: Washington
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ZIP: 98104-7092
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Sequence 8, Application US/09196387 Patent No. 6277613

RESULT 3 US-09-196-387-8 GENERAL INFORMATION:

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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLABSPEAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 673;
0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57; Indels
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION WHERE: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.9%; Score 92; DB 3 30.4%; Pred. No. 0.54; ive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., barid A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-23
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870-1876
                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 30.4%
Matches 35; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 673 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-09-196-387-8
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MEDIUM TYPE: Floppy
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: New Jersey
RY: USA
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
              TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
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201-343-1684
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                                                                                                             MOLECULE TYPE: protein US-09-196-387-10
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CITY: Hackensack
STATE: New Jersey
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GY: linear
                                                                                 TYPE: amino acid
TOPOLOGY: linear
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 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-196-387-10
Sequence 10, Application US/09196387
Fatent No. 6277613
FAPPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
8
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APPLICATION NUMBER: US/09/10f 1.2
CLACO DATE:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: Unue 10, 1998
AFTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                           600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92;
Pred. No. (
                                               APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson E94, David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CTELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                    11.98;
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157 6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64 Gaps Gaps 65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113 .. œ Query Match 11.9%; Score 92; DB 3; Length 949; Best Local Similarity 30.4%; Pred. No. 0.84; Matches 35; Conservative 15; Mismatches 57; Indels DB 4; Length 949; 57; Indels Version #1.30 Query Match 11.9%; Score 92; DB 4. Best Local Similarity 30.4%; Pred. No. 0.84; Matches 35; Conservative 15; Mismatches ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR

us-09-543-407-14.rai

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STATE: New
COUNTRY: US
ZIP: 07601
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                           158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLÉACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: de Lange, Titia
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
NUMBER OF SEQUENCES: 12
CORRESPONDEMEDE ADDRESS: 31
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.9%; Score 92; DB 3; Length 1327; Best Local Similarity 30.4%; Pred. No. 1.3; Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTONISY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-2:
TELECOMMUNICATION INFORMATION:
TELECHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                Sequence 2, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: OT601
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201-343-1684
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NO
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
TELEX: 13
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US-09-196-387-2
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Sequence 2, Application US/09841835 Patent No. 6506587 GENERAL INFORMATION:

RESULT 8 US-09-841-835-2

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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A PROTEIN THAT BINDS TO TRF1 AND METHODS
OF USE THEREOF
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.9%; Score 92; DB 4; Length 1327; 30.4%; Pred. No. 1.3; ive 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C
CURRENT APPLICATION UNMER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-16"
                                                                                                                          E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/03972115A Patent No. 6599728 GENERAL INFORMATION:
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTE
TITLE OF INVENTION: OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1327 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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LENGTH: 1327 amino aci
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
NO
                                                                                NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                                                                                                                       New Jersey
USA
                                                                                                                                             STREET: 411 Hack
CITY: Hackensack
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Best Local Similarity
Matches 35; Conserv
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MOLECULE TYPE:
HYPOTHETICAL: N
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Sequence 10, Application US/0896868A

Batent No.:6214981
GENERAL INFORMATION:
APPLICANT: TUCKER, KENNETH
APPLICANT: TUCKER, LAURA
TITLE OF INVENTION: PROPEILA CATARRHALIS OUTER MEMBRANE
TITLE OF INVENTION: PROPEILA CATARRHALIS OUTER MEMBRANE
TITLE OF INVENTION: PROPEILA CATARRHALIS OUTER MEMBRANE
TITLE OF INVENTION: PROPEILA CATARRHALIS OUTER MEMBRANE
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TITLE OUTER TO CATARRHALIS OUTER MEMBRANE
TITLE OUTER TO CATARRHALIS OUTER TO CATARRHALIS OUTER TO CATARRHALIS OUTER TO CATA
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                                                                                                       3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
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                                                                                                                                                                       23;
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,685A
FILING DATE: No. 6214981ember 12, 1997
CLASSIFICATION:
                                              26;
             Pred. No. 1.1;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31,232
ER: 7969-060
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                                                                                                                                                                                                                                                                                                  ----AALAAAGAGGELGGGGG 477
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NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERÊNCE/DOCKET NUMBER: 7969
TELEPHONE: (212) 796-9990
TELEPHONE: (212) 869-8864
                                                                                                                                                                                                                                      63 ARKSETTITQSGYGNGADVGQG
                35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2123 amino acids
             Best Local Similarity 35.49
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-968-685A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 -GFGNNATA 148
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-968-685A-10
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STATE:
                                                                                                                                                                                                                                                                                                  461
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Sequence 10. 6001592
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TO SAID POLYPEPTIDE
NAMER OF SEQUENCES:
A CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 738;
                                                                                                                                                                                                                                      11.9%; Score 92; DB 4; Length 1327; 30.4%; Pred. No. 1.3; ive 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Mie-pret. COUNTRY: JAPAN

ZIP: 514-01

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 987
FILING DATE: 15-0119-1996
ATTORNEY/AGENT INFORMATION:
MAME: C. Bruce Hamburg:
REFERENCE/DOCKET NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (712) 986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 89.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 738
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     812-5 Hirano
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.4<sup>§</sup>
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Isshinden
CITY: Tsu-city
STATE: Mie-prefecture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                         LENGTH: 1327
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                      ; OKGANISM: DOI
US-09-972-115A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-864-038A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-864-038A-3
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159 IGLIGSGLIGF-----GGLNSGTGN-----IGLFNSGTGNVGIGNSGTGNWGIGNSG 205
                                                                                                                                                                                                                                                                                                                                                 12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSD---ITVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYN 259
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity 25.4%; Pred. No. 6;
Matches 29; Conservative 16; Mismatches 50; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and north
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.8%; Score 83.5; DB 4; Best Local Similarity 25.4%; Pred. No. 6; Matches 29; Conservative 16; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-MAY-1998
CLEASIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 199, Application US/09072596 Patent No. 6458366 GENERAL INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                            LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 682-6031
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: USA
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CITY: Seattle
STATE: Washingt
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TOPOLOGY:
US-09-056-556-204
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                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32096
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS---- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TLNNYSNPNTASLSNSANNVSGNLG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 204, Application US/09056556
Patent No. 6350456
CENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.8%; Score 83.5; DB 4; Length 339;
Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 35; Conservative 28; Mismatches 53; Indels 4'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 -DITVGQYDQ----LVTRVVTHEMAHASVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 VNVAAGNFNQQKNDLAAAVSNGQYSTAGSAASQTSTG-NTTVN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 COLUMNIA:
STREET: 8aattle
STATE: Washington
COMPUTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDUTH YEB: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FTIING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                         Sequence 32096, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TSVLÓSGYGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32096
     213 NAFGTRATA 221
                                                                         RESULT 12
US-09-252-991A-32096
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266 IGLTGSGLLGF-----GGLNSGTGN-----IGLFNSGTGNVGIGNSGTGNWGÏGNSG 312
                               RESULT 15
US-09-477-135A-131
VS-09-477-135A
Sequence 131, Application US/09477135A
Patent No. 6572865
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION immunostimulatory Peptides
FILE REFERENCE: 52889
CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT APPLICATION NUMBER: US/09/477,135A
PRIOR PILING DATE: 1997-12-15
PRIOR FILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: 6/000,254
PRIOR PILING DATE: 1996-06-14
PRIOR PILING DATE: 1996-06-14
PRIOR PILING DATE: 1996-06-14
PRIOR SEQIENCE: 1998-06-15
NUMBER OF SEQIEN NUMBER: 6/000,254
SOFFWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50; Indels 19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    313 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYN 366
                                                                                                          69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYD 119
                                                                                                                                      206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSONTGGFNNGGYN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.4%; Pred. No. 6;
Matches 29; Conservative 16; Mismatches 50; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: August 2, 2004, 14:58:32 Job time : 13 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-131
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RESULT 1
US-09-741-873B-4
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775
1 MKLLKVAAFAAIVVSGSALA........HASVMVRQVGFGNNATANQY 151
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| cgn2_6/ptodata/2/pubpaa/PtoT NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PtoT NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PtoT NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Sequence 53421, A	Sequence 245046,	Seguence 49412, A	Sequence 8, Appli	Sequence 10, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 49960, A	Sequence 147748,
QI	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-425-114-53421	US-10-424-599-245046	US-10-282-122A-49412	US-09-841-835-8	US-09-841-835-10	US-09-841-835-2	US-09-972-115A-8	US-10-199-937-4	US-10-425-114-49960	US-10-437-963-147748
	12	12	12	12	15	12	12	12	σı	o,	σ	10	14	12	16
% Query Match Length DB	151	151	131	131	445	210	211	186	673	949	1327	1327	1327	263	145
% Query Match	67.7	67.7	57.7	57.7	13.4	12.6	12.6	12.3	11.9	11.9	11.9	11.9	11.9	11.7	11.4
Score	525	525	447	447	104	98	96	95	92	92	92	92	92	90.5	88.5
Result No.		7	m	4	ហ	9	7	8	6	10	11	12	13	14	15

604	equence 275	equence 5776	Н	equence	Sequence 64573, A	O١	equence 1						. 26, 7	2086,	934	1117	quence 131	equence 131	equence 131	equence 199	204	equence 643	equence 615	equence 113	e 116	equence 113	equence 116	equence 149	ce 149
119-10-425-114-5504	-10-424-599	US-10-425-114-57763	US-09-793-306-146	US-10-282-122A-5326	.0-282-1	US-09-813-214A-	9-712-363-15	US-10-080-170-34	US-10-080-170-34	US-10-156-761-876	US-10-369-493-2	US-10-437-963-1222	US-10-174-363-5	US-10-374-780A-20	US-10-156-761-9	10-156-761-117	US-09-996-634-131	US-09-997-182-13	US-09-997-181-1	US-10-193-002-19	US-10-084-843-20	US-10-282-122A-64	US-10-425-114-6152	US-09-880-748-113	19-880-748-1	US-10-293-418-113	US-10-293-418-116	US-09-880-748-149	US-10-293-418-149
0	700	1 70	97	28 1	78 1	22 9	527	27 1	27 1	32 1	36 1	70 1	048 1	18 1	438 1	71 1	43 9	43 1	43 1	43 1	43 1	00 1	42 1	54 1	54 1	54 1	54 1	57 1	57 1
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ALIGNMENTS

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ye-uy-141-873B-4

y Bequence 4, Application US/09741873B

y Dublication No. US20020081722A1

y Dublication No. US2020081722A1

y Dublication No. US2020081722A1

y Dublication No. US202008172A1

y PAPLICANT: Oleen, Arne

y TILE REPREBRENCE: 10289-09-04

y CURRENT APPLICATION NUMBER: US 09/9741,873B

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/3770,846

y PRIOR APPLICATION NUMBER: US 08/978,876

y PRIOR APPLICATION NUMBER: US 08/187,865

y PRIOR PRIING DATE: 1992-01-03

y PRIOR PRIING DATE: 1992-11-03

y PRIOR PRIING DATE: 1992-11-03

y PRIOR PRIING DATE: 1994-10-05

y PRIOR APPLICATION NUMBER: US 08/187,865

y PRIOR FILING DATE: 1994-10-05

y SOFTWARE: Percentin version 3.0

y SOFTWARE: Percentin version 3.0

y SOFTWARE: PRIOR CONSTRUCT ON NUMBER: US 08/318,519

y TYPE: PAT

ORGANISM: Escherichia coli

US-09-741-873B-4

QUENTY MATCH 68-28; DB 12; Length 151;

Best Local Similarity 68-28; Mismatches 27; Indels 0; Gaps 0;
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PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1989-05-04
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/7789,437
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1992-11-03
PRIOR PILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-8
NUMBER: US 08/18,519
PRIOR FILING DATE: 1994-10-05
NUMBER: PREDICATION NUMBER: US 08/18,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ 1D NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09741873B Publication No. US20040096965A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 64.9%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Escherichia coli
US-09-741-873B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Escherichia coli
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Publication No. US20040096955A9
GENERAL INFORMATION:
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT APPLICATION NUMBER: US 08/0749,878
PRIOR APPLICATION NUMBER: US 08/0783-1
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1999-1-10-06
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1999-1-10-06
PRIOR FILING DATE: 1999-1-10-06
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
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                                                                                                   61 SDARKSETIITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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Publication No. US20020081722A1
GENERAL INFORMATION:
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012899-084
CURRENT APPLICANTON UNMER: US/09/741,873B
CURRENT PILING DATE: 2003-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.7%; Score 525; DB 12; Length 151; Best Local Similarity 68.2%; Pred. No. 2.1e-45; Matches 103; Conservative 21; Mismatches 27; Indels
                                                                                                                                                               121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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SOFTWARE: PatentIn version 3.0
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ORGANISM: Escherichia coli
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US-09-741-873B-2
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| GENERAL INFORMATION:
| GABREAL INFORMATION:
| APPLICANT: Normark, Staffan
| APPLICANT: Olsen, Are
| TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
| TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
| TITLE OF INVENTION: E003-084
| CURRENT APPLICATION NUMBER: US/09/741,873B
| CURRENT FILING DATE: 2003-04-04
| PRIOR APPLICATION NUMBER: US 08/978,878
| PRIOR FILING DATE: 1997-11-26
| PRIOR FILING DATE: 1997-11-26
| PRIOR FILING DATE: 1997-11-06
| PRIOR APPLICATION NUMBER: US 07/970,846
| PRIOR APPLICATION NUMBER: US 07/970,846
| PRIOR FILING DATE: 1994-01-28
| PRIOR APPLICATION NUMBER: US 08/187,865
| PRIOR FILING DATE: 1994-01-28
| PRIOR FILING DATE: 1994-01-28
| PRIOR FILING DATE: 1994-01-28
| PRIOR FILING DATE: 1994-10-05
| NUMBER OF SEQ ID NOS: 10
| SEQ ID NO 2
| TENGTH: 131
                                                                                                                                                                                                                                                                                                              61 VGQGSDDSSIDLIQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                          21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                                                                                                                                                                                                                       81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHEMAHASVMVRQV
                                                                       .
0
   Length 131;
                                                                       Indels
57.7%; Score 447; DB 12;
64.9%; Pred. No. 1.5e-37;
iive 20; Mismatches 26;
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DB 12; Length 131;

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us-09-543-407-14.rapb

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US-10-424-599-245046
US-204040 US/10424599
Sequence 245046, Application US/10424599
Publication No. US20040031072A1
Publication No. US20040031072A1
Sequence 245046, Application No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENDER: 32-1(55223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 WGGGGGGGGGGGSASNVRATYHYYEPEQHGWDLNAVSAYCSTWDASKPYSWRSKYGWT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 ADVG----QGADN--STIELTQNGPRNNA---TIDQWNAKNSDITVGQYDQLVTRVVTHE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 WGGGGGGGGGGGSASNVRATÝHÝYEPEQHGWDLNÁVSÁYCSTWDAŠKPYSWRSKÝGWT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 WGGGGUHNGGGNSSGPDSTLSIYQY-----GSANAALALQSDARKSETTITQSGYGNG 78
  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53421
LENGTH: 210
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12.6%; Score 98; DB 12; Length 211;
Best Local Similarity 26.7%; Pred. No. 0.08;
Matches 36; Conservative 18; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                Query Match 12.6%; Score 98; DB 12; Length 210; Best Local Similarity 26.7%; Pred. No. 0.08; Matches 36; Conservative 18; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: PAT_MRT3847_63306C.1.pep
US-10-424-599-245046
                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: 700839445_FLI.pep
US-10-425-114-53421
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US-10-282-122A-49412
; Sequence 49412, Application US/10282122A
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ORGANISM: Glycine max
                                                                                                                                                                                                     TYPE: PRT ORGANISM: Glycine max
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Sequence 20638, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Gao, Vongwei

APPLICANT: Gater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (5.052) BI

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

NUMBER OF SEQ ID NOS: 47374
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CENDIGATION NO. US20040034888A1
CENDIGATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Stou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110
                                                                                                                                                                                                                                    61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
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                                                                                                                                                                                                     VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHEMAHASVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 77
                                                                                                                             21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY
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                                               Gaps
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                                            Indels
                                            26;
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13.4%; Score 104; DB 15;
Best Local Similarity 26.6%; Pred. No. 0.051;
Matches 45; Conservative 25; Mismatches 61;
                   Pred. No. 1.5e-37;
); Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Rhodopseudomonas palustris
64.9%; Fil
                                               85; Conservative
                                                                                                                                                                                                                                                                                                               GFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
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CURRENT APPLICATION: UNMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-22

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PLING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

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PRIOR PLING DATE: 2001-12-0

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PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-0

PRIOR PLING DATE: 2001-12-16

PRIOR PLING DATE: 2001-12-16
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 IDOWNAKNSDITVGQYDQLVTRVVTHEMAHASVMVRQVGFGNNATAN 149
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12.3%; Score 95; DB 12; Length 18
Best Local Similarity 29.9%; Pred. No. 0.14;
Matches 50; Conservative 20; Mismatches 59; Indels
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                                                        APPLICANT: Wang, Liangsu
APPLICANT: Amundio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                   Robert
                                                                                                                                                                                                                                                                                        Trawick, John
Carr, Grant
Yamamoto, Rober
Forsyth, R.
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US-09-841-835-8
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99 VAAAPUVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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Patent No. US2002007679541
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack Avenue, 4th Floor
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%; Score 92; DB 9; Length 673; Ilarity 30.4%; Pred. No. 1.4; Conservative 15; Mismatches 57; Indels
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                            STREET: 411 Hackensack Avenue, 4th Floor CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600-1-230 CIP1
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/841,835 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORWATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 673 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-841-835-8
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MEDIUM TYPE: Floppy
                                                                                              New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
Matches 35; Conserv
                                                                      STATE: NC.
COUNTRY: USA
07601
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Score 92; DB 9;
Pred. No. 3.3;
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PRIOR APPLICATION NUMBER: US/09/606,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4. Application US/10199937
Publication No US20030190739A1
GENERAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
                                                                                                                                                           Query Match
Best Local Similarity 30.4%;
Matches 35; Conservative 1
                                                                      HYPOTHETICAL: NO -841-97F
                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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US-10-199-937-4
                                                                                                                        US-09-841-835-2
LENGTH:
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Patent No. US20020076795A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Get Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPENDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 92; DB 9; Length 949; 30.4%; Pred. No. 2.2; tive 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack Avenue, tun Filori
CITY: New Jersey
CONTRY: USA
ZIP: 07501
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DEADELTIN Release #1.0, Version #1.30
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECHONE: 201-487-5800
TELEPRAK: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                    600-1-230 CIP1
                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECHONE, 201-343-1684
                                                             09/196,387
                                                                                                                                                                                                                                          TELEX: 13351
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 30.4
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-841-835-10
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSBLABSPEAA 157 99 VAAAPVVPAVGTSSAAGVAPNPAGGGGNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA 157 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64 6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64 Gaps 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212 65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212 65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113 Query Match
Best Local Similarity 30.4%; Pred. No. 3.3;
Matches 35; Conservative 15; Mismatches 57; Indels 57; Indels Publication No US20030032769A1

Sequence 8: Application US/09972115A

Publication No US20030032769A1

GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Matler, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFRENCE: 080/003C

CURENT APPLICATION NUMBER: US/09/972,115A

CURENT FILING DATE: 2001-10-05

PRIOR FILING DATE: 2000-04-10

PRIOR APPLICATION NUMBER: US 60/128,577

PRIOR APPLICATION NUMBER: US 60/129,123

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PATENTIN VERSION 3.1 APPLICANT: Demaggio, Anthony J.
APPLICANT: Goldman, Phyllis S.
APPLICANT: McElligott, David L.
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
FILE REPERENCE: 27866/38559
CURRENT APPLICATION NUMBER: US/10/199,937 us-09-543-407-14.rapb

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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Research E
APPLICANT: Research E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-11(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                            99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPGSPGSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 263;
                                                                                                                                                                                                                                                                                              Query Match
11.9%; Score 92; DB 14; Length 1327;
Best Local Similarity 30.4%; Pred. No. 3.3;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 -----YGNGA--DVGQGADNSTIEL--TQNGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: 700071884_FLI.pep
US-10-425-114-49960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 147748, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: AROSE, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 49960, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION WUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO SEQ ID NOS ID NOS: 178
LENGTH: 1327
                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-10-199-937-4
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ORGANISM: Zea mays
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US-10-437-963-147748
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US-10-425-114-49960
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## APPLICANT: Barbazuk, Brad
### PAPPLICANT: Li, Ping
### PAPPLICANT: Li, Ping
### TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
### TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
### TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
### CURRENT FILING DATE: 2003-65-14
### CURRENT FILING DATE: 2003-65-14
### CURRENT FILING DATE: 2003-65-14
### CURRENT FILING DATE: 2003-65-14
### CURRENT FILING DATE: 2004966
### CORRENT FILING DATE: 2004 | 11.4%; Score 88.5; DB 16; Length 145;
### CORRENT PROPRATION: Clone ID: PAT_MRT4530_48247C.1.pep
### CORRENT PROPRATION: Clone ID: PAT_MRT4530_48247C.1.pep
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### CORRENT PROPRATION: Clone ID: PAT_MRT4530_48247C.1.pep
### CORRENT PROPRATION: Clone ID: PAT_MRT4530_48247C.1.
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Sequence 12, Appli Sequence 5, Appli Sequence 57, Appl Sequence 30, Appl Sequence 26, Appl

Sequence 3

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq

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PEPTIDE SEQUENCES
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Sequence 14, Application US/09543407
Sequence 14, Application US/09543407
GENERAL INFORMATION:
APPLICANT
APPLICANT
COLLINEON, S. Karen
APPLICANT
COLLINEON, S. Karen
APPLICANT
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP'
TITLE OF INVENTION: 20004-3.406
CURRENT APPLICATION NUMBER: 2000-04-05
CURRENT APPLICATION NOS: 59
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
19 US-09-543-407-14
19 US-09-543-407-12
19 US-09-543-407-12
19 US-09-543-407-12
19 US-09-543-407-12
19 US-09-543-407-20
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US-09-678-411-10
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ORGANISM: Artificial Sequence
FEATURE:
        Q ID NO 14
LENGTH: 151
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            2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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| cgn2_6/ptodata/2/paa/USO6_COMB.pep: *
| cgn2_6/ptodata/2/paa/USO6_COMB.pep: *
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| cgn2_6/ptodata/2/paa/USO66_COMB.pep: *
| cgn2_6/ptodata/2/paa/USO96_COMB.pep: *
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                             protein search, using sw model
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Minimum DB Maximum DB

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Sequence 4, Appliance 2, Appliance 2, Appliance 34, Appliance 5834, Appliance 5833, Appliance 5833, Appliance 5833, Appliance 5833, Appliance 5833, Appliance 6, Appliance 5833, Appliance 6, Appliance 5833, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, Appliance 6, App

58833, AB 58833, AB 86, AB 206388, AB 66, AB 66, AB 67, AB 68, AB 68, AB 10, AB 11, AB 88, AB 11, AB 88, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB 11, AB

Sequence Sequence

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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
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US-08-233-642A-57
US-08-233-642A-57
i Sequence 57, Application US/08233642A
i GENERAL INFORMATION:
APPLICANT: Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-543-407-5; Sequence 5, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CORGANISM: Salmonella enteritidis US-09-543-407-5
                                                                                           LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.6%;
Matches 141; Conservative C
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US-09-543-407-12
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Oznan, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BREEFRIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BREEFRIATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: UNMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: PASKSEQ for Windows Version 4.0

LENGTH: 151
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Sequence 12, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Hay William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
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                                                Length 151;
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92.1%; Score 714; DB 19; Length 151;
Best Local Similarity 91.1%; Pred. No. 2.4e-68;
Matches 144; Conservative 0; Mismatches 0; Indels 1
                                                                                              Indels
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100.0%; Pred. No. 6.1e-75;
iive 0; Mismatches 0;
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                                      Query Match
Best Local Similarity 100.
Matches 151, Conservative
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-09-543-407-24
US-09-543-407-14
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                   20;
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                      Length 151;
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                                                                                                                                                Score 696; DB 19;
Pred. No. 2.1e-66;
0; Mismatches 0;
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89.4%; Score 693; DB 19;
Best Local Similarity 90.7%; Pred. No. 4.4e-66;
Matches 137; Conservative 3; Mismatches 11;
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121 LVTRVVTHEMAHASVMVRQVGFGNNATANOY 151
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
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ORGANISM: Artificial Sequence
          TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-543-407-26
                                                                                                         US-09-543-407-30
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LENGTH: 151
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US-09-543-407-30

Sequence 30, Application US/09543407

Sequence 30, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Mares L.
TILLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRECENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: BRECENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF SEQ ID NOS: 5900-04-05

NUMBER OF SEQ ID NOS: 59 for Windows Version 4.0

SEQ ID NO 30

LENGTH: 151
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APPLICANT: Collinsou, Sharon C.
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS: -
ADDRESSEE: 6300 Columbia Center, 701 Fifth Avenue
STREET: ---:-
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                                                                                                                                                             Score 692; DB 6;
Pred. No. 5.6e-66;
3; Mismatches 11;
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Best Local Similarity 90.7
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collings S. Karen
APPLICANT: Collings S. Karen
APPLICANT: Kay, William K.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 92049.3,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SUFFMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.9%; Pred. No. 2.1e-62;
Matches 136; Conservative 0; Mismatches 0; Indels 30;
                                          Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment
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FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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81 VGQGADNSTIELFQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHEMAHASVMVRQV 140
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 151
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                           APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 92043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
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78.2%; Score 606; DB 19; Length 131;
Best Local Similarity 89.3%; Pred. No. 9e-57;
Matches 117; Conservative 3; Mismatches 11; Indels
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ilarity 80.8%; Pred. No. 2.3e-56;
Conservative 4; Mismatches 25; Indels
                                                                                                       121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                          ; Sequence 31, Application US/09543407; GENERAL INFORMATION:
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Best Local Similarity
Matches 122; Conserv
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US-09-543-407-31
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US-09-543-407-28
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FactSEQ for Windows Version 4.0
LENGTH: 151
TYPE: ...
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043,407
CURRENT FILIGO DATE: 2000-04-05
SOFTWAREN FILIAGO DATE: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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78.6%; Score 609; DB 19; Length 151;
Best Local Similarity 81.5%; Pred. No. 5.2e-57;
Matches 123; Conservative 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.8%; Score 611; DB 19; Length 151; Best Local Similarity 81.5%; Pred. No. 3.2e-57; Matches 123; Conservative 6; Mismatches 22; Indels
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US-09-543-407-20
Sequence 20, Application US/09543407
GENERAL INFORMATION:
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LENGTH: 151
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                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                          SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT: White, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: PASTSEQ for Windows Version 4.0
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
SUTMERN FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.7%; Score 602; DB 19; Length 151; Best Local Similarity 81.5%; Pred. No. 3e-56; Matches 123; Conservative 5; Mismatches 23; Indels C
                                                                                                                                                                                 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 151
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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US-08-978-878-4

US-08-978-878-4

Sequence 4, Application US/08978878

SEQUENCE 4. Application US/08978878

SERVERAL INFORMATION:
APPLICANT: OLSEN, Arne
TITLE OF INVENTION:
FILE REPERENCE: 012889-081

CURRENT APPLICATION NUMBER: US/08/978,878

CURRENT APPLICATION NUMBER: US/08/978,878

CURRENT PLING DATE: 1998-11-26

SEALLIER APPLICATION NUMBER: SE 8801723-1

EARLIER FILING DATE: 1988-05-06
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GENERAL INFORMATION:
APPLICANT White, Aaron P.
APPLICANT Doran, James L.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESTRY TION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543.407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRSESEQ for Windows Version 4.0
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                             Length 151;
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                                                                                                                                          Query Match 74.6%; Score 578; DB 19; Length 15
Best Local Similarity 80.8%; Pred. No. 1.2e-53;
Matches 122; Conservative 6; Mismatches 23; Indels
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68.9%; Pred. No. 2.9e-48;
tive 20; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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US-09-543-407-7
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Matches 104; Conservative
                                                                                       US-09-543-407-16
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US-09-543-407-7
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Search completed: August 2, 2004, 15:26:42 Job time : 167.9 secs

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11109, A
309662,
342526,
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Sequence 741, App
Sequence 49, Appl
Sequence 300390,
Sequence 31234,
Sequence 312468,
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48, App
46132,
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9194, Ap
273, App
96, Appl
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285216,
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17306, A
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Sequence 88, Appl
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Sequence 2, Appli
                                                                   August 2, 2004, 14:49:38; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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Sequence 34
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Sequence 2
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1 MKLLKVAAFAAIVVSGSALA.......HASVMVRQVGFGNNATANQY
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(cgn2 6/ptodata/2/paa/VCT NEW COMB.pep:*
(cgn2 6/ptodata/2/paa/US06 NEW COMB.pep:*
(cgn2 6/ptodata/2/paa/US07 NEW COMB.pep:*
(cgn2 6/ptodata/2/paa/US08 NEW COMB.pep:*
(cgn2 6/ptodata/2/paa/US09 NEW COMB.pep:*
(cgn2 6/ptodata/2/paa/US0 NEW COMB.pep:*
(cgn2 6/ptodata/2/paa/US0 NEW COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-170-205E-3551
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US-10-170-205E-351
US-10-425-115-303390
US-10-425-115-312468
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US-09-248-796A-17306
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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-	US-09-952-267B-13	7	US-10-872-769-13	US-09-952-267B-5	US-10-872-768-5	US-10-872-769-5	US-10-425-115-351875	PCT-US03-24982A-317	US-10-100-683-7608	90	US-60-579-062-7907	PCT-US04-09385-4	US-10-809-790-4	PCT-US04-12070-2	PCT-US04-21492-198	US-10-425-115-193207	US-10-425-115-254355	US-10-425-115-329691	US-10-425-115-190187	
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APPLICANT: NOLSEL, Arne
TITLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation
FITLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation
FITLE OF INVENTION PRIMER: US/09/741,873C
CURRENT APPLICATION NUMBER: EB 8801723-1
FRIOR FILING DATE: 1998-05-06
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1994-01-28
FRIOR APPLICATION NUMBER: US 08/18,519
FRIOR FILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-01-05
FRIOR APPLICATION NUMBER: US 08/318,519
FRIOR FILING DATE: 1994-01-05
FRIOR APPLICATION NUMBER: US 08/318,519
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68.2%; Pred. No. 2.3e-38;
ive 21; Mismatches 27; Indels
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                                ; Sequence 4; Application US/09741873C; GENERAL INFORMATION:
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Best Local Similarity 68.2
Matches 103; Conservative
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US-10-170-205E-741

US-10-170-205E-741

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOA1381

CURRENT APPLICATION NUMBER: US/10/170,205E

CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                            65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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Best Local Similarity
Matches 35; Conserv
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPRENCE: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION NUMBER: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFWARE: Patentin version 3.2
SEQ ID NO 35751
LENGTH: 299
                                                                                                                                                                                 APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE REFRENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: SE 8801723-1
FRIOR APPLICATION NUMBER: US 08/978,878
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR PELING DATE: 1999-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR PELING DATE: 1992-11-03
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ 1D NOS: 11
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.7%; Score 447; DB 5; Length 131; Best Local Similarity 64.9%; Pred. No. 1.2e-31; Matches 85; Conservative 20; Mismatches 26; Indels
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Best Local Similarity 30.4%; Pred. No. 2.2;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35751, Application US/10170205E GENERAL INFORMATION:
                                                               Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                                                                        APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Escherichia coli
US-09-741-873C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 GFGNNATANOY 151
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US-10-170-205E-35751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-10-170-205E-35751
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NS-10-425-115-312468
Sequence 312468 Application US/10425115
GENERAL INFORMATION:
GENERAL INFORMATION:
TOTAL APPLICANT: Exovalic, David K.
APPLICANT: Exovalic, David K.
APPLICANT: APPLICANT: A Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369326
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; Sequence 21, Application US/10479638
; GENERAL INFORMATION:
APPLICANT: Bandolph V. Lewis
APPLICANT: The University of Wyoming
APPLICANT: The University of Spider Silk Proteins in Higher Plants
; TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
; TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
; TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
; TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
; TITLE OF INVENTE: 2003-02-03
; TITLE OF INVENTE: 2003-02-06
; PRIOR PRIOR APPLICATION NUMBER: 60/296,184
; PRIOR FILING DATE: 2001-06-06
; PRIOR FILING DATE: 2001-06-06
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NOS: 54
; SEQ ID NO 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 35.1%; Pred. No. 3.9;
Matches 33; Conservative 10; Mismatches 39; Indels
                                                            73 SGYGNGAD-----VGQGADNSTIEL--TQNGFRNNATID 104
                                                                                                                  134 GGMGGGADGAYGSGAGGGVGKGQGESGVALAPSSDGYYNGGAAD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:;
; COTER INFORMATION: Clone ID: MRT4577_48027C.1.pep
[S-10-422-115-312468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 NNLSSGYNSNGRYN--TIG-----SSDGNTGGYN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 DNSTIELTQNGFRNNATIDQWNAKNSDITVGQYD 119
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, ORGANISM: Argiope trifasciata
US-10-479-638-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.2%
Matches 36; Conservative
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ORGANISM: Zea mays
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                                                                                                                                                                                               Sequence 300390, Application US/10425115
Sequence 300390, Application US/10425115
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihuai
APPLICANT: Zhou, Yihuai
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 30390
LENGTH: 258
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 301334
LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA----RKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
11.7%; Score 90.5; DB 6; Length 25%;
Best Local Similarity 27.9%; Pred. No. 2.5;
Matches 29; Conservative 15; Mismatches 39; Indels 21; Gaps
                                                                                         158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 256;
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11.5%; Score 89.5; DB 6; Length 25:
Best Local Similarity 27.9%; Pred. No. 3;
Matches 29; Conservative 14; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 GGMGGGANGAYGSGAGGGVGKGEGVSGVALAPSSNGYYNGGAAD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 -----TQNGA--DVGQGADNSTIEL--TQNGFRNNATID 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_37025C.1.pep
US-10-425-115-300390
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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PCT-US04-05654-2086
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  32;
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APPLICANT:
Matches
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                                                                                                                                                                                                                                                                   JAPENANT: COLE, STEWART

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

TILE REFERENCE: 05394.0019

CURRENT APPLICATION NUMBER: US/10/468,356

CURRENT APPLICATION NUMBER: 10/080,170

PRIOR APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2002-02-22

PRIOR PALING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 655

SOFTWARE: PRECEIN Ver. 3.2

LENGTH: 527
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con Yihua
APPLICANT: APPLICANT: A Sequence of the Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 346132
LENGTH: 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GOGADNSTIELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- 113
                                        403 GYGAGAAAGAGAGAAAGAGSYSGSISRLSSAEAVNRVSSNIGAVASGGASALPGVISNIF 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -STLSIYQYGSANAALALQSDARKSE
                                                                                   114 -----TVGQYDQLVTR-----VVTHEMAHASV-MVRQVGFGNNATANQ 150
                                                                                                                463 SGVSSSAGSYEEAVIQSLLEVLSVLLHILSNSSIGYVGAEGLGDSLAVVQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 527;
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  74 GYGNGADVGQGADNSTIELTQNG-FRNNATIDQWNAKNSDI-
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; OTHER INFORMATION: Clone ID: MRT4577_78839C.1.pep
US-10-425-115-346132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.2%; Score 86.5; Di
Best Local Similarity 22.9%; Pred. No. 13;
Matches 35; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GVVPQWGG----GGNHNGGGNSSGPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mycobacterium tuberculosis
US-10-468-356-348
                                                                                                                                                                                                               US-10-468-356-348
; Sequence 348, Application US/10468356
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 BQLSVEQGAPSQAIQPIPSSSKAFKFPMRPGKGQSGKRCIVKANHFFAELPDKDLHHYDV 213
                                         ---NHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----YQYGSANAALALQSDARKSETTITQSGYG
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24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: PIJGTIM, MATSHA L

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR PRIOR DATE: 2003-02-25
PRIOR PRIOR PILING DATE: 2003-02-26
PRIOR SEQ ID NOS: 2950
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: Patentin Version 3.2
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                                                                                                                                   71 TOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
  40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.0%; Score 85.5; DB 1; 25.7%; Pred. No. 34; iive 17; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: G1152 Paralogous to G1146
Mismatches
                                                                                                                                                                                                                                                                                            Sequence 2086, Application PC/TUS0405654
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US04-21492-88; Sequence 88, Application PC/TUS0421492; GEWERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LVTRVVTHEMAHASVMVRQV 140
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reuber, T. Lynne
Keddie, James
Dubell III, Arnold N
Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 GGGGNHNGGGNSSGPDSTLSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kumimoto, Roderick W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 NGADVGQGADNSTIE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broun, Pierre E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.75
Matches 36; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gutterson, Neal
Yu, Guo-Liang
                                           19 LAGVVPQWGGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repetti, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Century, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                    Haake, Volker
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APPLICANT Baum, James A
APPLICANT Baum, James A
APPLICANT Larosa, Thomas J
APPLICANT Larosa, Thomas J
APPLICANT Lu, MacJong
APPLICANT Lu, MacJong
APPLICANT Roberts, James K
APPLICANT Roberts, James K
APPLICANT Roberts, James K
APPLICANT RANG, Wei
APPLICANT CANAG, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: WOMBER: US/60/579,062
CURRENT APPLICATION WNBER: US/60/579,062
CURRENT APPLICATION WNBER: US/60/579,062
CURRENT RIUNG DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOCTHARE: PatentIn version 3.2
SEQ ID NO 9194
LENGTH: 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7,
  77 GHENNGHGYGSSSTKTQTITQTSSSS-----SQGGNLEQTIL-NGHGNNG-IGYGSGSK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 TIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE-MAHASVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 VIE------TTVTKHLGGNNEKHLGKLDQVV--LTGHENNGH------GYGSSST 169
                                                                                                              129 VIE-----TTVTKHLGGNNEKHLGKLDQVV--LTGHENNGH------GYGSSST 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GHENNGHGYGSSSTKTQTITQTSSSS-----SQGGNLEQTIL-NGHGNNG-IGYGSGSK 128
                                                                                 TIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE-MAHASVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 GGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.6%; Score 82; DB 7; Length 758; 26.8%; Pred. No. 47; tive 21; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2, 2004, 15:29:51
                                                                                                                                                                                                                                                                                                                                                                  Sequence 9194, Application US/60579062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , TYPE: PRT
, ORGANISM: Diabrotica virgifera
US-60-579-062-9194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.8%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: August
                                                                                                                                                                                     148 ANO 150
                                                                                                                                                                                                                                   170 KTQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 ANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 KTQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Job time : 18.8 secs
                                                                                                                                                                                                                                                                                                                    RESULT 15
US-60-579-062-9194
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APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Laroaw, Thomas J.
APPLICANT: Laroaw, Thomas J.
APPLICANT: Laroaw, Thomas J.
APPLICANT: Wu, Weil
APPLICANT: Wu, Weil
APPLICANT: Whing, Bei
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION TOWNER: US/60/565,632
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILE PATENTING DATE: 204-04-07
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9194
APPLICANT: Diversa Corporation
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: GUUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN TITLE OF INVENTION: THEM
FILE REFRENCE: 564462009540
CURRENT FILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: 60/484,725
PRIOR FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 518
SOFTWARE: Patent In version 3.1
SEQ ID NO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 IVVNGQTRQAENQSVNTGVWANNQCGGSGNSEWLHCNGYISFGNVSGSSSSSSSSSSSSSS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 NAALALQSDARKSETTITQ-----SGYGNGADVGQGADNSTIELT-QNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 IVVSG-----SALAGVVP--QWGGGGN----HNGG----GNSSGPDSTLSIYQYGSA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 535;
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10.6%; Score 82; DB 7; Length 758;
Best Local Similarity 26.8%; Pred. No. 47;
Matches 33; Conservative 21; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Obtained from an environmental sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.6%; Score 82.5; DB
Best Local Similarity 26.2%; Pred. No. 29;
Matches 38; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 WNAKN----SDITVGQYDQLVTRV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WGVSNFTGRTISVTVNGSGTAVTTI 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9194, Application US/60565632 GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Diabrotica virgifera
US-60-565-632-9194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
PCT-USO4-21492-88
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-60-565-632-9194
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29 GGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNS

•

OM protein - protein search, using sw model

Run on:

August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545:204 Million cell updates/sec

Title: Perfect score:

US-09-543-407-14 775 1 MKLLKVAAFAAIVVSGSALA.......HASVMVRQVGFGNNATANQY 151 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein a	urlin	curlin protein csg	curlin major subun	prot	curlin nucleator p	anpr	curlin minor chain	prote	probable PPE prote			hypothetical glyci	hypothetical prote	DNA-binding protei	ovo protein - frui	conserved hypothet	hypothetical prote	nucleation compone	rot	-1	tail fiber protein	F3F19.21 protein -	metalloproteinase	probable PPE prote	leishmanolysin (EC	probable PPE prote	metalloproteinase	hypothetical prote
SUMMARIES	JD	603	063	S70788				C90806												AH0635	JN0891	T03371	S00275	C86266	$\overline{}$		819916		JN0892	7070
	DB	5	N	N	N	N	Ŋ	N	N	Ŋ	C)	Ŋ	Ŋ	N	N	~	N	N	7	N	7	7	7	0	N	7	Н	~	N	0
	Length		151	151	152	152	151	151	151	151	552	770	1748	2174	301	1028	1213	145	145	151	479	256	262	573	479	590	646	678	478	527
9,6	Query Match	0	g	68.1	S	IJ	m	m	3	2	N	N	N	3	Ч	н	Н	11.7	н	ц	Н	н	ч		-	н	Н	Н	\vdash	_
	Score	693	σ	528	. 90	06.	94.	•	04.	œ.	ė.	96	95	93	91	91	91	ö	90.5	ö	o,	89.5	σ.	89	88.5	87	87	87	86.5	v.
	Result No.		7	m	4	Ŋ	9	7	œ	σ'n	10			13																

	probable disease r	leishmanolysin (EC	leishmanolysin (EC	protein kinase sgg	merozoite 45K surf	hypothetical prote	probable sugar ABC	hypothetical prote	leishmanolysin (EC	leishmanolysin (EC	hypothetical prote	hypothetical prote	hypothetical prote		probable PPE prote
F70825	G84687	B42049	A44951	835327	B39112 .	S66852	AD1539	T21956	A45621	PL0221	H84219	A83401	T15352	S35423	D70575
N	7	7	7	7	N	(7)	N	(7)	П		0		N	N	N
645	447	599	599	575	347	196	440	407	590	602	285	340	440	1067	3300
11.2	11.1	11.1	11.1	11.0	11.0	11.0	10.9	10.8	10.8						10.8
			.8				84:5	9.4	9.4	9.4	83.5	83:5	83.5	83.5	83.5
30	31	32	33	34		36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	JC6039
	fimbrin protein agfA precursor - Salmonella enteritidis
	C;Species: Salmonella enteritidis
	C,Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999
	C;Accession: JC6039; PC6015; A44898
	R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
	J. Bacteriol: 178, 662-667, 1996
	A, Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
	A; Reference humber: JC6039; MJID: 96146512; PMID: 8550497
_	A;Accession: \(\text{CC6039} \)
_	A;Molecule type: DNA
	A;Residues: 1-151 <col/>
	A, Cross-references: GB: U43280; NID: 91184712; PIDN: AAC43599.1; PID: 91184714
	A, Accession: PC6015
	A, Molecule type: protein
	A;Residues: 21-52 <co2></co2>
	A, Experimental source: strain 27655-3b
	A; Note: the authors translated the codon ACG for residue 44 as Ile
	R;Collinson, S.K., Emody, L., Muller, K.H., Trust, T.J., Kay, W.W.
	J. Bacteriol 173, 4773-4781, 1991
	A, Title: Purification and characterization of thin, aggregative fimbriae from Salmonell
	A; Reference number: A44898; MUID: 91310586; PMID:1677357
_	A:Contents: 27655

A;Contents: 27655
A;Accession: A4898
A;Accession: A4898
A;Accession: A4898
A;Accession: A4898
A;Residues: 21-33 <C03>
A;Residues: 21-33 <C03>
A;Acession: agray
C;Genetics: agray
C;Genetics: agray
C;Function: major component of thin aggregative fimbriae
A;Description: major component of thin plasminogen, tissue plasminogen activator
C;Function: Eimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
C;Keywords: fimbria
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: fimbrin protein agfA #status experimental <WAT>

Gaps ., Query Match

89.4%; Score 693; DB 2; Length 151;
Best Local Similarity 90.7%; Pred. No. 5e-52;
Matches 137; Conservative 3; Mismatches 11; Indels

0

09

MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120 09 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 61 임 ò g

121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151

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Curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C;Species: Escherichia coli Cipate: 18-Unl-2001 #sequence_revision 18-Unl-2001 #text_change 18-Unl-2001 C;Accession: D90806 C;Accession: D90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Altie: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gent A;Reference number: A99629; MUID:21156231; PMID:11258796
A.Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csg;
A.Reference number: S31202; MUID:93211294; PMID:8459772
A.Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A) Description: major component of wild-type curli, interaction between CsgA and CsgB tr. A;Note: curli are thin, coiled fibers expressed on the surface of Escharichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F,21-20/Domain: signal sequence #status predicted <SIG>F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1.133, RQRDSGWLW' <0LS3>
A;Cross_references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLIKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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ilarity 67.1%; Pred. No. 3.6e-36;
Conservative 21; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 528; DB 2;
; Pred. No. 5.4e-38;
20; Mismatches 27.
                                                                                                   A; Molecule type: DNA
A; Residues: 1-6, 'V', 8-151 < OLS1>
A; Cross-references: EMBL: L04979
A; Accession: S34560
A; Molecule type: protein
A; Residues: 21-42; 44-50 < OLS2>
R; Olsen, A.N.; Arnqvist, A.M.
Submitted to the EMBL Data Library, October 1992
A; Reference number: S34559
A; Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY
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68.98;
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 23.15
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Matches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: csgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    curlin protein csgA precursor - Escherichia coli (strain K-12)

NyAlternate names: csgA protein; major curlin protein
Cippecies: Becherichia coli
Cipace: 12-Reb-1998 #sequence revision 20-Reb-1998 #text_change 01-Mar-2002
Cipace: 12-Reb-1998 #sequence revision 20-Reb-1998 #text_change 01-Mar-2002
Cipace: 12-Reb-1998 #sequence revision 20-Reb-1998 #text_change 01-Mar-2002
Cipacesion: S70788; G64846; S31202; S34560; S34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Marcobiol. 18, 661-670; J995
A;Fitle: Expression of two csg operons is required for production of fibronectin- and CcA;Reference number: S70788
A;Fitle: Expression of two csg operons is required for production of fibronectin- and CcA;Residues: J0788
A;Fatus: nucleic acid sequence not shown; translation not shown
A;Residues: 1-151 c4AA>
A;Residues: 1-151 c4AA>
A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Residues: 1-151 c4AA>
A;Cross-references: EMBL:X90754; NID:g1147558; PEDN:CAA62282.1; PID:g1147564
A;Residues: D.J.; Mau, B.; Shao, Y.
A;Rose, D.J.; Mau, B.; Shao, Y.
A;Rose, D.J.; Mau, B.; Shao, Y.
A;Rose, D.J.; Mau, B.; Shao, Y.
A;Reference number: A64720; MUD:97426617; PMID:9278503
A;Reference number: A64720; MUD:97426617; PMID:9278503
A;Reference number: DNA
A;Reference number: A64720; MUD:97426617; PMID:9278503
A;Reference number: DNA
A;Reference number: A64720; MUD:97426617; PMID:9278503
                                                                                                                                                                Major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Tycscies: Salmonella enterica subsp. enterica serovar Typhi G.Species: Salmonella enterica subsp. enterica serovar Typhi G.Species: Description ob een called Salmonella typhi G.Species has also been called Salmonella typhi G.Saccession: Al0635 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 #sparkhilly J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Waite, N.; Farrar, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.; Cronin, A.; Davis, P.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serovals A; Accession: Al0635 #scarus; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Residues: 1-151 <PAR>
A,Crossic references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
C;Genetics:
A,Gene: STY1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 693; DB
Pred. No. 5e-52
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
          NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 90.7%;
Matches 137; Conservative
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A; Residues: 1-151 <BLAT>
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          121
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à q ò q à Pb

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A, Description: minor component of wild-type curli, interaction between CsgA and CsgB tr A,Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kiningeni in the absence of CsgA, CsgB can self-assemble into polymers
F;1-21,Domain: signal sequence #status predicted <SIG>
F;22-151/Product: minor curlin chain #status predicted <MAT>
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Potamousis, K.; Apodaca
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A;Molecule type: DNA
Residues: 1-151 - STO>
A;Cxoss-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
A;Cxoss-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DO806
minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain Ols/:n/, oucyobacies Escherichia coli (strain Ols/:n/, oucyobacies Escherichia coli (species Escherichia coli Cippecies: Escherichia coli Cippecies: Ba-dul-2001 #sequence_revision 18-Jul-2001 #sequence_revision 18-Jul-2001 #sequence_revision 18-Jul-2001 |
C;Accession: C90806 | R; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 |
A;Tile: Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and charactus: preliminary A;Reference number: A;Residues: A;Residues: DNA A;Residues: 1-151 cHAY>
A;Residues: 1-151 cHAY>
A;Residues: 1-151 cHAY>
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A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics: A;Gene: ECS1419
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G8565

G8565

curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (st
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession, G85665
Iller, L.; Groubeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
Nature 409, 529-531, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-OYGSANAALALQSDARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
    source: strain K-12, substrain MG1655
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; Pred. No. 0.054;
19; Mismatches
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Best Local Similarity 29.2%
Matches 35; Conservative
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nes 35; Conserv
                                                                                                                                             23.15
                                                          C;Genetics:
A;Gene: csgB
A;Map position: 2
C;Function:
         A; Experimental
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NiAlternate names: csgB protein; curlin nucleation component; minor curlin protein
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S7078; F6484 Es
Mol. Microbiol. 18, 661-670, 1995
A;Rithe: Expression of two csg operons is required for production of fibronectin- and Cc
A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-151 - 4AAM
A;Residues: 1-151 - 4AAM
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A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein csqA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Accession: H8565
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhen, Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: H8565
A; Status: preliminary
A; Residuas: 1-152 < 470>
A; Cross_references: GB:AB005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:216
A; Cross_references: Strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: csgA
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A;Residues: 1-151 <BLAT>
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278;
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Best Local Similarity 67.13
Matches 102; Conservative
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related to C2H2 zinc finger transcription factor D-Spl [imported] - Neurospora crassa N;Alternate names: protein B7F21.50
C)Species: Neurospora crassa
C;Species: Neurospora crassa
C;Species: 1-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C;Accession: T51024
C;Accession: T51024
C;Accession: T51024
C;Accession: T51024
C;Accession: T52024
C;Access
     A,Molecule type: DNA
A,Residues: 1-522 <COL>
A,Gross-references: GB:Z92774, GB:AL123456; NID:g3261729; PIDN:CAB07133.1, PID:g1877289
A,Experimental source: strain H37Rv
A,Gene: cs:
C,Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 RKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVT 123
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C;Species: Tetrahymena thermophila
C;Date: 19-Mar.1977 #sequence revision 18-Jul-1997 #text_change 07-Dec-1999
C;Accession: S42136; S42135; S03650
R;Taylox, P.M.; Martindale, D.W.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SGSALAGV-----VPQWGGGGNHNGGGNSSGPD---STLSIYQYGSANAALALQSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 SGSGNIGVENTGANTLVP---GDLMMLGVGNSGNANIGFGNAGVLNTGFGNASILNTGLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           12.5%; Score 96.5; DB 2; Length 552; 28.5%; Pred. No. 1.1; ive 10; Mismatches 62; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: T51024
A,Status: preliminary
A,Molecule type: DAA
A,Residues: 1-70-80A
A,Cross-references: EMBL:AL389901; GSPDB:GN00116; NCSP:B7F21.50
A,Cross-references: BAC clone B7F21; strain OR74A
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12.4%; Score 96; DB 2
Best Local Similarity 22.8%; Pred. No. 1.8;
Matches 31; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 RVVTHEMAHASVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -IIIDSGLINS-----GFGNIGT 476
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R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.

B;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.

B;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.

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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: D70604
R;Coles: N. - 17 Brosch, R.; Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R;Colnor, R.; Davies, R.; Devlin, K.; Peltwell, T.; Gentles, S.; Hanris, D.; Gordon, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mauthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genoma A;Recession: D70604
A;Accession: D70604
A;Accession: D70604
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C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
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                                                                                                                                                                                                                               Length 151;
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A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: csgB
                                                                                                                                                                                                                   ; Score 104.5; DB 2;
; Pred. No. 0.054;
19; Mismatches 59;
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ilarity 29.2%;
Conservative 13
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Best Local Similarity
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hypotherical protein At2g15770 (imported) - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana 0.2-Feb-2001 (S.) Accession: B84533 (S.) Accession: B84533 (S.) Species: A.) Shea, M. I.; Town, C.D.; Fujii, C.Y.; Riin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Riin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999 (C.) Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999 (C.) MID:20083487; PMID:10617197 (A.) Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197 (A.) Arabidopsis thaliana. A; Residues: preliminary A; Molecule type: DNA A; Residues: 1-301 (STO)
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                                                                                                                                                                                                                                                                                          737
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DNA-binding protein ovo - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Species: D1-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000

C;Accession: A56038

R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.

Mol. Cell. Biol. 14, 6809-6818, 1994

A;Title: Multiple products from the shavenbaby-ovo gene region of Drosophila

A;Reference number: A56038; MUID:95021209; PMID:7935398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSALA----GVVPOWGGGGNH-NGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
                                                                                                                                                                                                                         11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
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A,Molecule type: mRNA
A,Residues: 1-1028 cGAR>
A,Cross-references: GB:U11383; NID:g520526; PIDN:AAB60216.1; PID:g520527
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                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                          693 AIATAGAGAVGILAQSIGGGGGN---GGNATGGDAGFGSFQIGGGGGG---
                                                                           ; Score 93; DB 2; Length 2174; ; Pred. No. 11; 15; Mismatches 32; Indels '
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Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 HEMAHASVMVRQV---GFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SHAAGIVAQSVGGGGGTGGTASSY 781
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24.5%;
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                                                                                             Query Match
Best Local Similarity 24.5
Matches 36; Conservative
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A;Gene: SMb21548
A;Genome: plasmid
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A,Map position: 2
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C'Species: Sinorhizobium meliloti
R'Finan, T.M.; Wendner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A., 98, 9889-9894, 2001
A,TTitle: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endc
A,Resion: ES5965
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-2174 < KURN>
A,Residues: 1-2174 < KURN>
A,Resperimental source: strain 1021, megaplasmid pSymB
R'Galibert, E.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler, P.; Ghain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
D.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A,Reteriore number: Asenome of the legume symbiont Sinorhizobium meliloti.
A,Reterence number: A96039; MUID:21368234; PMID:11474104
A,Contents: annotation
C'Species of the legume symbiont Sinorhizobium meliloti.
                                                                                                                                                                                                                                                                  A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-: A;Cross-references: BMEL:L03710
R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila. A;Reference number: S03650, MUID:88189811; PMID:3357771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Genetic code: SGC5
A/Genetic code: SGC5
A/Genetic code: SGC5
A/Introns: 85/3: 136/1: 157/3: 201/2: 290/2: 327/3; 499/1: 573/2: 607/3: 708/3: 777/3: 6/geywords: zinc finger code code: SGC6
E/1464-1450/Region: glycine-rich
F/1451-1464/Region: zinc finger CCHC motif
F/1451-1464/Region: zinc finger CCHC motif
F/1530-1514/Region: zinc finger CCHC motif
F/1530-1543/Region: zinc finger CCHC motif
F/1530-1592/Region: zinc finger CCHC motif
F/1530-1592/Region: zinc finger CCHC motif
F/150-1592/Region: zinc finger CCHC motif
F/150-1592/Region: zinc finger CCHC motif
F/1602-1615/Region: glycine-rich
                                                                                                                                                                  repeats in a protein encoded by
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                        A)Residues: 1-1748 <TAY>
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1686 QTGGGWGSNDN-----QQQQNENTGGGGWGSSNSNQT 1717
                                                                                         R; Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich xA;Reference number: 542135; MUID:94051569; PMID:8233798
A;Accession: 842135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 GADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDIT 114
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A; Residues: 256-250, I', 252-255, 'N', 257-773 < MAR>
A; Cross-references: EMBL: X06462
C; Genetics:
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32.0%; Pred. No. 5.6;
ive 11; Mismatches
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Best Local Similarity 32.03
Matches 31; Conservative
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RESULT 13

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A;Gene: cnjB

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C;Genetics:
A;Gene: ovo
A;Cense: ovo
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Best: Local Similarity 31.2%; Pred
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Search completed: August 2, 2004, 14:56:21 Job time: 9.4 secs

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August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec
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1 MKLLKVAAFAAIVVSGSALA......HASVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_42:*

Database :

Description	salmonella escherichi escherichi escherichi escherichi salmonella drosophila drosophila drosophila drosophila erwinia ch erwinia ch erwinia ch erwinia ch leishmania mycopacter leishmania caenorhabd drosophila mycoplasma r outer me drosophila homo sapie pepper mil pepper mil erwinia ch arkobacter drosophila homo sapie pepper mil escherichila drosophila homo sapie pepper mil escherichila drosophila homo sapie pepper mil erwinia ch arkobacter drosophila homo sapie pepper mil erwinia ch arkobacter drosophila
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ALIGNMENTS

A PARKNII O., Dougsin V., Cancer K., English M.T.G., Sebaihia B. Churcher C., Mungail Y.L., Bentley S.D., Holden M.T.G., Sebaihia B. Churcher S., Basham D., Brooks K., Chillingworth T., Connerton P., RA Croin A., Davis P., Dowd L., White N., Farra J., R. Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K. RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C. RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., R. Mitchead S., Barrell B.G., Simmonds M., Skelton J., Stevens K., RT enterica serovar Typhi CI18."; RI Mature 413:848-852(2001). RN SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RP SEQUENCE ROW N.A. RP SEQUENCE STOM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 21-33.

SPECIESES.enterritidis, STRAIN=27655-3B;

MEDLINE=9110586; PubMed=1677357;

Collinson S.K., Emoedy L., Mueller K.-M., Trust T.J., Kay W.W.;

Collinson and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).

-!- FONDTION: CUBLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                     SPECIESS. enteritidis. STRAIN=27655-3B;
MEDLINE=94013373; PubMed=8104955;
MEDLINE=94013373; PubMed=8104955;
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae.";
(7)
                                                                       SEQUENCE FROM N.A.
SPECIES-S.-encertitidis; STRAIN=27655-3B;
MEDLINE=96146512; Pubmed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W. "Salmonella enteritidis agf8AC operon encoding thin, aggregative fimbriae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVMVRQVGFGNNATANQY -> DSYTQVAS (IN
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4.9e-53;
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Pred. No. 4.9e
3; Mismatches
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                                   Bacteriol. 185:2330-2337(2003)
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                                                                                                                                                                                   Bacteriol. 178:662-667(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE008749; AAL20074.1;
EMBL, AL627269; CAD08268.1;
EMBL, AE016840; AA069399.1;
EMBL, U43280; AA043599.1;
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Best Local Similarity 90.7%;
Matches 137; Conservative
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StyGene; SG10608; csgA.
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SEQUENCE OF 21-31.

MEDLINES-9110/586; PubMed=1677357;

Collinson S.K., Emcedy L., Trust T.J., Kay W.W.;

Collinson S.K., Emcedy L., Trust T.J., Kay W.W.;

Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

J. Bacteriol. 173:4773-4791 (1991).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES TRAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96414468; PubMed=8817489; Hammar M., Anguyis A., Bian Z., Olsen A., Normark S.; Anguyis A., Bian Z., olsen A., normark S.; Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                    STRAIN=K12 / W3110;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A., Olsen A., Arnqvist A., i"The Rpos sigma factor relieves H-NS-mediated transcriptional repression of cggA, the subunit gene of fibronectin-binding curli in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=7061202; PubMed=8905232;
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Kashimoto K.,
Ilemoto K., Inada T., Inch T., Kajihara M., Kanai K., Kashimoto K.,
Mori H., Moromura K., Nakamura Y., Mashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
A. 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIR=HZ, MG1655;
MEDLINE=97426617, PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.; "The Cr! protein activates cryptic genes for curli formation and fibronectin binding in Escherichia coli HB101."; Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Bscherichia coli K-12."; Science 277:1453-1474(1997).
                                                                         01.DEC-1992 (Rel. 24, Created)
01-007-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
                                      151 AA.
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STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.";
Mol. Microbiol. 7:523-536(1993)
                                      STANDARD;
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                                                                                                                                                                    Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                               NCBI_TaxID=562;
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
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EMBL, AR005315; AAG55788.1; --
EMBL, AP002254; BAB34843.1; --
PIR; D90806; D90806.
                                                                                                                                                                                                                                                                                                                                                                                                                       15099 MW;
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Best Local Similarity 67.1:
Matches 102; Conservative
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152
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152 AA;
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ID CSGB ECOLI
AC P39828;
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SEQUENCE
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STRAIN=0157-117 / ACCC 43895;
MEDIJINE=21218556; PubMed=11119125;
Whlich G.A., Keen J.E., Elder R.O.;
"Mutations in the cagD promoter associated with variations in curli
expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli O157:H7.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                   Score 528; DB 1; Length 15:
Pred. No. 7.98-39;
Ni mismatches 27; Indels
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Nature 409:529-533(2001).
                                                                                                                                                                                                                                         MAJOR CURLIN SUBUNIT.
A -> E (IN REF. 1).
; C003470D208D395F CRC64;

    -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.

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Last annotation update)
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                                                                                                                                                                                                            Fimbria; Signal; Complete proteome.
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28-FEB-2003 (Rel. 41, Last seque
28-FEB-2003 (Rel. 41, Last annot
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
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                                                                                                                         EMBL, L04979; AAA23616.1; -.
EMBL, X90754; CAA62282.1; -.
EMBL, AE0002026; AAC74126.1; -.
EMBL, D90741; BAA35832.1; -.
EMBL, D90742; BAA35840.1; -.
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68.9%;
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EcoGene; EG11489; csgA.
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Q93U24;
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1 MKLLKVAAFPAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Antrovist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MAJOR CURLIN SUBUNIT.
EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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01-CCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
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MEDLINB=2115631; PubMed=11258796;
MEDLINB=2115631; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kinagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.,
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SEQUENCE FORM STATE / MG1655,
MEDLINE=97426617, PubMed=9278503,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rose C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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SEQUENCE FROM N.A.

WEDLINE=21074935, PubMed=11206551,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Link S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97061202; PubMed=8905232;
                              Mol. Microbiol. 18:661-670(1995).
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EMBL; X90754; CAA62281.1; -.

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J. Bacteriol. 178:662-667(1996).
J. Bacteriol. 178:662-667(1996).
J. Bacteriol. CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720, MEDLINE=21534948; PubMed=11677609, McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                     33 FAVNELSKSSFNQAII----GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES—S. typhimurium; STRAIN=SR-11; MEDLINE=98117058; PubMed=9457880; Remling U., Bian Z., Hammar M., Sierralta W.D., Normark S.; "Curli fibers are highly conserved between Salmonella typhimurium ar Escherichia coli with respect to operon structure and regulation."; J. Bacteriol. 180:722-731(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                   Length 151;
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                                                                                                                                                                                                   151 MINOR CURLIN SUBUNIT.
15882 MW, B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                   13.5%; Score 104.5; DB 29.2%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA
                                                                                                                                                                                                                                                                                                         19; Mismatches
                                                                                                                                                                                      POTENTIAL.
EMBL, AE000205, AAC74125.1; --
EMBL, D90741, BAA35831.1; --
EMBL, AP005315, AAG55787.1; --
EMBL, AP00254; BAB4842.1; --
PIR, C90806, C90806.
PIR, S70787, S70787.
ECGGene, EG12621, CsgB.
Fimbria, Signal; Complete protecome.
Fimbria; Signal; Complete Protecome.
FIGNAL
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                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                       22 1
151 AA;
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Best Local Similarity
Matches 35; Conserv
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FUNCTION,
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AIIQKGSGNKANITQYGTQK------TAVVVQK 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARVRQEGSKLLSVISQ--EGGNNRAKVDQAGNYNFAYİEQTGNAN-------DAS
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MEDLINE=99454782; PubMed=10523501;
Smith S., de Lange T.;
"Cell cycle dependent localization of the telomeric PARP, tankyrase, to nuclear pore complexes and centrosomes.";
J. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20556282; PubMed=10988299;
Chi N.-W., Lodish H.F.;
Tankyrase is a Golgi-associated mitogen-activated protein kinase
substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith S., Giriat I., Schmitt A., de Lange T.; "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
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                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                Score 98.5; DB 1,
NO. 0.074; 1ndels
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                                                                                                                                                                                                                                                                                                                               MINOR CURLIN SUBUNIT.
  SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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                                                                                                                                                                                         EMBL, AJ002301; CAA05316.1; -.
EMBL, AE008749; AAL20073.1; -.
EMBL, U43280; AAC4598.1; -.
EMPL, JC6040; JC6040.
Stydene; SG10669; csgB.
Fimbria; Signal; Complete proteome.
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MEDLINE=99040105; PubMed=9822378;
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TNK1_HUMAN
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PREVIOUS, AND WINGERNESS OF HIS-1184 AND GLU-1291.

MEDILINES-GC22074; Debaded11393745;

A COOK B.D. Dyned II. Cook B.D. Speed II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. Dyned II. She will be seen to be cook B.D. She to be seen to be cook B.D. She to be seen to be cook B.D. She to be seen to be cook B.D. She to be seen to be cook B.D. She to be seen to be cook B.D. She to be seen to be seen to be cook B.D. She to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be seen to be se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Gaps
                                                                                                                                                                                                                                                                                                                                                     SMRT, SM0035, ZnF CH2, 4.
PROSITE, PS0028, ZINC FINGER C2H2 1; 3.
PROSITE, PS00157, ZINC FINGER C2H2 2; 3.
Zinc-finger, Metal-binding, DNA-binding; Repeat; Nuclear protein;
     ITS CONTINUED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R (IN REF. 2).
D7068BB2BC0F6F77 CRC64;
BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR L'
PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
SIMILARITY: Contains 4 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą.
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C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
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EMBL; X59772; CAB36921.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                   FlyBase; FBG0003028; ovo.
InterPro; IRRO00089; Znf C2H2.
Pfam; PF00096; Zf-C2H2; 3
SWART; SM00355; ZnF_C2H2; 4.
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Q8Z7M3;
28-FEB-2003 (Rel. 41, Created)
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Best Local Similarity 31.2%;
Matches 34; Conservative
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IRANSFAC; T00669; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pranscription
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ID CSGB S
AC Q827M3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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TISSUE=Ovary;
MEDLINE=95021209; PubMed=7935398;
MEDLINE=95021209; PubMed=7935398;
Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity.";
[2]
                                                                                                                                                                                                                                                                                    /FTIG=VSP_004538.
Missing (in isoform 2).
/FTIG=VSP_004539.
H-A: LOSĞ OF ACTIVITY, WHEN ASSOCIATED WITH A-1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212
                                                                                                                                                                                                                                                                                                                                                                            E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota, Noptera; Endopterygota, Diptera, Brachycera; Muscomorpha, Ebhydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 92; DB 1; Length 1327;
; Pred. No. 3.3;
15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                             WITH A-1184.
W; E14DE985C710B957 CRC64;
                                                                                                                                                                                                                                                                     (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OVO DROME STANDARD; PRT; 1028 AA. P51521; 09XZU4; 10-0CT-1996 (Rel. 34, Last sequence update) 10-0CT-2003 (Rel. 34, Last annotation update) 10-0CP-2003 (Rel. 42, Last annotation update) OVO Drotein (Shaven baby protein).
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/FTId=VSP 0
   ANK 7.
ANK 8.
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ANK 10.
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PARP
POLY-PRO.
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EST -> GH
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MEDLINE=91293102; PubMed=1712294;
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30.4%;
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Best Local Similarity 30....
Best 4 Jone 15, Conservative
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VARSPLIC
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δ q ઠે d annotation update)

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003297; 018421; 018422; P91721; P91722; 01-0CT-1993 (Rel. 27, Created) 15-UU-1998 (Rel. 36, Last sequence update) 16-UU-1998 (Rel. 36, Last sequence update) Period Aironale
                                                                      Period circadian protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                              Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Chillingworth T., Farrar J., Feltwell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                            STRAIN-TY2 / ATCC 700931, MEDLINE-2251367; PubMed=12644504; Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R., "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 ARVRQEGSKILSVISQ--EGENNRAKVDQAGNYNFAYIEQTGNAN------DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                      Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MINOR CURLIN SUBUNIT.
161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
     28-FEB-2003. (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Innor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.36
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EMBL, AE016840; AA069400.1; -.
Fimbria; Signal; Complete proteome.
                                                                                                                                       STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                      Bacteria, Proteobacteria, Gamme
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AA; 16254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Conservative
                                                                                                                                                                                                                                                                                                     Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSHMAIRVTÓ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 ISQSAYGNSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 MAHASVMVRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                            SEQUENCE FROM N.A.
                                                              Salmonella typhi
                                                                                                  NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
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PER JONGTION: ESSENITIAI LOS DISCIPLIANTS AUGUSTONS.

PER JOSSE laads to shortened circadian rhythms; an increase in period length of circadian rhythms and a decrease leads to lengthened circadian rhythms and a decrease leads to lengthened circadian rhythms and a decrease rhythmic ty of locomotor activity, eclosion behavior, and for the rhythmic component of the male courtship song that originates in the thoracio nervous system. The biological cycle depends on the rhythmic component of the male courtship song that originates in the thoracio nervous system. The biological cycle depends on the rhythmic formation of PER, Nuclear activity of the heterodime of the TIM-PER complex. Light induces the degradation of TIM, which promotes elimination of PER, Nuclear activity of the heterodima accordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional inhibition (By similarity).

SUBUNIT: Forms heterodimer with timeless (TIM); the complex then transcriptional inhibition (By similarity).

First accumulates in the perinuclear region about one hour before transcription into the nucleus. Interaction with TIM is required for, nuclear localization (By similarity).

THE: STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER PER-TIME PROPHER AND IN THE FORMATION GOMES HERE ARMY-SIM) dimerization domains.

SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biological clock functions. Determines the
                                                                                                                                                                                                                                                                                                                                                                                         of the period locus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE$93196482; PubMed=8450754;
Peixoto:A.A., Campesan S., Costa R.H., Kyriacou C.P.;
"Molecular evolution of a repetitive region within the per gene of
Drosophila willistoni (Fruit fly).
Bukaryoča, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7260;
                                                                                                                                                                                                                                                                      STRAIN=Various strains,
MEDLINE=97357421; PubMed=9214747;
Gleason J.M., Powell J.R.;
"Interspecific and intraspecific comparisons in the Drosophila willistoni sibling species.";
Mol. Biol. Evol. 14:741-753(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila.";
Mol. Biol. Evol. 10:127-139(1993)
-!- FUNCTION: Essential for biolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCÈ OF 579-646 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; US1055; AAB41360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB41363.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB41364.1;
AAB41365.1;
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EMBL;
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RESULT 9 PER_DROWI

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Bacteriophage T2.
Viruses; dsDNA viruses, T4-like viruses.
MCBI_TAXID=10664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erwinia chrysanthemi
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 30; Conserv
                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=B374;
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                                                                                                                                                                                                                                           T -> A (IN STRAIN 0811.4).
S -> F (IN STRAIN 0811.4).
G -> V (IN STRAIN GUANA).
G -> A (IN STRAIN MANAUS 2).
G -> S (IN STRAIN NANTA MARIA).
MISSING (IN STRAIN PORTO ALEGRE 3).
MISSING (IN STRAIN PORTO ALEGRE 4).
MISSING (IN STRAIN PORTO ALEGRE 4).
                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN STRAINS MANAUS 4, PORTO
ALEGRE 1 AND PORTO ALEGRE 2).
S - A (IN STRAINS GUADELOUPE AND GUANA).
MISSING (IN STRAIN MANAUS 3).
A -> T (IN STRAIN 0811.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD
                                                                                                                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                           MISSING (IN STRAINS LIMA B, L'HABITATUE
                                                                                                                                                                                                                                                                                                                                          G -> V (IN STRAIN PORTO ALEGRE 4).
MISSING (IN STRAINS GUADELOUPE, MANAUS
PORTO ALEGRE 2, PORTO ALEGRE 1 AND
                                                                                                                        Biological rhythms; Repeat; Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 90; DB 1; Length 1093; 27.7%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 115896 MW; AB6DE050267EC187 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      771 ----SCSGLGGNGNVGSGNGNNSQPSTNOYTO 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
Receptor recognizing protein (Protein Gp38).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                   POLY-LYS.
POLY-GLY.
POLY-GLY.
POLY-SER.
POLY-GLY.
POLY-ALA.
POLY-ALA.
                                                                  EMBL, L06342; AAA28765.1; -- FlyBase, FBGn0013161; Dwil\per. InterPro, IPR000014; PAS_domain. Pfam; PF00989; PAS; 2.
                                   AAB41374.1; -.
AAB41375.1; -.
AAB41376.1; -.
         US1066; AAB41371.1; -. US1067; AAB41372.1; -. US1068; AAB41373.1; -.
                                                             US1072; AAB41377.1; -.
 AAB41370.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                          202
209
359
411
625
734
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886
1093
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Matches 26; Conserv
                                   US1069; #
US1070; #
US1071; #
 US1065;
                                                                                                                                Polymorphism.
NON_TER
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VG38 BPT2
ID VG38 BPT2
AC P07875;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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VARIANT
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                                                                                                       SMART;
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EMBL;
EMBL;
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 EMBL;
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                                                                                                                                                                                                                     Riede I., Drexler K. Eschbach M.L., Henning U.,
"DNA sequence of genes 38 encoding a receptor-recognizing protein of
Dacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
-!- FUNCTION: Vg38 is at the tip of the long tail fibers and serves as
the phage recognition site for the cellular receptor.
-!- MISCELLANBOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTR
AS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89255387; PubMed=2722818; Delepelaire P., Wandersman C.; "Protease secretion by Erwinia chrysanthemi. Proteases B and C are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delepelaire P., Wandersman C.;
hordein secretion in Gram-negative bacteria. The extracellular
metalloprotease B from Erwinia chrysanthemi contains a C-terminal
secretion signal analogous to that of Escherichia coli alpha-
no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 89.5; DB 1; Length 262; 34.1%; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X05312; CAA28935.1; -.
PIR; S00275; S00275.
InterPro; IPR07932; Tail_fibre_GP38.
Fibar pro5268; G738; Tecognition.
Fibar protein; Phage recognition.
SEQUENCE 262 AA; 25801 MW; 0567366918F6C745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Secreted protease C precursor (EC 3.4.24.-) (ProC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 NSTIELTQNGFRNNATIDQWNAKNSDIT 114
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STRAIN=B374;
MEDLINE=91009140; PubMed=2211614;
                                                                                                                                                                                                    MEDLINE=87283911; PubMed=3302276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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J. Bidl. Chem. 264:9083-9089(1989).
-!- COFACTOR: Binds 1 zinc ion and 7 calcium ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOWAIN: THE GLY-RICH REPEATS MAY BE IMPORTANT IN THE EXTRACELLULAR SECRETRON OF THIS METALLORPOTRASE.
-!- SIMILARITY: Belongs to peptidase family M10B. | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | PEPOIDIGASE | MICHEPPO: | PRO006025 | PEPLIGASE | MICHEPPO: | PRO006025 | PERLOCATION | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | MICHEPPO: | ZINC (CATALYTIC) (BY SIMILARITY).
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PDB; IGO7; 17-OCT-02.
PDB; IK7G; 19-OCT-02.
PDB; IK7G; 20-OCT-02.
PDB; IK7G; 20-OCT-02. 297 302 341 350 359 267 300 348 357 364 297 302 341 348 350 359 267 300 357 364 METAL METAL METAL METAL METAL METAL METAL METAL METAL METAL METAL METAL

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365 36 36 36 36 36 36 36 36 36 36 36 36 36	1 70 0 0 1 1 70 0 0 1	373 373 375 375 381 381 382 382 383 383 384 384 386 386 395 395 412 412 412 412 79 AA; 51600	Tarity 28.8% Conservative SMHNGGGNSSGPDS SNDILVGNSAD ADVGGGADN AYDWIADFQKGID- HEWAHASVMVRQ	DARD; 2, Creat 2, Last 2, Last 2, Last 2, Last 2, Last 2, Last 2, Last 2, Last 2, Last 2, Last 2, Last 379; 379; 1010 3 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host 1 n host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 WGSGNIGSYNLGGGN-----LGSYNLGSGN------TGDTNFGGGNTGNLN 306
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAINS-COT 1551 / Oshkosh;
MEDIJINE-22206494; PubMed-12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobb W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Indels 46; Gaps
              MEDLINE=8829587; PubMed=9634210;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elglameier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skeiton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 87; DB 1; Length 678; 26.2%; Pred. No. 4.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Transmembrane; Complete proteome. TRANSMEM 14 34 POTENTIAL. TRANSMEM 180 200 POTENTIAL. CONFLICT 258 258 D -> G (IN REF. 2). SEQUENCE 678 AA; 66736 MW; 209F1593D52533A2 CRC64;
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InterPro; IPR002899; Mycobac_Dentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
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TIGR; MT1599; -.
Tuberculist; Rv1548c; -.
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                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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InterPro; IPR001625; Pept M Zn BS.

InterPro; IPR00157; Peptidase M8.

Pfam; PF01457; Peptidase M8. 1.

PROSTE; PR00782; LSHWANOLYSIN.

PROSTE; PS00142; ZINC PROTESSE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Simon, Signal; Cell adhesion; Multigene family.

Inc. 1. 39

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 87; DB 1; Length 646; 73.1%; Pred. No. 3.9;
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15-UUL-1999 (Rel. 38, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
110-0CT-2003 (Rel. 42, Last annotation update)
RVJC48C OR MTISS9 OR MTCX48.17.
                          -!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 QYDQLVTRVVTHEMAHASVMVRQVGF 142
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                                                                                                                                                                                                                                                                                                   EMBL; X64394; CAA45733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399
                                                                                                                                                                                                                                                                                                                                PIR; S19916; S19916.
                                                                                                                                                                                                                                                                                                                                                          P08148; ILML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501
646 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                       HSSP; P08148; ILN
MEROPS; M08.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1773;
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Query Match

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RESULT 13 YF48_MYCTU

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746730AE8E2A2E7C CRC64;

similarity)

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63848 MW;
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                599 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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               SEQUENCE
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                                                Query Match
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                                                                                                                                                                                                                                                                                             ACIUVALON PERILDE.

LEISRAANOLYSIN.

REMOVED IN MATURE FORM (BY SIMILARITY).

SINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

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MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
                                                                                        Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania
NCBI_TaxID=44271;
                                                                                                                                                      MEDIINE=90205976; PubMed=2320059; Millar R.A., Reed S.G., Parsons M.; "Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Gly-Asp sequence.";
             Leishmanolysin precursor (BC 3.4.24.36) (Cell surface protease) (Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00625; Pept M Zn BS.
InterPro; IPR006277; Peptidase_M8.
PEfam; PP01477; Peptidase M8; 1.
PRINTS; PR01427; Peptidase M8; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Pydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPT-anchor; Lipoprotein.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION PEPTIDE.
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                      1y-Asp sequence.";
Biochem. Parasitol. 39:267-274(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M80672; AAA29238.1; -.
EMBL; M28827; AAA29235.1; -.
PIR; A44951; A44951.
HSSP; P08148; ILML.
MEROPS; M08.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383
152
                                                                            Leishmania chagasi
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
252
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04442660
8446660
                                              endopeptidase)
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PROPEP
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DISULFID
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DISULFID
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CARBOHYD
LIPID
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SEQUENCE FROM N.A.

STRAIN=CV. Columbia:

MIDINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MIDINE=21016719; PubMed=11130712;

MIDINE=21016719; PubMed=11130712;

MIDINE=21016719; PubMed=11130712;

MIDINE=0: Alonso J. Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

MIDINE O: Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

MIDINE O: Alonso J., Altafi H., Araujo R., Bromman C.L., Chin C.W.,

MIDINE D. Etgu P., Feddblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

MIDINE O: Molekins J., Johnson-Hopson C., Khan S., Khaykin E.,

MIDINE O.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

MIDINE O.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,

Lin X., Liu S.X., Liu Z.A., Lee J.M., Lonz C.A., Li J.H., Y.-P.,

MILISCHET J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

MILISCHERSON T., Maranda M., Nguyen M., Nierman W.C., Osborne B.I.,

MILISCHERSON T., Salaberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

MUD., Yu G., Fraser C.M., Venter J.C., Davis R.W.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

C STRAIN=cv. Columbia;

MEDLINE=2954850; Pubmed=14593172;

A Radlin F., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

A Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Danch H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A Arakawa T., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Khan S., Meyers C., Nakajima M., Narusaka M., Sakim., Sakurai T.,

A Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamura Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia, TISSUE=Leaf;
MEDINE=S800466; PubMed=9427751;
Bobmert.K., Camus I., Bellini C., Bouchez D., Caboche M., Benning C.;
"AGGI défines a novel locus of Arabidopsis controlling leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Argonaute protein..., ruce ammoration upuate;
AGO1 OR[ATIG48410 OR F11A17.3 OR TINI5.2.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                Gaps
                                                                                .,
    Length 599;
                                                                                6; Indels
Score 86; DB 1;
Pred. No. 4.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                             AGO1_ARATH

ID AGO1_ARATH
STANDARD; PRT; 1048 AA.

ID AGO1_APATH
STANDARD;
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                 117 QYDQLVTRVVTHEMAHASVMVRQVGFGNNA 146
                                                                                                                                                                                                                                          250 RYDOLVTRVVTHEMAHA--LGFSVGFFEGA 277
                                          Best Local Similarity 66.7%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 GGYGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQF- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 NGADVGQGADNSTIE------LIQNGFRNNATIDQMNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 GGGGNHNGGGNSSGPDSTLSI-----YQYGSANAALALQSDARKSETTITQSGYG 76
                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the argonaute family.
-!- SIMILARITY: Contains 1 PAZ domain.
-!- SIMILARITY: Contains 1 PAZ domain.
-!- SAULIARITY: Catains 1 Piwi domain.
-!- CAUTION: Ref. 2 (AAFT)18) sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Gaps
                                 Science 302:842-846(2003).
-!- FUNCTION: Essential for proper development of leaves and floral organs, and formation of axillary meristems.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing, Named isoforms=1;
Comment-A number of isoforms are produced. According to EST
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                             Isold=004379-1; Sequence=Displayed;
TISSUE SPECIFICITY: Widely expressed at low levels.
DEVELOPMENTAL STAGE: Expressed throughout all developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.0%; Score 85.5; DB 1; Length 1048; Best Local Similarity 25.7%; Pred. No. 9.2; Matches 36; Conservative 17; Mismatches 60; Indels 27;
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13 104 GLY-RICH.
1048 AA; 116190 MW; 3E5146343A09C541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50821; PAZ, 1.
PROSITE; PS50822; PIWI; 1.
Developmental protein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC007992; AAD49755.1; --
EMBL; AC000898; AAF79718.1; ALT_SBQ.
EMBL; BT000941; AAN41341.1; --
INTERPRO; IPR003100; PAZ.
INTERPRO; IPR003165; Piwi.
PF02170; PAZ; 1.
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Search completed: August 2, 2004, 14:49:28 Job time : 6.3 secs

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2, 2004, 14:39:17 ; Search time 29.7 Seconds (without alignments) 1604.150 Million cell updates/sec
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775
1 MKLLKVAAFAAIVVSGSALA........HASVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                         OM protein - protein search, using sw model
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1: SP_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_numan:*
5: Sp_numan:*
5: Sp_numan:*
5: Sp_numan:*
6: Sp_page:*
6: Sp_page:*
6: Sp_plant:*
6: Sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*

sp_archeap:

	Description	O33802 salmonella	Q7x243 citrobacter	Q7x240 citrobacter	Q8cw63 escherichia	Q7x237 enterobacte	Q54069 salmonella	Q9s3j5 escherichia	O33801 salmonella	Q7x238 enterobacte	Q8eih3 shewanella	Q7x241 citrobacter	Q8cw64 escherichia	Q8eih4 shewanella	Q7x244 citrobacter	Q7ucz1 shigella fl	Q83ru7 shigella fl
SUMMARIES	ID	033802	Q7X243	Q7X240	Q8CW63	Q7X237	Q54069	0983J5	033801	Q7X238	QBEIH3	Q7X241	Q8CW64	Q8EIH4	Q7X244	Q7UCZ1	Q83RU7
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RA WEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

RA Asko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

RA Maybew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

RT "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

RT of uropathogenic Escherichia coli.";

R. Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

REMBL; ABO16759; AAN79779.1; ... 1818.5734C1240E83 CRC64;
                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYDQ 120
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Enterobacteriaceae; Enterobacter.
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4154(2003).
EMBL; AJ515701; CAD566751; -
SEQUENCE 149 AA; 15260 WW; 946DD52017F648FD CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter.
CMCBI_TaxID=213763;
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Enterobacteriaceae, Citrobacter.
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EMBL, AJ515700, CAD56672.1, -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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76.8%; Pred. No. 3.7e-39;
iive 13; Mismatches 21
  LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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Matches 116; Conservative
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4156(2003).
EMBL; AJ515702; CAD56678.1; -. SEQUENCE 150 AA; 15112 MW; SD8BB2D872DF15F3 CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Enterobacteriaceae; Salmonella.
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                                                                                                                                  56.6%; Score 438.5; DB 2; Length 150; 58.9%; Pred. No. 7e-28; Live 28; Mismatches 33; Indels 1.
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Pred. No. 6.3e-24;
0; Mismatches 1; Indels
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Cox J.M., Eglezos S., Woolcock J.B.;
"Virulence of Salmonella enteritidis in chickens correla
colony morphology and expression of SE17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SEF17 fimbrin (Fragment).
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01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fragment).
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TRANSPOSON=Insertion sequence 181;

MEDLINE=99314153; PubMed=10386375;

La Ragione R. M., Collighan R. J., Woodward M.J.;

Lon-curiliation of Escheriolia coli 078:K80 isolates associated with

IS1 inserti on in csgB and reduced persistence in poultry infection.";

FEMS Microbiol. Lett. 175:247-253(1999).

EMBL; Ali31756; CAB4580.1; -.

NON TER

SEQUENCE 29 AA:
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MEDLINE=98053981; PubMed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes interaction of
Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
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EMBL; AJ000514; CAA04150.1; -
SEQUENCE 179 AA; 19318 MW; A2BCCB648B3C0B0B CRC64;
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Last sequence update)
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01-OCT-2003 (TrEMBLrel. 25, Created)
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01-OCT-2003 (TrEMBLrel. 25, Last annotat
Nucleation component of curlin monomers.
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Best Local Similarity 89.7%;
Matches 26; Conservative
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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AGFB.
Salmonella typhimurium.
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Escherichia coli 06
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Best Local Similarity
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nes 35; Conserv
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SEQUENCE 160 AA;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=546;
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                                                                                                                                                                                              STRAIN=Fec4;
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                                                                                                                                                                                                                                    10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 69
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                                                                                                                                                                                                                                                                                       70 ITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVV 126
                                                                                                                                                                                                                                                                                                    Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Deboy T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Beboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White C., Wolf A.M., Wanathevan J., Weidman J., Umpraim M., Lee K., Berry K., Lee C., Wolf A.W., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 SCPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGRDNLIDLVÓQGTANQGIVFQSGSDNS-AYVTQAGNDNISLVTQIGTNNEVQLLQVGAQ
                                                                                      Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515702; CAD566771; -.
SEQUENCE 151 AA; 15985 WW; F0B82BD2A27882B7 CRC64;
                                                                                                                                                                                                            Gaps
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            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                  Length 151;
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SEQUENCE 139 AA; 14811 MW; 41EC1CFA76957920 CRC64;
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Last annotation update)
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                                                                                                                                                                                  DB 2;
                                                                                                                                                                               13.9%; Score 107.5; DB
30.8%; Pred. No. 0.31;
ive 14; Mismatches
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EMBL; AE015532; AAN53942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Minor curlin subunit CsgB, putative
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STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
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                                                                                                                                                                                  Query Match
Best Local Similarity 30.89
Matches 36; Conservative
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Enterobacter sakazakii.
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Best Local Similarity
                                                              SEQUENCE FROM N.A.
                                     NCBI_TaxID=28141;
                                                                            STRAIN=Fec39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 GSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY
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STRAIN=06.H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; FubMed=12471157;
MEDLINE=22388234; FubMed=12471157;
MWEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnanberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD566741.; -
SEQUENCE. 152 AA; 16149 MW; D063A527D45D4329 CRC64;
                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=217992;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016759; AAN79778.1; -.
                                                                                   Last sequence update)
Last annotation update)
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29.2%; Pred. No. 0.58;
tive 19; Mismatches
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29.1%; Pred. No. 0.55;
tive 13; Mismatches
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                      Q7X241;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequenc
01-0CT-2003 (TrEMBLrel. 25, Last annotat
Nucleation component of curlin monomers.
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PRELIMINARY;
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NCBI_TaxID=623;
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98 NLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRV 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2297666; PubMed=12368813; MEDLINE=2297666; PubMed=12368813; MEDLINE=2297666; PubMed=12368813; Meddelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Umayam L.A., Mhite O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Wanthevan J., Weidman J., Impraim M., Lee K., Medbonald L.A., Melblyur T.V., Smith H., Gill J., Utterback T.R., McDonald L.A., "Genome, sequence of the dissimilatory metal ion-reducing bacterium
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL; AE015532; AAN53941.1; -.
                                                                                                                                                 PRT;
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26.0%;
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Best Local Similarity 26.0%
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STRAIN=2457T / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152.

Web J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

Schwartz D.C., Blattner F.R.;

Complete genome sequence and comparative genomics of Shigella

flexneri serotype 2a strain 2457T.";

Infect: Immun. 71:275-2786(2003).

EMBL, AE016981; AAP16542.1;

EMBL, AE016981; AAP16542.1;

SEQUENCE 151 AA; 15868 MW; 5D5D266B964014A0 CRC64;
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Enterobacteriaceae; Shigella.
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                                 36671.1; -.
16158 MW; BD00AF57E1400704 CRC64;
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Last annotation update)
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                                                                                             ;; Score 103.5; DE
;; Pred. No. 0.65;
13; Mismatches
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Infect. Immun. 72:4151-4158(2003).
EMBL, AJ515700, CAD56671.1; -.
SEQUENCE 151 AA; 16158 MW; BD00
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28.8%;
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                                                                                     Query Match
Best Local Similarity 28.89
Matches 32, Conservative
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Best Local Similarity
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:35:42; Search time 44.9 Seconds
(without alignments)
950.215 Million cell updates/sec
Perfect score: 757
Sequence:
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 200000000

Minimum DB Maximum DB

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Salmonell AGÉA::PT3 AGÉA::PT3 AGÉA::PT3 AGÉA::PT3 AGÉA::PT3 AGÉA::PT3 AGÉA::PT3 AgfA sequ Salmonell E. coli C Fibronect Salmonell Salmonell Aab36348 AqfA::PT3 Escherich curli Escherich Salmonell Salmonell Salmonell Salmonel Description Aab36353 A Aab36352 A Aab36350 A Aab36354 A Aab36351 A Aar62761 Aaw23569 S Aab36343 B Abr82651 B Aar52664 B Aaw23570 8 Aab36346 Aab36347 A Aab36326 Aab36338 Aab36344 Aab36325 SUMMARIES AAB36346 AAB36347 AAB36353 AAB36352 AAB36350 AAB36354 AAB36351 AAB36351 ABR82651 AAR52664 AAB36348 AAB36343 AAB36316 AAB36325 AAB36349 Length Query Score Result No.

Aab36339 Salmonell	Aab36320 Salmonell	Aab36342 Salmonell	Aab36322 Salmonell	Aab36327 Salmonell	Aab36337 Salmonell	Aab36340 Salmonell	Aab36324 Salmonell	Aab36319 Salmonell	Abr82649 E. coli V	Abr82645 E. coli c	Aaw32312 Leishmani	Aae36891 Plectreur	Aab36323 Salmonell	Aab36336 Salmonell	Aab36328 Salmonell	Abr82647 E. coli c	Aae36890 Plectreur	Abu44579 Protein e	Aab36331 Escherich
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (BEFIT/TAF) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant of a recombinant gene back into the chromosome of the homologous species; replacing the native Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; AgfA::PT3#3 amino acid sequence SEQ ID NO:16. Kay ww; Disclosure, Page 136; 139pp; English. vaccine; immune response; immunogen. AA. Collison SK, standard; protein; 151 99US-0127888P 05-APR-2000; 2000WO-CA000356 (first entry) Salmonella enteritidis. Escherichia coli. (UYVI-) UNIV VICTORIA Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64624. WO200060102-A2. 05-APR-1999; 26-FEB-2001 12-OCT-2000 White AP, Synthetic. AAB36348 AAB36348; RESULT 1 AAB36348

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copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonalla, E. coli or Enterobacteriacese host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent (1) is useful for the expression of recombinant AgfA protein which is useful foliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inspensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                      AgfA
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Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 151; Conservative 0; Mismatches 0;
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N-PSDB; AAQ87467.
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The Salmonella AgfA protein and DNA are used in vaccine and genetic

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                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                     09
                                                                                                                                                                                                  9
                                                                                                                                                                                                                                     1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                      Length 151;
                                                                                                                                                          Indels
                                                                                                                  86.9%; Score 658; DB 2; L
larity 90.1%; Pred. No. 1.6e-57;
Conservative 3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 135, 139pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36341 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-672631/65.
                                                                                                                                       Best Local Similarity
Matches 136; Conserv
                                                                               Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC64617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36341;
                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                             9
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copiess/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                          1 MKILKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                               Score 658; DB 3;
Pred. No. 1.6e-57;
3; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNOTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis 27655-3b agfA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-00233788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-00054452
                                                                                                                                                                                                                                 y Match
Local Similarity 90.1%;
hes 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-309886/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT74142
                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1994;
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29-SEP-1997
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                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epirope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coil and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, csgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALAQ
                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                       Length 151;
                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                     Score 653; DB 2;
Pred. No. 5.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                                                                                                                                                                                                                                                                                                                                                                                        151
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                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             NNPALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collison SK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36349 standard; protein; 151
                                                                                                                                                                                   86.3%;
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                                                                                                                                                                                                                      Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC64625
                                                                                                                                                       Sequence 151 AA;
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sent sequence represents agfA encoded by the full agfA gene from Salmonella enteritidis 27655-3b. The nucleic acid can

Example 2; Fig 7; 85pp; English

The present derived from

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directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequence grown on a fallow of incoducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to Show) on coppless/cell), the hybrid fimbria protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response considerate the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- YDQLVTRVVTHEMAHASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVWYRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 618; DB 3; Lu
Pred. No. 1.6e-53;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.68;
76.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 131; Conservative
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Escherichia coli.
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N-PSDB; AAC64622.
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI7/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and Enterphaceaeleriaceae for the production of fimbriae comprising recombinant of incerting recombination of a recombinant gene into the chromosome of the honologous species; a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, copy of that gene or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or chromosome of the comprising secondinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or sequence or sequences grown on a Salmonella, E. coli or susful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which he heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to committee the contraction properties relevant for an efficient live in a contraction in the properties of immunogenicity and adhesion properties relevant for an efficient live in a contraction and contraction and contraction are efficient live and contraction and contraction are efficient live and contraction and contraction are efficient live.
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protein useful for eliciting immune response in animal.
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Pred. No. 9.8e-50;
7; Mismatches 23
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                                              Page 135; 139pp; English.
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Matches 121; Conserv
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Synthetic.
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Salmonella enteritidis.

Escherichia coli. Synthetic.

WO200060102-A2

12-OCT-2000.

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seqment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEI)/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of a recombinate on the chromosome of the homologous species, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a replacement segment comprising arecombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the aversasion of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the recombinant protein are efficient live warding a mannel contains a melficient live warding a mannel contains a melficient live warding a mannel contains a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding a melficient live warding and melficient live warding a melficient live warding and melficient live warding and melficient live warding and melficient li
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Pred. No. 1.5e-49;
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                                                                                                                                                                                             Kay WW;
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                                                                                                                                                                                   Collison SK,
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05-APR-1999;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbried (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enerother and AgfA-homologue fimbrins ubunits, respectively; (2) directing recombinant of a recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologue species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or coli or coli or interpretation of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xpensive to purify in large amount. The present sequence is given in exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.2%; Score 577; DB 3; Length 151; 80.8%; Pred. No. 1.9e-49; ive 5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                                                                                                                                                                                                                                                                                          M.W.
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                                                                                                                                                                                                                                                                                                                                                                          Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                                                                                                                                                                                                                   JS-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                        99US-0127888P
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                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672631/65.
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Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC64629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                                                                        05-APR-1999;
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임
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σ١ RESULT

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;

vaccine; immune response; immunogen.

AgfA::PT3#8 amino acid sequence SEQ ID NO:26.

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Ор
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(I) use of thin aggregative finbriae (SEPT/7/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are combinant AgfA protein containing a replacement segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein sare usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in an abilitie are easy and since the inserted epitope, and hybrid fimbriae are easy and since the inserted epitope, and hybrid fimbriae are easy and since in the contains are presented and an effection in the contains the inserted epitope, and hybrid fimbriae are easy and since in the contains the inserted epitope, and hybrid fimbriae are easy and since the contains the inserted epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                           Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.0%; Score 575; DB 3; Length 15: Best Local Similarity 81.5%; Pred. No. 3.1e-49; Matches 123; Conservative 5; Mismatches 23; Indels
                                                                                                                                                                 AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 138; 139pp; English.
                          AAB36352 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA000356.
                                                                                                                   26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                Salmonella enteritidis.
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran JL,
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                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                       AAB36352;
AAB36352
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA cequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and directing recombination of a recombinant gene into the chromosome of the bomologue species; (3) directing recombination of a recombinant gene back into the chromosome of the homologus species; replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA confined in containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the comprising an immune response in an animal. In a fimbrial presentation containing an immuner response in an animal. In a fimbrial presentation containing the hybrid fimbrin protein possesses both the immune, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response contains an immune response contains the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKAYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
                                                                                                                     HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                                                                                                                                                                                                                                             AAB36350 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC64626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                   RESULT 10
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05-APR-1999;
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                                                                                                                                                                                           Matches
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                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                        SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                       1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                           Length 151;
                                         Score 574; DB 3; Length 15
Pred. No. 3.9e-49;
5; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
                                                                                                                                                                                151
the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kay WW;
                                                                                                                                                                                NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collison SK,
                                                                                                                                                                                                                                                               AAB36354 standard; protein; 151 AA
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                                          Query Match
Best Local Similarity 80.8%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
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N-PSDB; AAC64630.
                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                         RESULT 11
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for
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                                                                                                                                                                                                                                                                                                        ij.
Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 568; DB 3;
Pred. No. 1.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#6 amino acid sequence SEQ ID NO:22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36351 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%;
80.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAC64627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060102-A2
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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of Enterobacteriaceae for the production subunits, respectively; (2) directing recombination of a recombinant gene into the Chromosome of the homologue species, replacing the native composition of the homologue species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino composition or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequence or sequenc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 567; DB 3; Length 15:
Pred. No. 1.9e-48;
5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36355 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.8%;
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000
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AAB36355
ID AAB36
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: sequence which encodes a foreign epitope or antigen. Also described are: or sequence which are (SEPI)/TAFA) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant confinences production of finbriae comprising recombinant of directing recombination of a recombinant gene homologous species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal copy of that gene, and (4) eliciting an immune response in an animal coli described and animo acid polymer comprising a replacement segment comprising a recombinant AgfA protein which is useful for the expression on a salmonalla, B. coli or collymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the expression or recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the control of the compression or electronic are presented in high numbers (in the control of the compression of the compression of the compression of the complex relevant for an efficient live in the control of the complex relevant for an efficient live in the control of the complex relevant for an efficient live in the control of the complex relevant for an efficient live in the control of the complex relevant for an efficient live in the control of the complex relevant for an efficient live in the control of the complex r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                         Recombinant agfA gene having a segment replaced by a foreign DNA seg
which encodes foreign epitope or antigen, expresses recombinant AgfA
protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine, the carrier fimbrial subunit proteins are usually strong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 566; DB 3;
Pred. No. 2.4e-48;
5; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR62761 standard; protein; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.8%;
80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella; AgfA; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.8
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
N-PSDB; AAC64631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA sequence
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26-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR62761;
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Example 2; Fig 7; 85pp; English.

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The sequence represents the Salmonella enteritis 27655-3b InphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct DN field.) (Updated on 27-MG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                         37 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG 96
                                                                                                                                                                Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis 27655-3b TnphoA mutant agfA fragment.
                                                                                                                                                                                                                                                                                                                                                     Score 487; DB 2; Length 120;
Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRNNATIDOWNAKONSDITVGOYGGNNAALVNQTASDS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 FRNNATIDOWNAKWSDITVGOYGGNNAALVNOTASDS 133
                                                                                                 Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                            UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                 Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW23569 standard; protein; 120 AA
                                                                                                                                                                                                         7A; 95pp; English.
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                                                                                                                                                                                                                                                                                                                                                     64.3%;
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         94WO-IB000207
                                  93US-00054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                  95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collinson SK, Kay WW,
                                                                                                 Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-309886/28.
                                                                                                                         WPI; 1994-358275/44.
N-PSDB; AAQ73066.
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT74141
                                                                                                                                                                                                                                                                                                                             Sequence 120 AA;
                                                                                                                                                                                                         Disclosure; Fig
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           26-APR-1994;
                                  26-APR-1993;
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29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW23569;
                                                          (UYVI-)
(KING/)
                                                                                                   Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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                               The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The mucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                      37 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG 75
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                             Score 487; DB 2; Length 120;
Pred. No. 1.3e-40;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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ne : 45.9 secs
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Best Local Similarity
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Sequence 49, Appl
Sequence 32096, A
Sequence 2, Appli
Sequence 5, Appli
Sequence 6167, Ap
Sequence 7854, Ap
Sequence 2, Appli
Sequence 2, Appli
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Sequence 199, App
Sequence 204, App
Sequence 6562, Ap
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                            Sequence 2, 1
Sequence 49,
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APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier. Sharon C.
APPLICANT: Clouthier. Sharon C.
APPLICANT: OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 653; DB 1; Length 151;
Pred. No. 1.8e-60;
3; Mismatches 13; Indels
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COUNTRY: US.A.
COUNTRY: US.A.
COUNTRY: US.A.
CONFUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: BATENIT Release #1.0, Version #1.25
CURRENT: APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASS!FICATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELEPHONE: (206) 682-601
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US-08-804-227C-3

US-09-043-123-2

US-09-043-123-2

US-09-252-991A-32096

US-09-134-001C-3

US-09-134-001C-3

US-09-336-447A-5

US-09-328-335-6167

US-09-328-335-6167

US-08-687-379-2

US-08-687-379-4

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US-08-687-379-4

US-08-687-379-4

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US-09-072-56-199

US-09-072-56-199

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US-09-072-56-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.4%;
Matches 135; Conservative
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Sequence 57, Appl
Sequence 131, Appl
Sequence 26438, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
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Sequence 67, A
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Sequence 2, Al
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/cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/2/iaa/PCTUS_COMB.pep:*
                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-247-188A-57

US-09-477-183A-131

US-09-477-183A-131

US-09-477-183A-131

US-09-252-991A-2438

US-08-614-377A-7

US-09-134-010-3214

US-09-134-010-3214

US-09-336-115C-12

US-09-336-115C-6

US-09-336-115C-6

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US-09-36-115C-6

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US-09-641-2

US-08-69-880-2

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US-08-119-641-2

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US-09-540-236-3739

US-08-541-780-2

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Maximum Match 100% .
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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757
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Match 1
                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
    9
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
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NESOUR 2.

Sequence 57, Application US/08233788A

Sequence 57, Application US/08233788A

Sequence 57, Application US/08233788A

Septent No. S6354T

APPLICANT: Manual W.

APPLICANT: Colineon, Karen S.

APPLICANT: Coluthier, Sharon C.

TITLE OF INVENTION: OF SALMONELA

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSED Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREE: Washington

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Pred. No. 2.5e-43;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER REPARABLE FORM:
MEDUTOR TYPE: 10ppy disk
COMPUTER: 1BM PC compatible
OMPUTER: 1PM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 FRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 FRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                           121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: TOTAL STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG STRONG S
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US-09-543-681A-5434
Sequence 5434, Application US/09543681A; Patent No. 6605709; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-6031
TELERA: (206) 682-6031
TELERA: 372384 SEEDANBERRY
INFORMATION FOR SEO ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 97.9%;
Matches 95; Conservative
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TITLE OF INVENTION: WOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT PAPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS 6344
LENGTH: 2315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 DVIVIIILINDAGHASAPDYSTLAGSQH---DGKIALHGDTGK----VTYDGASTVTVVI 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 QGADNS-----TIELTQNGFRNNATIDQWNAKNSDITVGQYGG--NNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 DQLVTRVVTHEMAHASGPD-STLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVG 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.4%; Score 86.5; DB 4; Length 943; 24.8%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 2315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REPRENCE: 52888
CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: US/09/823
PRIOR PILING DATE: 1997-12-15
PRIOR PELING DATE: 1997-12-15
PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR APPLICATION NUMBER: 60/000,254
PRIOR PILING DATE: 1996-06-15
NUMBER OF SEQ ID NOS: 169
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 131, Application US/09477135A Patent No. 6572865 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.0%;
Matches 37; Conservative 1
                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Proteus mirabilis
US-09-543-681A-5434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1804 GASATGVIYDGN 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 SVMVRQVGFGNN 145
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Matches 39; Conserv
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TIIIQSGYGNGADVGQGA-----DNSTIELTQNGFRNNATI-DQWNAKNSDIIVGQYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                        11 AIVVSGSALAGVYDQLVTRVVTHEMAHA---SGPDSTLSIYQYGSANAALALQSDARKSE
                                                                                                                                                                                                                                                                                                         463 AAATAGATVAGRVNGAVT--ITDSAAASATTAGKIATVTLGSFGAA----TIDSSAL---
                                                                                                                                                                                                                   20;
                                                                                                                                                             Query Match
10.8%; Score 82; DB 1; Length 1026;
Best Local Similarity 24.8%; Pred. No. 7.9;
Matches 34; Conservative 28; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7; Application US/08614377A

Patent No. 5976864

GENERAL INFORMATION:
APPLICANT: Smit, John
APPLICANT: Bingle Wade H.
APPLICANT: Bingle Wade H.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTRY: USB

CONTRY: USB

CONTRY: USB

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT: APPLICATION DATA:

APPLICATION NUMBER: US/08/614,377A

FILING DATE: 12-MAR-1996

CLASSIFICATION: 435

APPLICATION NUMBER: US 08/194,290

FILING DATE: 09-FEB-1994

CLASSIFICATION: 435

APPLICATION: 435

APPLICATION: 435

ALTONEN PATENTINE OB-JUNE-1992

CLASSIFICATION: 435

ATPONEY/AGENT INFORMATION:

NAME: TAGO, Y. ROCKY

REGISTRATION NUMBER: 34053

REGISTRATION NUMBER: 34053

REGISTRATION NUMBER: 34053

REGISTRATION NUMBER: 34053

REGISTRATION NUMBER: 34053

REBERBUCK-POCKET NUMBER: BELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 NAA--LVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 TASSTIASLVAADATTL 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 Franklin Street
LENGTH: 1026 anino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-194-290-7
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617-542-8906
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TOPOLOGY: 11
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INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-614-377A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                          Sequence 26438, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 DQLVT---RVVTHEM-----AHASGPDSTLSIYQYGSANA------ALA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LQSDARKSETTITQSGYG-----GFR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         477 GVTVVQSQNGANIGSGASGITVVQ--SQNGANIGSGASGISVVQSQSG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 NNATIDQWNAKN----SDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 85; DB 4; Length 1415; 1 Similarity 25.6%; Pred. No. 6.1; 43; Conservative 19: Minner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08194290
Patent No. 5500353
GENERAL INFORMATION:
APPLICANT: Smit, John
APPLICANT: Bringle, Wade H
TITLE OF INVENTION: Bacterial surface protein expression
NUMBER POWDENCES: 10
COMMERS.POWDENCE ADDRESS:
ADDRESSER: Shlesinger, Arkwright & Garvey
STREET: 3000 South Eads Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Garvey, George A
REGISTRATION NUMBER: 17737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: USA
                      RESULT 5
US-09-252-991A-26438
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US-08-194-290-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 STLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR---- 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 SAFAAI----ANGGTYNNAHSIQKVVTHEGDTIEYEHTSHKAMKDYTSYMLAEILKGTF
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09336115C
Sequence 22, Application US/09336115C
Sequence 22, Application US/09336115C
Sequence No. 6576244
Sequence No. 6576244
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Sequence
                                                                                                                                                                                                                                                                         Length 746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 YOYGSANAALALQSDARKSETTITQSGYGNGADVGQGA---
                                                                                                                                                                                                                                                                                                                                  43:
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                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                   Query Match
10.8%; Score 81.5; DE
Best-Local Similarity 26.5%; Pred. No. 5.7;
Matches 39; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 81; DB 19.0%; Pred. No. 5.7; ive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              7 AAFAAIVVSGSALAGVYDQL--VTRVVTHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GESPEYTMSVWMGFNK---VKQYGTNS 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 GFRNNATIDQWNAKNSDITVGQYGGNN 122
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 746
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                                                                                                                                                 TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3214
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; Sequence 12, Application US/09336115C
Partent No. 6576244
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 19.0%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-336-115C-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SIGNAL LOCATION: (1).
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US-09-336-115C-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 690
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Sequence 7. Application US/09142648B

Patent No. 6210948

CENDERAL INFORMATION:

APPLICANT: Smit. John
APPLICANT: Smit. John
APPLICANT: Bingle, Wade H.
APPLICANT: No. 6210348ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULC FILE REFERENCE: 08106/00202

CURRENT FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: US/09/142,648B

PRIOR APPLICATION NUMBER: US/09/142,648B

PRIOR APPLICATION NUMBER: US/09/142,648B

PRIOR APPLICATION NUMBER: US/09/14377
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: UNGBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                          68 TTITÇSGYGNGADVGQGA-----DNSTIELTQNGFRNNATI-DQWNAKNSDITVGQYGGN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                    11 AIVVSGSALAGVYDQLVTRVVTHEMAHA---SGPDSTLSIYQYGSANAALALQSDARKSE 67
                                                                                                                                                                                                                                                                                                         TTITQSGYGNGADVGQGA-----DNSTIELTQNGFRNNATI-DQWNAKNSDITVGQYGGN
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10.8%; Score 82; DB 3; Length 1026;
Best Local Similarity 24.8%; Pred. No. 7.9;
Matches 34; Conservative 28; Mismatches 55; Indels
                                                               10.8%; Score 82; DB 2; Length 1026; 24.8%; Pred. No. 7.9;
                                                                                                                           28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                              122 NAA--LVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574 TASSTIASLVAADATTL 590
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                                                                                                                           Conservative
                                                                                              Local Similarity
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US-09-134-001C-3214
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US-09-142-648B-7
      US-08-614-377A-7
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                                                                  Query Match
                                                                                                                              Matches
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RESULT 13
US-09-206-942-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 STLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR---- 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 NNIIEHYYTENGKEIPVSYSGGSSFSPTIQLTYHNNAENLLQQAATIMQVLITQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09336115C

Sequence 6, Application US/09336115C

Patent No. 657624

GENERAL INFORMATION:
APPLICANT: Weltzin, Richard A.
APPLICANT: Weltzin, Richard A.
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/05502

CURRENT APPLICATION NUMBER: US/09/336,115C

CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: US 09/100,258

PRIOR APPLICATION NUMBER: US 09/100,258

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FRSTSEQ for Windows Version 4.0
                  APPLICANT: Guy, Eruno
ITTLE OF INVENTION: LT and CT in Parenteral Immunization
ITTLE OF INVENTION: Methods Against Helicobacter Infection
ITTLE OF INVENTION: Methods Against Helicobacter Infection
ITTLE REPERENCE: 06123/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT APPLICATION NUMBER: US 09/100,258
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.7%; Score 81; DB 4; Length 691;
Best Local Similarity 19.0%; Pred. No. 5.7;
Matches 33; Conservative 27; Mismatches 66; Indels
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10.7%; Score 81; DB 4; Length 745;
Best Local Similarity 23.1%; Pred. No. 6.4;
Matches 27; Conservative 18; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 721
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AFAAIVVSGSALAGVYDQLVTRV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Helicobacter pylori
APPLICANT: Weltzin, Richard A. APPLICANT: Guy, Bruno
                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SIGNAL LOCATION: (1)...(20)
                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: SIGNAL
; LOCATION: (1)...(18)
US-09-336-115C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-336-115C-6
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91 ELTONGERNATIONAMANINDITYOCYCCANNALAUNCEASSESSIVUTTYTYTYNNAAT 264
RESULT 13
125 ERECTADINGGYVOCKANGASSESSIVGANGSSTOTTATTYGGOVITTYTYNNAAT 264
RESULT 13
125 SAPPLEASE 5
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17 TITLE OF INVARIATION: Nocedular Waight Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SGSALAGVYDQ--LVTRVVTH----EMAHASGPDSTLSIYQYGSANAALALQS-DARKSET 68
                                                                                                                                                                                                                                                                                                                                                                                            27; Gaps
                                                                                                                                                                                                                                                                                                                                                10.6%; Score 80.5; DB 1; Length 1536; 26.4%; Pred. No. 20; tive 22; Mismatches 60; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2. Application US/08302832
Patent No. 5603938
GENERAL INFORMATION:
APPLICANT Barenkamp, Stephen J
TITLE OF INVENTION:
TITLE OF INVENTION:
FINE OF INVENTION:
Of No. 5603938-Typeable Haemophilus
NUMBER OF SEQUENCES:
ADDRESSEE: Shoemakkr and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bidg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: TEACHER STORY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,832
FILING DATE: 16-SEP-1994
CLASSIFICATION NUMBER: US 9205704.1
APPLICATION NUMBER: US 9205704.1
APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MAR-1992
ATPONEY/AGENT INFOMMATION:
NAME: BERKETERSER' USTY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1281 NTVNVTANAGDLTV-----GNGAEIN 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 NAALVNQTASDSSVMVRQVGFGNNATAN 149
             NAME: BERNSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
TELECOMUNICATION INPORMATION:
TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.48
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Bidg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: Z2202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-038-682-2
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US-08-302-832-2
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p SEQUENCE CHARACTERISTICS:
| LENGTH: 1536 amino acids
| TYPE: amino acids
| TYPE: amino acids
| STRANDEDNESS: single
| STRANDEDNESS: single
| STRANDEDNESS: single
| MOLECULE TYPE: DNA (genomic)
| WOLDCOULE TYPE: DNA (genomic)
| US-08-302-832-2
| Query Match
| Best Local Similarity 26.4%; Pred. No. 20, Matches 39; Conservative 22; Mismatches 60; Indels 27; Gaps 7;
| Matches 39; Conservative 22; Mismatches 60; Indels 27; Gaps 7;
| SGSALAGVYDQ--LVTRVVTH---EMAHASGEDSTLSIYQYGSANAALALGS-DARKSET 68
| SHORT TOSIGNESSGSVTLTATECALAVSNISG--NTVTVTANSGALTTLAGSTIKGTESVT 1225
| QY 69 TITQSGYGNGADVGQGADNSTIEL-----TQNGFRNNATIDGWNAKNSDITVGGYGGN 121
| STANDEDNESSSSYNVRQVGFGNNATAN 149
| DD 1226 TSSQSG-----DIGGTISGGTVESLTTQSNSKIKATTGEANVTSATGTIGGTISG 1280
| DD 1281 NTVNVTANAGDLTV------GNGAEIN 1301
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Search completed: August 2, 2004, 14:58:32 Job time : 12 secs

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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/USIO6_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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757
                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                 OM protein
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Seguence 4, Appli	Seguence 4, Appli	Seguence 2, Appli	Seguence 2, Appli	Sequence 20638, A	Seguence 72503, A	Sequence 49757, A	Seguence 1549, Ap	Sequence 146, App	Sequence 162284,	Sequence 131, App	Sequence 131, App	Sequence 131, App	Sequence 64369, A	Sequence 38, Appl
ID	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-282-122A-72503	US-10-282-122A-49757	US-10-238-075-1549	US-09-793-306-146	US-10-437-963-162284	US-09-996-634-131	US-09-997-182-131	US-09-997-181-131	US-10-282-122A-64369	US-10-383-930-38
DB	12	12	73	12	15	12	12	14	0	16	σ	10	10	12	16
% Query Match Length DB	151	151	131	131	445	290	1862	182	597	154	943	943	943	3300	1554
% Query Match	63.5	63.5	54.7	54.7	15.0	12.3	11.8	11.8	11.7	11.4	11.4	11.4	11.4	11.4	11.2
Score	481	481	414	414	113.5	93	89.5	89	88.5	86.5	86.5	86.5	86.5	86.5	85
Result No.		2	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15

	equence 107204,	equence 4985	equence 1, 1	4,	e 1, 7	equence 9411		ce 11,	e 7001	16, 7	equence 33,	1317	500	534			ce 105	equence 736	ce 709	e 497	12,	equence 22,	6, Appli	58683,	73345,	540	equence 65, App	eguence 2,	equence 63, App	146
	-10-437-963-10720	-282-	-984-334	-10-004-115A	-10	56-761-9	-185-990-	-10-185-990	5-10-282-122	19-996-19	-10-164-966-	-10-156-761-13	10-369-493-2009	0-369-493-534	3-379-93	0-223-5	19-769-78	10-282-122A-7367	-122A-7058	10-282-122A-497	-08-834-666A-1	08-834-666A	-08-834-666A-	3-10-282-122A-586	-10-282-122A-7334	82-122A-540	-10-193-764-	92-88	-10-193-764-63	US-10-437-963-146426
	16	12	10	14	14	14	14		12	σ	12	14	15	15	თ	14	10	12	12	12	ω	α	œ	12	13	12	14	13	14	16
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	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1

US-09-741-873B-4

US-09-741-873B-4

Sequence 4; Application US/09741873B

Publication No. US2020081722A1

GENERAL INFORMATION:
Publication No. US2020081722A1

GENERAL INFORMATION:
PED TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REPERENCE: 01289-049-04

FILE PREPART FILING DATE: 3003-04-04

PRIOR FILING DATE: 1990-05-06

PRIOR FILING DATE: 1990-05-06

PRIOR FILING DATE: 1991-11-26

PRIOR PRILING DATE: 1991-11-26

PRIOR PRILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR PRILING DATE: 1991-11-06

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEG ID NOS 4

LENGTH: 151

CAPPARE: Patentin Version 3.0

SEG ID NOS 4

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OCHERNY MATCH

GEN THE OF CALL SIMILATIVE COIS

SEC ID NOS 4

CHARLE OF CALL SIMILATIVE COIS

OCHERN MATCH

GEN THE OF CALL SIMILATIVE COIS

OCHERN MATCH

GEN THE OF CALL SIMILATIVE COIS

DESCRIPTION OF COMBERVARIVE 139; Mismatches 32; Indels 0; Gaps 0;
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1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60

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APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTATION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
PRIOR PELICATION NUMBER: US 08/978,878
PRIOR PEPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/399,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PELING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE PARCETIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR
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Best Local Similarity 69.9%; Pred. No. 3.6e-37;
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17; Mismatches 17;
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PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-16-26
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.7%;
milarity 69.9%;
Conservative 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-741-873B-2
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                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09741873B

bublication No. US20040096965A9

publication No. US20040096965A9

publication No. US20040096965A9

GARBEAL INFORMATION:

APPLICANT: Olsen, Arne

TILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE EFFRENCE: 012689-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 08/978,878

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-07

PRIOR PELING DATE: 1991-11-06

PRIOR PELING DATE: 1991-11-06

PRIOR PELING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR PELING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-05

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

LENGTH: 151

TANDER: DATE: 151

TANDER: DATE: 1994-10-05

SEQ ID NO 4

LENGTH: 151
                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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Publication No. US20020081722A1
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-087
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.5%; Score 481; DB 12; Length 151; 66.2%; Pred. No. 2.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                        121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.5
Best Local Similarity 66.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-741-873B-2
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Indels

Length 131;

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APPLICANT: Xu, H.

TITLE OP INVENTION: Identification of Essential Genes in Microorganisms
FILE REPREMENCE: ELITRA.034
CURRENT APPLICATION NUMBER: 00/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-11-27
PRIOR PRIING DATE: 2000-11-27
PRIOR PRIING DATE: 2000-11-27
PRIOR PRIING DATE: 2000-11-27
PRIOR PRIING DATE: 2000-11-27
PRIOR PRIING DATE: 2000-11-27
PRIOR PRIING DATE: 2000-12-22
PRIOR PRIING DATE: 2000-12-22
PRIOR PRIING DATE: 2000-12-29
PRIOR PRIING DATE: 2001-12-29
PRIOR PRIING DATE: 2001-12-29
PRIOR PRIING DATE: 2001-12-29
PRIOR PRIING DATE: 2001-02-09
PRIOR PRIING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALAL-- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KLIK-----SIAKSGSFRAYVLDSTET-VRTAQEEHQSLSSSTVALGRTLIANQILAANQ 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: Patentin version 3.1 SEQ ID NO 72503 LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%; Score 93; DB 12.1arity 26.7%; Pred. No. 0.12; Conservative 23; Mismatches
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49757, Application US/10282122A Publication No. US20040029129A1
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Rol
Forsyth, R.
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Best Local Similarity
Matches 40; Conserv
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US-10-282-122A-72503
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 10/369, 493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360, 039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 FNGNSGFLÓENGTLSGANLLTVKQSGNSNSVGRDIQGKQSGAGNSAAIFQEGTGSDVELQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 -----LQSDARKSETTI------TQSGYGNGADVGQGADNSTIELT 93
              3 LLKVAAFAAIVVSGSALAG----VYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALA
                                                                                                                               NNATIDOWNAKWSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 25.0%; Pred. No. 0.0013;
Matches 46; Conservative 18; Mismatches 63; Indels 57;
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LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
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Sequence 72503, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Ohlsen, Kari

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                   Sequence 20638, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 QNGFRNNATIDQWNAKN---
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Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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US-10-369-493-20638
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APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Skeify, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
ITILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
ITILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
ITILE OF INVENTION: Of Tuberculosis
TILE OF INVENTION: Of Tuberculosis
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 146
                                                                                                                                                                                                                                                                       57 SSLKDNAATSGLTPFAIRLTGCATGMNSAQNVKAYFEPSSNIDLATHNLKNTAT--PTKA 114
                                                                                                                                                                                                                  57 LALQSDARKSETT---ITQSGYGNGADVGQGA-----DNSTIELTQNGFRNNATIDQWNA 108
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                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVYDQLVT---RVVTHE-MAHASGPDSTLSIYQYGSANAA 56
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11.7%; Score 88.5; DB 9; Length 597;
Best Local Similarity 35.9%; Pred. No. 1;
Matches 28; Conservative 7; Mismatches 32; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                109 KNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                         115 DNVQIQLLNSNGTSTILLGEADNGQDVQSETIGSDGSAT 153
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Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 146, Application US/09793306
Patent No. US20020098200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bubkarov, Andrey A.
APPLICANT: Barbaruk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 DSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Campos-Neto, Antonio APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-437-963-162284
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US-10-238-075-1549
US-10-238-075-1549
US-10-238-075-1549
Sequence 1549, Application US/10238075
PUBLICATION NO. US20030148324A1
GENERAL INFORMATION:
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.Coli, and biological uses of these polynucleotides and of their CURRENT APPLICATION WUMBER: US/10/238,075
CURRENT PILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003-09-10
PRIOR APPLICATION NUMBER: 0000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1278 AAASAITATANGDVTVASAGKLAAGTTVGVTALNDINVAGAIESNGDAVLNA-QQGSLNA 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1337 TGGINSGA---ELTIT-----TGLDLSLGASTSAVGDVTLNAGRNAILNGTLVGQGNGYI 1388
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 7801-02-16
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llarity 26.8%; Pred. No. 3.7;
Conservative 16; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :99
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ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 39; Conserva
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Best Local Similarity
Matches 51; Conserv
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LENGTH: 1862
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LENGTH: 182
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57 L----ALOSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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US-09-997-182-131
; Sequence 131, Application US/0999182
; Publication No. US2030049263A1
; GENERAL INFORMATION:
; APPLICANT: Nano, Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
; FILE REFERENCE: 61258
; CURRENT APPLICATION NUMBER: US/09/997,182
; CURRENT FILING DATE: 2001-11-28
; PRIOR FILING DATE: 2000-01-03
; PRIOR PILING DATE: 1997-12-15
; PRIOR FILING DATE: 1997-06-15
; PRIOR FILING DATE: 1996-06-14
; PRIOR FILING DATE: 1996-06-14
; PRIOR FILING DATE: 1996-06-15
; NUMBER OF SEQ ID NOS: 169
; SOOFWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
TITLE OF INVENTION: Mamunostimulatory Peptides
FILE REFERENCE: 61257
CURRENT FILING DATE: 2001-11-28
PRIOR PILING DATE: 2001-11-28
PRIOR PILING DATE: 1997-12-15
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR APPLICATION NUMBER: 08/990,823
PRIOR FILING DATE: 1997-12-15
PRIOR FILING DATE: 1995-06-14
PRIOR FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
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24.8%; Pred. No. 3.1;
iive 22; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 943
TYPE: BRT
; ORGANISM: Mycobacterium tuberculosis
US-09-997-182-131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.8%
Matches 39, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KVAAFPAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 KLAALGFIVLLSIGLAS-----AVRVERYSNAQGSGTGSGEGTGSVNGAGAGLG----- 53
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Sequence 131, Application US/0996634

Sequence 131, Application US/0996634

GENERAL INFORMATION:
APPLICANT Nano, Francis
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: 09/497,135
PRIOR PLILING DATE: 2000-01-03
PRIOR FILING DATE: 1997-01-15
PRIOR PLILING DATE: 1996-06-14
PRIOR FILING DATE: 1996-06-14
PRIOR FILING DATE: 1996-06-14
PRIOR PLILING DATE: 1996-06-15
PRIOR PLILING DATE: 1996-06-15
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                                                                                                                                                                                                                                                                                                                                            Length 154;
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                                                                                                                                                                                                                                              ), OTHER INFORMATION: Clone ID: PAT_MRT4530_61390C.1.pep
US-10-437-963-162284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                      11.4%; Score 86.5; DB 16; 23.5%; Pred. No. 0.26; iive 21; Mismatches 56;
         CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162284
LENGTH: 154
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Best Local Similarity 23.5$
Matches 40; Conservative
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                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 39; Conserv
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US-09-996-634-131
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23;

Indels

Length 943;

Gaps 23; Length 943; Indels 11.4%; Score 86.5; DB 10; 24.8%; Pred. No. 3.1; ive 22; Mismatches 73; Query Match
Best Local Similarity 24.8'
Matches 39; Conservative

RESULT 12

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RESULT 15
US-10-383-930-38
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APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
FILE OF INVENTION INVENTION 134A
CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-09
FRIOR FILING DATE: 2000-09-09
FRIOR PRIOR APPLICATION NUMBER: 60/230,347
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR APPLICATION NUMBER: 60/257,531
FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-10-29
FRIOR FILING DATE: 2000-10-29
FRIOR FILING DATE: 2000-10-20
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR APPLICATION NUMBER: 60/209
FRIOR APPLICATION NUMBER: 60/209
FRIOR APPLICATION NUMBER: 60/209
FRIOR APPLICATION NUMBER: 60/209
FRIOR APPLICATION NUMBER: 60/209
FRIOR APPLICATION NUMBER: 60/209
FRIOR APPLICATION NUMBER: 60/209
FRIOR APPLICATION NUMBER: 60/209
FRIOR FILING DATE: 2001-02-09
FRIOR APPLICATION NUMBER: 60/209
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-16
                                    57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 VAGGCALVSAAAAQVTTRVFRNLGL-ANVGEGN-----VGNGNVGNFNLGSANIGNGN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
-SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AAFAAIVVSG-----SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA 56
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11.4%; Score 86.5; DB 12; Length 3300;
Best Local Similarity 24.8%; Pred. No. 17;
Matches 39; Conservative 22; Mismatches 73; Indels 23;
                                                                                                                                                                                                                                        113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                   IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 64369, Application US/10282122A Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Carnudóo, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Yamannoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 64369
LENGTH: 3300
7 AAFAAIWVSG--
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US-10-282-122A-64369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GNGADVGQGADNSTIEL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 TONGFRNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
TITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REPERBNCE: 25669-018
CURRENT APPLICATION NUMBER: US/10/383,930
CURRENT PILING DATE: 2003-03-03-03
PRIOR APPLICATION NUMBER: 60/402,483
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR APPLICATION NUMBER: 60/363,209
PRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 38
IENGTH: 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 1554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                               113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                             IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 85; DB 22.7%; Pred. No. 9; ive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: August 2, 2004, 15:36:10 Job time : 37.8 secs
                                                                                                                                                                                                                                                                  Sequence 38, Application US/10383930 Publication No. US20040127400A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Streptococcus sobrinus
US-10-383-930-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 22.74
Matches 27; Conservative
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- protein search, using sw model

OM protein

Run on:

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Sequence 55, Appliance of Appliance 1, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 31, Appliance 31, Appliance 31, Appliance 32, Appliance 31, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, Appliance 32, App
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US-09-543-407-16

Sequence 16, Application US/09543407

Sequence 116, Application US/09543407

Sequence 116, Aaron P.

APPLICANT White, Aaron P.

APPLICANT Colinson, S. Karen

APPLICANT RAP, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REPRENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16

LENGTH: 151
                                                                                                                                                             Sequence 24, P
Sequence 20, P
Sequence 28, P
                                   Sequence 57, A
Sequence 18,
                                                                                                                                                                                                                                            Sequence 30,
Sequence 34,
                                                                            Sequence 12,
                                                                                                    Sequence 31,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-791-537-29229
US-09-791-537-111372
US-09-791-537-111372
US-09-791-537-111371
US-09-791-537-94843
             9 US-09-543-407-5

US-08-233-642A-57

US-09-543-407-18

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9 US-09-543-407-14

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9 US-09-543-407-24

9 US-09-543-407-24

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9 US-09-522-691-5834

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US-09-739-449-8854
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                                                               August 2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALA........BSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

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Query Match Length DB

Score

Result No.

hits satisfying chosen parameters: 6019581 seqs, 976053577 residues

Total number of

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

US-09-543-407-16 757

Title: Perfect score:

Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

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61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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Sequence 18, Application US/09543407

Sequence 18, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Kazen

APPLICANT: Collinson, S. Kazen

APPLICANT: Kay, William W.

ITLE OF INVENTION: BRESENTAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 653; DB 6; Length 151;
Pred. No. 1.6e-64;
3; Mismatches 13; Indels
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/08/233,642A
PPLICATION NUMBER: US/08/233,642A
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81.6%; Score 618; DB 19; I
Best Local Similarity 76.6%; Pred. No. 1.4e-60;
Matches 131; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                        ATTILING DATE: 26-ABR-1994
CLASSIFICATION: 424
ATTONER/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REBRENCE/DOCKET NUMBER: 920043.403C3
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELESAX: 3723836 SEEDAMBERY
INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
LENGHY: 151 amino acids

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Best Local Similarity 89.4%;
Matches 135; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-233-642A-57
            Washington
                                         RY: U.S.A.
98104-7092
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                                                                                                                                                             Gaps
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: CAY, William W.
TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT PELLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Kay, william W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 58
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 86.9%; Score 658; DB 19; Length 151; Best Local Similarity 90.1%; Pred. No. 4.5e-65; Matches 136; Conservative 3; Mismatches 12; Indels (
                                                                                                                                                         Indels
                                                                          Query Match 100.0%; Score 757; DB 19; Best Local Similarity 100.0%; Pred. No. 3.4e-76; Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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; ORGANISM: Salmonella enteritidis
US-09-543-407-5
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US-09-543-407-16
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Length 151;

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ORGANISM: Salmonella enteritidis
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TYPE: PRT
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                                                                                                               41 PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN 100
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                                                             1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH---
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ION NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL SYSTEM FOR HETEROLOGOUS PEPTIDE SEQUENCES
                                                                                                                                                                                                           101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                      101 ATIDQMNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
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80.1%; Pred. No. 2.6e-56;
tive 7; Mismatches 23;
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|21 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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Sequence 31, Application US/09543407

Sequence 31, Application US/09543407

Sequence 31, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: Obran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, Milliam W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTE

TITLE OF INVENTION: PRESENTATION OF HETEROL

FILE REFRENCE: 92043.407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASISEQ for Windows Version 4.0

SENGTH: 131
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                        MKLLKVAAFAAIVVSGSALAGV
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 80.1<sup>3</sup>
Matches 121, Conservative
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US-09-543-407-12
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                                                                                                             37 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT White, ABRON P.
APPLICANT White, ABRON P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BREEBELAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPRESENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
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     Length 131;
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80.8%; Pred. No. 4.4e-56;
tive 6; Mismatches 23; Indels
                                                         Indels
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US-09-543-407-26

US-09-543-407-26

Sequence 26, Application US/09543407

GENERAL INFORMATION:

APPLICANT White, Aaron P.

APPLICANT Collinson, S. Kaxen

APPLICANT COllinson, S. Kaxen

APPLICANT Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPP

FILE REPERENCE: 920043 406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT RILIGATION UNMBER: 2000-04-05

NUMBER OF SEQ ID NOS: 59
                                                      0
Ouery Match
Best Local Similarity 98.3%; Pred. No. 2.8e-56;
Matches 113; Conservative 2; Mismatches 0;
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Best Local Similarity 80.8
Matches 122; Conservative
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
                                                                                                                        FEATURE:
CTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
CTHER INFORMATION: sequence containing the replacement fragment
CTHER INFORMATION: encoding FT3 from GP63 of Leishmania major.
US-09-543-407-26
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                                                                                                                                                                                                                                                                                         Length 151;
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                                                                                                                                                                                                                                                                                                                                        24; Indels
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76.2%; Score 577; DB 19;
Best Local Similarity 80.8%; Pred. No. 5.7e-56;
Matches 122; Conservative 5; Mismatches 24;
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US-09-543-407-24
Sequence 24, Application US/09543407
GENERAL INFORMATION:
                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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                        SEQ ID NO 26
LENGTH: 151
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RESULT 10 US-09-543-407-20 ; Sequence 20, Application US/09543407

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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, P. TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.40
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICANTON NUMBER: US/09/543,407
CURRENT APPLICANTON NUMBER: US/09/543,407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.8%; Score 574; DB 19; Length 151;
80.8%; Pred. No. 1.2e-55;
ive 6; Mismatches 23; Indels
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Best Local Similarity 80.1%; Pred. No. 5.8e-55;
Matches 121; Conservative 4; Mismatches 26;
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Best Local Similarity 80.83
Matches 122; Conservative
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Length 151;

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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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Sequence 30 Application US/09543407

Sequence 30 Application US/09543407

SERBEAL INFORMATION: Aaron P.

APPLICANT DOTAIN JAMES I.

APPLICANT COllinson, S. Karen

APPLICANT KAY, William W.

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE REFERENCE: 920043.406

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 109
                                                                                                                                                                                                                                                                           43 STLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT
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GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen;
APPLICANT: Collinson, S. Karen;
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
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6300 Columbia Center, 701 Fifth Avenue
                                                                       74.8%; Score 566; DB 19;
80.8%; Pred. No. 9.7e-55;
iive 5; Mismatches 24;
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73.2%; Score 554; DB 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 109; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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ORGANISM: Salmonella enteritidis
                                                                           Query Match
Best Local Similarity 80.8
Matches 122; Conservative
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STATE: Washingto
COUNTRY: U.S.A.
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   US-09-543-407-30
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61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQMNAKNSDITVGQYGG 120
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| Sequence 30, Application US/09543407
| GENERAL INFORMATION:
| APPLICANT: White, Aaron P. |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: KAY, William W. |
| TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| FILE REFERENCE: 920043.406 |
| CURRENT APPLICANTON NUMBER: US/09/543,407 |
| CURRENT PILING DATE: 2000-04-05 |
| NUMBER OF SEQ ID NOS: 59 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Maron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
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APPLICANT: Collinson, S. Caren
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Caren
APPLICANT: Collinson, S. Caren
APPLICANT: Collinson, S. Caren
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                       121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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ORGANISM: Artificial Sequence
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Indels

Length 109;

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16 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG 75
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,642A

FILING DATE: 26-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: King, Joshua

REGISTRATION NUMBER: 35.70

REGISTRATION NUMBER: 35.70

REGISTRATION NUMBER: 35.70

REJERHONE: (206) 622-4900

TELLEFAX: (206) 622-4900

TELLEFAX: (206) 622-6031

TELLEFAX: (206) 626-6031

TELLEFAX: (206) 626-6031

TELLEFAX: (206) 682-6031

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Search completed: August 2, 2004, 15:26:43 Job time : 168.9 secs

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Sequence 2, Appli
Sequence 1453, Appl
Sequence 109, Appl
Sequence 109, Appl
Sequence 69, Appl
Sequence 67, Appl
Sequence 11455, A
Sequence 11455, A
Sequence 11456, A
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                                                                                     2, 2004, 14:49:38; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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3. /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

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3. /cgn2_6/ptodata/2/paa/USO0_NEW_COMB.pep:*
            version 5.1.6
- 2004 Compugen Ltd.
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US-09-741-873C-2
US-10-004-115B-34
US-60-556-841-1453
US-10-784-592-35
US-10-784-592-35
US-10-170-205E-32312
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US-10-170-205E-11455
US-09-806-709-69
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Maximum Match 100%
Listing first 45 summaries
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            GenCore (c) 1993
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Perfect score:
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APPLICANT O'LSEN, Arne
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TITE OF INVENTION'S Fibronectin Binding Protein As Well As Its Preparation
FILE STREEN O'LSES-084
CURRENT FILING DATE: 0200-12-22
FRIOR APPLICATION NUMBER: US 08/974,873
CURRENT FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-04
PRIOR FILING DATE: 1998-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-03
PRIOR FILING DATE: 1991-05-04
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
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PRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 4
FUNDALL: 151
Sequence 5, Appli
Sequence 52, Appl
Sequence 7905, Ap
Sequence 7905, Ap
Sequence 3413, Ap
Sequence 19565, A
Sequence 2, Appli
Sequence 78, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 12923, A
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Sequence 255, App
Sequence 24, App
Sequence 20202, A
Sequence 218336,
Sequence 6541, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels
US-10-872-769-5

US-60-56-63-7905

US-60-56-63-7905

US-60-579-062-7905

US-10-1170-208-3413

US-10-1170-208-3413

US-09-248-796A-19565

PCT-US04-12070-2

PCT-US04-1277-7

PCT-US04-1277-7

US-10-831-070-78

US-60-56-841-1245

US-60-556-841-1245

US-10-748-796A-20202

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US-10-1425-115-218336

US-10-1425-115-23328
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                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4; Application US/09741873C GENERAL INFORMATION:
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; TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-873C-4
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Matches 100; Conservative
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30; Gaps

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60 QSDARKSETTITQSGYGNGADV----GQGADNSTIBLTQNGFRNNATIDQWNAKNS--- 111
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                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQY-GSANAALAL
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12.3%; Score 93; DB 6; Length 348;
Best Local Similarity 24.8%; Pred. No. 0.43;
Matches 40; Conservative 26; Mismatches 65; Indels
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11.1%; Score 84; DB 7; Length 385;
Best Local Similarity 25.9%; Pred. No. 3.7;
Matches 30; Conservative 21; Mismatches 53; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 145.1

Sequence 145.1

GENERAL INFORMATION:

APPLICANT: Abad, Mark S.

APPLICANT: Abad, Mark S.

TITLE OF INVENTION: Genes and Uses for Plant Improvement

FILE REPERBOR: 38-21/53450)

CURRENT APPLICATION NUMBER: US/60/556,841

CURRENT FILING DATE: 2004-03-25

NUMBER OF SEQ ID NOS: 12463

SEQ ID NO 1453

LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 LIDLAHAGIFDISVETFSLDNGAEAYRRLAAGTLSGRAVVV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 ------DITVGQYGGNNAA----LVNQTASDSSVMV 137
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NAME/KEY: SIGNAL
LOCATION: (1). (49)
FEATURE:
NAME/KEY: (50). (597)
OTHER INFORMATION: multi copper oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT CORGANISM: Corynebacterium sp. ST-10 US-60-556-841-1453
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APPLICANT: Wilting, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-60-556-841-1453
US-10-004-115B-34
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US-10-784-592-35
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                                      US-V9-741-81/C-Z
US-V9-741-81/C-Z
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT FILING DATE: 2000-12-22
FRICH REPPLICATION NUMBER: US 09/741,873C
CURRENT FILING DATE: 1998-08-06
FRICH REPLICATION NUMBER: US 08/978,878
FRICH RELING DATE: 1998-05-06
FRICH REPLICATION NUMBER: US 08/978,878
FRICH RELING DATE: 1999-11-26
FRICH RELING DATE: 1999-11-26
FRICH RELING DATE: 1999-11-06
FRICH RELING DATE: 1991-11-06
FRICH RELING DATE: 1991-11-06
FRICH RELING DATE: 1991-11-06
FRICH RELING DATE: 1991-11-03
FRICH RELING DATE: 1991-11-03
FRICH RELING DATE: 1991-11-03
FRICH RELING DATE: 1991-01-28
FRICH RELING DATE: 1994-01-28
FRICH RELING 
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APPLICANT: ASAKO, HIROYUKI
APPLICANT: ASAKO, HIROYUKI
APPLICANT: SHIMZU, MASATOSHI
APPLICANT: SHIMZU, MASATOSHI
APPLICANT: SHIMZU, MASATOSHI
APPLICANT: HITO, NOBUYA
APPLICANT: WAKITA, KTUHEI
ITILE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
TITLE OF INVENTION: PROCESS 10/004,115B
CURRENT APPLICATION NUMBER: US/10/004,115B
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: UP 2001-06144
PRIOR APPLICATION NUMBER: UP 2001-06144
PRIOR PELING DATE: 2001-01-15
PRIOR PELING DATE: 2001-01-15
PRIOR PELING DATE: 2001-01-15
PRIOR PELING DATE: 2001-06-11
PRIOR SPELING DATE: 2001-06-11
PRIOR SPELING DATE: 2001-06-11
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PATENTIN Ver: 3.2
SOFTWARE: PATENTIN VER: 3.2
LENGTH: 3R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-10-004-115B-34
Sequence 34, Application US/10004115B
GENERAL INFORMATION:
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ORGANISM: Corynebacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 79; Conserv
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12; Gaps

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; Sequence 32312, Application US/10170205E; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 TTIDEYSDNNPSFTDDSSGDES 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 366, Application US/10501035; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-170-205E-32312
                                                                                                                                                                                                                                             RESULT 7
US-10-170-205E-32312
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Indels 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 -----KSETT-----ITQSGYGNG----AD-VGQGADNST-----IELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSS------VMVRQVGFGN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.8%; Score 82; DB 6; Length 1236; Best Local Similarity 26.0%; Pred. No. 25; Matches 39; Conservative 16; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE LOCATION: (514). (514)
OTHER INFORMATION: putative copper binding site
LOCATION: (139)..(139)
OTHER INFORMATION: putative copper binding site
FEATURE:
                                                                                                                                                                      NAME/KEY: MISC FEATURE
LOCATION: (1817., (181)
OTHER INFORMATION: putative copper binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE

LOCATION: (566)...(566)

/ OTHER INFORMATION: putative copper binding site

US-10-784-592-35
                                                                                                    LOCATION: (141)...(141)
OTHER INFORMATION: putative copper binding site
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT' Mid-robial Technics Limited
APPLICANT' Mid-robial Technics Limited
APPLICANT:
Hansbro, Fhilip M
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT FILING DATE: 2004-06-23
CURRENT FILING DATE: 2004-06-23
FRICR APPLICATION NUMBER: US/09/769/778
FRICR APPLICATION NUMBER: US/09/769/778
FRICR APPLICATION NUMBER: US/09/769/778
FRICR PILING DATE: 1998-03-27
FRICR PILING DATE: 1998-03-27
FRICR PILING DATE: 1998-03-27
FRICR PILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PARCENT IN VET: 2.1
                                                                                                                                                                                                                                                              NAME/KEY: MISC FEATURE LOCATION: (183). (183) OTHER INFORMATION: putative copper binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pneumoniae
                                                                                   NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 109
LENGTH: 1236
TYPE: PRT
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US-10-873-528-109
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16 GSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYG-SANAALALQSDARK-.

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APPLICANT Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINAS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TILE REPERENCE: DOINGS FOT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT PILING DATE: 2004-07-09
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: PATHWAYE: Actenin version 3.2
SOFTWARE: Actenin version 3.2
SEQ ID NO 366
LENGTH: 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEVICES, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION NUMBER: US/206-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 32312
LENGTH: 1158
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                                                                                                                    295 DKNGRQVLSYNTSIMTTQGSGYTWGNGAQMNGFFAKKGYGLISSWTVPIT--GTDTSFTF 352
                                                                      -----SETTITQ-SGY--GNGADV------GQGADNS-TIBLTQNGFRNNATI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 RLAAMARLQENGOKDVGSY----QLPKGMSSHINGQARTSSSKIMASKSSATVFQNPMG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 KSETTITQSGYGNGAD---VGQGADNS-----TIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 IIPSSPKNAGYKNSLERNNIKQAANNSLLLHLLKSQTIPKPMNGHSHSERGSIFEESSTP 411
235 GSKLIFTYTVTYVNPKTNDLGNISSMRPGYSIYNSGTSTQTMLTLGSDLGKPSGVKNYIT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDAR 64
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10.8%; Score 81.5; DB 6; Length 11
Best Local Similarity 21.1%; Pred. No. 26;
Matches 30; Conservative 28; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Indels
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Best Local Similarity 21.1%; Pred. No. 26;
Matches 30; Conservative 28; Mismatches 67;
                                                                                                                                                                                                                         104 DOWNAKNSDITVGQYGGNNAALVNQTASDS 133
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                                                                                 352 IIPSSPKNAGYKNSLERNNIKQAANNSLLLHLLKSQTIPKPNNGHSHSERGSIFEESSTP 411
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INPLUENZAE HIGH
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
TITLE OF INVENTION NUMBER: US/09/0038
FILE REPRENCE: 1038-1138 MIS
CURRENT APPLICATION NUMBER: D67/CA99/00938
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-11-08
PRIOR FILING DATE: 1998-11-08
PRIOR APPLICATION NUMBER: 09/206,942
PRIOR APPLICATION NUMBER: 09/206,942
PRIOR PLING DATE: 1999-11-08
                                                                                                                                                                                                                                                                                                                                              APPLICANT: YANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: PROTECTIVE WEIGHT PROTEINS
FILE REFERENCE: 1038-1138 MIS
CURRENT APPLICATION NUMBER: US/09/806, 709
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: PCT/CA99/00938
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR FILING DATE: 1998-10-07
PRIOR PLING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN VET. 2.1
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727 TGSILGGIESSSGSVTLTATEGALAVSNISG--NTVTVTANSGALTTLAGSTIKGTESVT
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                                                                                                                                113 ITVGQYGGNNAALVNQTASDSS 134
                                                                                                                                                              TTIDEYSDNNPSFTDDSSGDES 433
                                                                                                                                                                                                                                                                                 Sequence 69, Application US/09806709
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
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Sequence 1130, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: CAPTURE, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT PAPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Parentin version 3.2
SEQ ID NO 1130
LENGTH: 503
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US-10-106-205E-11455
US-10-170-205E-11455, Application US/10170205E
| GENERAL INFORMATION:
| APPLICANT: ADAMS, Mark |
| TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF |
| TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF |
| TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF |
| TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF |
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| TITLE OF INVENTION: CAPTURE AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGENTS AGEN
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                                                                                                                                                                                                                                                                                                    10.6%; Score 80.5; DE 26.4%; Pred. No. 46; cive 22; Mismatches
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                                                                                                                                                                         ; ORGANISM: Haemophilus influenzae US-09-806-709-67
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Best Local Similarity 26.4%
Matches 39; Conservative
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Best Local Similarity
Matches 35; Conserv
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US-10-170-205E-11130
SOFTWARE: Pater
SEQ ID NO 67
LENGTH: 1536
TYPE: PRT
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144 YGEHWRQARKLVTAHLFTVKRVHSYRRARKEEVRLVVAKVREAAVAGTATDMS---LAMN 200
                                                                                                                                                                                                                                                                                                                                                                                   60 QSD----------ARKSETTITQSGYGNGADVGQGADNSTIELTQN
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10.6%; Score 80; DB 6; Length 546;
Best Local Similarity 27.2%; Pred. No. 14;
Matches 34; Conservative 14; Mismatches 43; Indels
                                                                                                           ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_94013C.1.pep
US-10-425-115-362763
                     FEATURE: | NAME/KEY: unsure LOCATION: (1)..(546) OTHER INFORMATION: unsure at all Xaa locations
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US-60-579-902-7335
  ORGANISM:
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Sequence 11456, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Parentin version 3.2
SOFTWARE: Parentin version 3.2
SEQ ID NO 11456
LENGTH: 503
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103-10-425-115-362763, Application US/10425115
15 Gequence 362763, Application US/10425115
15 Gequence 362763, Application US/10425115
16 GENERAL INFORMATION:
17 APPLICANT: La Rosa, Thomas J.
18 APPLICANT: Cao, Youguei
18 APPLICANT: Cao, Yongwei
19 APPLICANT: Cao, Yongwei
10 TITLE OF INVENTION: Plants
10 TITLE OF INVENTION: Plants
10 TITLE OF INVENTION: Plants
11 CURRENT APPLICATION UVMBER: US/10/425,115
11 CURRENT FILING DATE: 2003-04-28
12 NUMBER OF SEQ ID NOS: 369326
13 SEQ ID NO 362763
14 TYPE: PRT
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                                                                                                                                     Gaps
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                                                                                        ; Score 80; DB 6; Length 503;
; Pred. No. 13;
14; Mismatches 53; Indels
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                                                                                        Query Match
Best Local Similarity 28.2%;
Matches 35; Conservative 1.
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Best Local Similarity 28.2%
Matches 35; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-11130
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; ORGANISM: Homo sapiens
US-10-170-205E-11456
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474 HDEL----SYORKHKFQLNLSQNLSDYGSIYVSGYLQDDWGSRSTTRSLNVGYSVNYAD 528
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Sequence 7335, Application US/60579902
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Wu, Wei
TITLE OF INVENTION: Nucleotide and Amino Acid Sequences from Xenorhabdus;
TITLE OF INVENTION: Nucleotide and Amino Acid Sequences from Xenorhabdus;
TITLE OF INVENTION: 18-21 (53444) A
CURRENT APPLICATION NUMBER: US/60/579,902
NUMBER OF SEQ ID NOS: 14985
SEQ ID NOS: 14985
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Best Local Similarity 25.2%; Pred. No. 24;
Matches 36; Conservative 24; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 2, 2004, 15:29:52
Job time : 18.8 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 LVNQTASDSSVM--VRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 GLSGTALDGNVLGYSLQQRYGNN 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Xenorhabdus bovienii
US-60-579-902-7335
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec Run on:

US-09-543-407-16 757 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
2: pir1:*
3: pir2:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

ga & 8

outer membrane pro	hypothetical prote	prc	probable PPE prote	atio	nucleoskeletal-Īik	probable PPE prote	ice nucleation pro	hypothetical prote	hypothetical prote	paracrystalline su	S-layer protein Rs	hemolysin (importe	cell wall surface	hypothetical prote	딦	
\$21408	C29349	C86266	D70575	A25547	S14055	E70969	SNPSO	869589	T32020	A48995	C87374	AI0452	E95206	C90739	E85589	
7	7	7	7	7	N	N	Н	N	0	7	N	N	~	N	7	
331	455	573	3300	1210	823	3716	1200	528	534	1026	1073	1635	4776	760	760	
11.5	11.5	11.5	11.4	11.3	11.1	11.1	11.0	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	
	87	87	86:5	85.5 85.5	84	84	83.5	82	85	82	85	82	82		i.	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

ж.р. н	RESULT 1 JC66039 Finhyin nyotain arfa nyaquyeov . Galmonalla antaritidia
100	Limini process gara predictor. C.Species: Salmonolla enteritidis C.Sate: 31-Dec-1996 #sequence revision 31-Dec-1996 #text change 08-Oct-1999
	Accession: JC6039, PC6015, A44898
¥ b	k;collinson, s.k.; cloutnier, s.c.; boran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996
ৰ ব	A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039: MUID:96146512: PMID:8550497
4	A, Accession: JC6039
4 4	A;Molecule type: DNA A;Residues: 1-151 <col/>
4.	A, Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714
4 4	A;Accession: recul.
4	A;Residues: 21-52 <cc2></cc2>
A.	
ξ α	A;NOCE: THE AUTHORS TERBIZICED THE COOD AUG TOT FESTICE 4 AS ILE R:COllingon S.K. FRANCAY I. Miller K H Trief T T Kay W W
; b	7. Bacteriol: 173, 4773-4781, 1991
Æ	A, Title: Purification and characterization of thin, aggregative fimbriae from Salmonell
4	Reference number: A44898; MUID:91310586; PMID:1677357
A F	A; Contents: 27655
₹ •	A; Accession: A444898
4,4	Afstatus: preliminary
	Afrocacute type: protectin A:Residues: 21-33 <co3></co3>
A	A;Note: sequence extracted from NCBI backbone (NCBIP:45936)
υ	C, Genetics:
۷ 	A;Gene: agfA;
0	C; Function:
4 , A	A;Description; major component of thin aggregative fimbriae a. Note: fimbrise bind to fibronectin misseminomer figure misseminomer setimetor
	de: fimbria
) [14	Fil-20/Domain: signal sequence #status predicted <sig></sig>
ш	;21-151/Froduct: fimbrin protein agfA #status experimental <mat></mat>
	ביסי לסופקד למרבילה כן הדפוומרטונפט בלים מלקם ס', פקלם
δ	/ MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
qq	: ::

csg;

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Curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C.Species: Escherichia coli (5Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C.Accession: D90806 C.Accession: D90806 C.Accession: D80806 C.Accession: T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A; Shiba, T.; Hattori, M.; Shinagawa, H. A; Pitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A; Accession: D90806 A; Ascession: D90806 A; Astatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Doscription: major component of wild-type curli; interaction between CsgA and CsgB trianscription: are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogeni, in the absence of CsgA, CsgB can self-assemble into polymers
F:1-20/Domain: signal sequence #status predicted <SiG>
F:21-151/Product: curlin #status experimental <MAT>
A,Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A,Reference number: S31202; MUID:93211294; PMID:8459772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:913360880; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-133,'RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.9%; Score 484; DB 2;
66.9%; Pred. No. 2.7e-36;
iive 18; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.7%; Score 474.5; DB 65.8%; Pred. No. 2e-35; cive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 21-45-44-50 <0LS2>
R;Olsen, A.N.; Arngvist, A.M.
submitted to the EMBL Data Library, October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                  A; Accession: 331202
A; Molecule; type: DWA
A; Residues; L'6, VV, 8-151 <OLS1>
A; Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity 66.9
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S34559
A;Accession: S34559
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A;Residues: 1-152 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 23.15
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Best Local Simi
Matches 100;
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A,Note: the mucleotide sequence was submitted to the EMBL Data Library, August 1995
R,Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617; PMID:9278503
A,Recession: G64846
A,Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                Cyactes (2) Accession: Alo635
RyParkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L. T.; Connectron, P.; Connectron, P.; Connectron, P.; Connectron, P.; Connectron, P.; Connectron, P.; Connectron, P.; Connectron, P.; O'Gaora, P. Nature 413, 848-852, 2001
Ayathors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Athachers: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; A; A; Competer genome sequence of multiple drug resistant Salmonella enterica servy A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Accession: A10635
A; Anchoeule type: DNA
A; Residues: 1-151 < PAR>
A; Residues: 1-151 < PAR>
A; Residues: 1-151 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
G; Genetics:
A; Gene: STX1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      curlin protein csgA precursor - Escherichia coli (strain K-12)
NyAlternate names: csgA protein; major curlin protein
C;Species: Escherichia coli
C;Daccies: L2-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70788; Gs4846; S31202; S34550; S34559
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18; 661-670, 1995
A;Title: Expression of two csg operons is required for production of fibronectin- and A;Title: canmber: S70783; MUID:96414468; PMID:8817489
                                                                                                                                                                          major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Cybocies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi .
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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A;Molecule type: DNA
A;Residues: 1-151 <HAM>
A;Residues: 1-151 <HAM>
A;Coss-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 658; DB 2; Lt
Pred. No. 7.5e-52;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNOTASDSSVMVROVGFGNNATANOY 151
             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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ilarity 90.1%;
Conservative
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Best Local Similarity
Matches 136; Conserv
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us-09-543-407-16.rpr

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A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Genetics:
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             minor curlin, subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, subs C;Species: Bscherichia coli C;Date: 18-uh-2001 #sequence_revision 18-Juh-2001 #text_change 18-Juh-2001 C;Accession: C90806 B:Hayashi, T:; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A;Reference mumber: A99629; MUID:21156231; PMID:11258796 A;Accession: C90806 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-151 < HAX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain 0157:H C;Species: Escherichia coli (5pecies: Escherichia coli (5pecies: Escherichia coli (5pecies: Escherichia coli (5,Species: Escherichia coli (5,Species: Escherichia coli (5,Species: Escherichia coli (5,Species: Escherichia coli (1,Species: Escherichi
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 MAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 118.5; DB 2; Length 151; ; Pred. No. 0.0014; 13; Mismatches 62; Indels . 5;
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1 Similarity 31.6%;
37; Conservative 1
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Best Local S
Matches 37
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R; Hammar, M.; Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S.

Mol. Microbiol. 18, 661-670, 1995

A; Title: Expression of two csg operons is required for production of fibronectin- and CC
A; Reference number: S70783; MUID:96414468; PMID:8817489

A; Reference number: S70783; MUID:96414468; PMID:8817489

A; Reference number: S70783; MUID:96414468; PMID:8817489

A; Reference number: S70783; MUID:96414468; PMID:8817489

A; Reference number: S70783; MUID:9147558; PIDN:CAA62281.1; PID:91147563

A; Roseidues: 1-151 cHAM>
A; Residues: 1-151 cHAM>
A; Roseidues: EMBL:X90754; NID:91147558; PIDN:CAA62281.1; PID:91147563

A; Experimental source: strain K12, substrain W3110

A; Experimental source: strain K12, substrain W3110

A; Rose: D.J; Mau, B.; Shao, Y.
Science 277, 1452-1462, 1997

A; Itle: The complete genome sequence of Escherichia coli K-12.

A; Roseidues: A64720; MUID:97426617; PMID:9278503
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A)Residues: 1-152 <STO>
A)Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z16
A)Experimental source: strain 0157:H7, substrain EDL933
C)Genetics:
A)Gene: csgA
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DALATA
A;Residues: 1-151 <BLATA
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C,5pecies Escherichia coli C,5pecies Escherichia coli C,5pecies Escherichia coli C,5pecies Escherichia coli C,Accession: H85665
C,Accession: H85665
No.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Altitles Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A88480; MUID:21074935; PMID:11206551
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N;Alternate names: csgB protein; curlin nucleation component; minor curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70787; F64846
119
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65.8%; Pred. No. 2e-35;
ive 19; Mismatches 32;
                                                                                                                                                                                                                                   152
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                                                                                                                                       120 GNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                             Query Match 62.77
Best Local Similarity 65.8
Matches 100; Conservative
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A;Status: preliminary
A;Molecule type: DNA
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A; Description: catalyzes the hydrolysis of peptide bonds between two hydrophobic residus A; Note: the activated form can activate the proenzyme form C; Superfamily: leishmanolysin
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N;Alternate names: surfase endopeptidase glycoprotein gp63
C;Species: Leishmania donovani
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jan-2000
C;Accession: A45621
                                                                                                                                                                                                                                                                                                                                                                                     GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISO
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A;Molecule type: DNA
A;Residues: 1-590 (MEB>
A;Experimental source: LV9
A;Note: sequence extracted from NCBI backbone (NCBIN:74958, NCBIP:74959)
                                                                                                                                                                                                                                                                                                GSANAALALOSDARKSE-----TTITQSGYGNGADVGQ-GADNST--
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Mol. Biochem. Parasitol. 48, 173-184, 1991
A;Title: Heterogeneity of the genes encoding the major s
A;Reference number: A45621; MUID:92107220; PMID:1762629
A;Accession: A45621
                                                                                                                 ; Score 111.5; DB 2; Pred. No. 0.0057; 17; Mismatches 46
                                                                                                                      14.7%;
30.5%;
                                                                                                                                                                                                           Conservative
                                                                                                                                                                Similarity
                                                                                                                                                                                                           36;
                                     A;Gene: STY1180
                                                                                                                          Query Match
Best Local
C,Genetics:
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A.Note: this species has also been called Salmonella typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C.Accession: AH0635
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, P.P. Connetton, P.; Cronin, A.; Davis, P.; Daviss, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.;Althors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.;Althors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A. A.;Althors: A.
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R; Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
A; Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A; Reference number: JC6039; MUID:96146512; PMID:8550497
A; Reference number: JC6040
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 NGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                    MAHASGPDSTLS1YQYGSANAALALQSDARKSETT1TQSGYGNGADVGQGADNST1ELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
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                                                                                                                                                                          Length 151;
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source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 111.5; DB 2;
llarity 30.5%; Pred. No. 0.0057;
Conservative 17; Mismatches 46;
                                                                                                                                                                     15.7%; Score 118.5; DB 2; ilarity 31.6%; Pred. No. 0.0014; Conservative 13; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 36, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
Residues: 1-151 <PAR>
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                                                                                                                                                                                        Local Sim.
    A; Experimental
                                                                                                                                                                          Query Match
Best Local S:
Matches 37
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                                          C;Genetics:
A;Gene: csgB
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surface glycoprotein of Leishman

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#status
fide bond
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C,rcycurds: blocked carboxyl end; cell adhesion; glycoprotein; hydrolase; lipoprotein; C,rcycurds: blocked carboxyl end; cell adhesion; glycoprotein; hydrolase; lipoprotein; F;1-39/Domain: signal sequence #status predicted <SIG>F;40-87/Domain: activation peptide #status predicted <ATP>F;80-55/Product: leishmanolysin #status predicted <AMP>F;86-590/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;81,255,321/Binding site: zinc, catalytic (Cys, His, His, His, His) (inhibited) #status F;251,255,321/Binding site: zinc, catalytic (His) (active) #status predicted F;251,255,321/Binding site: zinc, catalytic (His) (active) #status predicted F;257,321/Binding site: carbohydrate (Asn) (covalent) #status predicted F;555/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ი</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SETTITOS--GYGNGA-----DVGQGADNSTIELTQNGFRNNATIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 AVGVINIPAANIASRYDQLVTRVVTHEMAHALG----FSVVFFRDARILESISNVRHKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 DVPVINSSTAVAKAREQYGCGTLEYLEMEDQGGAGSAGSHIKM-----RNAQ-DELMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 590;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.4%; Score 101.5; DB Best Local Similarity 28.8%; Pred. No. 0.24; Matches 46; Conservative 20; Mismatches
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A;Cross-references: GB:Z82098; GB:AL123456; NID:g3261664; PIDN:CAB05045.1; PID:e280737; A;Experimental source: strain H37Rv C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-U1-1998 #sequence_revision 17-U1-1998 #text_change 15-Sep-2003
C;Date: 17-U1-1998 #sequence_revision 17-U1-1998 #text_change 15-Sep-2003
C;Dates: 17-ISTOSCH, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Nature 393, 537-54, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Accession: F70675
A;Accession: F70675
             F;122-139,188-227,311-383,390-451,403-422,412-486,463-507,512-562,532-555/Disulfide F;261,265,331/Binding site: zinc, catalytic (His) (active) #status predicted F;263/Active site: Glu #status predicted (F:263/Active site: Glu #status predicted (Asn) (covalent) #status predicted F:394/Binding site: carbobyydrate (Asn) (covalent) #status predicted F:574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature are 57574/Modified site)
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R.Medina-Acosta, E.; Karess, R.E.; Russell, D. submitted to the EMBL Data Library, February 1992 A.Bescription: Structurally distinct genes for the surface prot A.Reference number: S19916
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R;Ramamoorthy, R.; Donelson, J.E.; Paetz, K.E.; Maybodi, M.; Roberts, S.C.; Wilson, M.E. Biol. Chem. 257, 1888-1895, 1992
A;Title: Three distinct RNAS for the surface protease gp63 are differentially expressed A;Reference number: A42049; MUID:92112918; PMID:1370484
A;Accession: B42049
A;Accession: B42049
A;Accession: B42049
A;Residue: preliminary
A;Molecule Lype: mRNA
A;Residues: 1-599 <RAM>
A;Cross-references: GB:M80669; NID:g159324; PIDN:AAA29236.1; PID:g159325
C;Function:
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A; Residues: 1-599 < MIL.>

A; Residues: 1-599 < MIL.>

A; Residues: 1-599 < MIL.>

A; Cross-references: GB: M28527; NID: 9159322; PIDN: AAA29235.1; PID: 9159323

R; Ramamoorthy, R.; Donelson, J.E.; Paetz, K.E.; Maybodi, M.; Roberts, S.C.; Wilson, M.E..

C Biol. Chem. 257, 1888 1895; 1992

A; Title: Three distinct RNAs for the surface protease gp63 are differentially expressed

A; Reference number: A42049; MUID: 92112918; PMID: 1370484
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N;Alternate names: glycoprotein gp63; surface metalloproteinase, log phase
C;Species: Leishmania chagasi
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Jan-2000
C;Accession: A44951; A42049
R;Miller, R.A.; Reed, S.G.; Parsons, M.
Mol. Biochem. Parasitol. 39, 267-274, 1990
A;Title: Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Gly-Asp
A;Reference number: A44951; MUID:90205976; PMID:2320059
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A.Note: the activated form can activate the proenzyme form
C.Superfamily: leishmanolysin of the proenzyme form
C.Keywords: blocked carboxyl end; cell adhesion; glycoprotein; hydrolase; lipoprotein;
F.1-39/Domain: signal sequence #status predicted <archive.
F.40-97/Domain: activation peptide #status predicted <ARP>
F.98-574/Product: leishmanolysin #status predicted <ARP>
F.575-599/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F.48,261,265,331/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
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A; Residues: 1-599 «RAM»
A; Crossreferences: GB: M86672; NID:g159328; PIDN:AAA29238.1; PII
A; Note: sequence extracted from NCBI backbone (NCBIN:76040, NCBI
A; Note: the source is designated as Leishmania donovani chagasi
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13.1%; Score 99.5; DB 1; Length 646;
Best Local Similarity 30.8%; Pred. No. 0.4;
Matches 40; Conservative 15; Mismatches 66; Indels
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August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec US-09-543-407-16 757 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence: Run on:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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NCBI_TaxID=562;
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                                                                                  01-DEC-1992
01-OCT-1996
                                    CSGA ECOLI
P28307;
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SEQUENCE 1
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEPECTESS-S.entertidis; STRAIN=27655-3B;
MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
Collinson A.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from "Salmonella enteritidis.";
Dacteriol. 173:4773-4781(1991).
-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
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                                                                                    SEQUENCE FROM N.A. STRAIN=27655-3B; SPECIES=8. entertidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthler S.C., Doran J.L., Banser P.A., Kay W.W.; "Salmonella entertidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                      SEQUENCE OF 21-151 FROM N.A.
SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE-94013373; PubMed-81049646-810.
Doran J.L. Collinson S.K., Buttan J., Sarlos G., Todd B.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic testes for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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Pred. No. 4.9e-50;
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    Bacteriol. 178:662-667(1996).

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MEDLINE=91310586; PubMed=1677357;
Collineon S.K., Emcedy L., Trust T.J., Kay W.W.;
Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991)
J. Bacteriol. 173:4773-4781(1991)
J. Bacteriol. STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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Oshima T., Alba H., Baba T., Fuljita K., Hayashi K., Honjo A.,
Oshima T., Alba H., Baba T., Fuljita K., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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STRAIN=K12 / W3110;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A.;
"The RpoS signa factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding curli
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MEDLINE=97426617, PubMed=9278503,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                    Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
                                                              (Rel. 24, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
151 AA.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.";
Mol. Microbiol. 7:523-536(1993)
                                                                                                                                                                                      Major curlin subunit precursor
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
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STRAIN=K12 / MG1655;
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                         1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTH-EMAHASGPDSTLSIYQYGSANAALAL
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MEDLINE=96414468; PubMed=8817489;
Hammar M., Anqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of
fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                    COLÍED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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01-FBE-1995 (Rel. 31, Created)
01-FBE-2099 (Rel. 34, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor.
CSB OR B1041 OR 21675 OR ECS1419.
Bscherichia coli ol57:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.7%; Score 474.5; DB 1; Length 152; 65.8%; Pred. No. 3.2e-34; ive 19; Mismatches 32; Indels 1;
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nes 32; Indels
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EMBL; AP005315; AAG55788.1; -.
EMBL; AP005554; BAB34843.1; -.
PIR; D90806, D90806.
PIR; H85665; H85665.
Finbria; Signal; Complete proteome.
SIGNAL 21 152 BY SIMILARITY.
CHAIN 21 152 MAJOR CURLIN SUBUNIT; CHAIN 152 AA; 15099 MW; EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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Best Local Similarity 65.8
Matches 100; Conservative
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   [3]
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                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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STRAIN=0157:H7 / ATCC 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli 0157:H7.",
Appl. Environ. Microbiol. 67:2367-2370(2001).
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BOBLINE=21074955;
Perna N.T., Plunkett G. III, Buzland V. Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of entrohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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A -> E (IN REF. 1).
C003470D208D395F CRC64;
   SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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Last annotation update)
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EcoGene; EG11489; csgA.
Fimbria; Signal; Complete proteome.
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CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                             EMBL, AE000205; AAC74126.1; -.
EMBL, D90741; BAA35832.1; -.
EMBL, D90742; BAA35840.1; -.
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28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last anno
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                                                                                                                                                                                                                                                                                                      L04979; AAA23616.1; -. X90754; CAA62282.1; -.
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Q93U24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7 / KIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Chnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara M., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arngvist A., Olsen A., Normark S.,

*Sigma S-dependent growth-phase induction of the csgBA promoter in

*Sigma S-dependent growth-phase induction of the csgBA promoter in

*Escherichia coli can be achieved in vivo by sigma 70 in the absence

of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).

-: FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE

COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH

TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO

FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                             STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-O157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao, Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                         Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 27:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95157246; PubMed=7854117;
                                       Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-21 FROM N.A. STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          Gregor J., La.
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or send an email to license@isb-sib.ch).

EMBL; X90754; CAA62281.1; -.

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                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                         35 MAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQ 94
                                                                                                                                                                                                                                                                                                                                                                                 73
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-!- FUNCTION: CURLIN 187 THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERRYTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRORECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.

-!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
STRAIN=TY2 / ATCC 700931;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baken S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Hien T.T., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Goora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete ganome sequence of a multiple drug resistant Salmonella enterica serovar Typhi. CT18.",
                                                                                                                                                                                                                                                                                                                                                                               18 IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
                                                                                                                                                                                                                                                                                                   5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     95 NGFRUNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                 151 MINOR CURLIN SUBUNIT.
15882 MW, B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                            15.7%; Score 118.5; DB 1;
31.6%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA
                                                                                                                                                                                                                                                                                                   13; Mismatches
                                                                                                                                                                                    POTENTIAL.
                                                                                                                                     EcoGene; EG12621; csgB.
Fimbria; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21534947; PubMed=11677608;
EMBL; AE000205; AAC74125.1; -.
EMBL; AB0741; BAA55831.1; -.
EMBL; AE005515; AAG55787.1; -.
EMBL; AP002554; BAB34842.1; -.
PIR; C98066; C98066.
PIR; C98066; C98066.
PIR; S70787; S70787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                     22 1
151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SALTI
                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                        GSANAALALQSDARKSE----TITIQSGYGNGADVGQ-GADNST-----IELTQ 94
                                                                                                                                                                                                                                                                                                        14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                            129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPACE STRUCTURES THAT ASSEMBLE PREPERENTIALLY AT GROWTH TEMPERATURES BELOW 3.7 DEGREES CELSTIGS. CURLI. CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=S. typhimurium, STRAIN=SR-11;
SPECIES=S. typhimurium, STRAIN=SR-11;
MEDIJNE=99117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium an "Curli fibers are highly conserved between Salmonella typhimurium an Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                          NGFRNNATIDOWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                            EGENNRAKVDQ--AGNYNPAYIEQIGNANDASISQSAYGNSAAIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
NCBL_TaxID=602, 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                       DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  minor subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720,
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                   161C54326E573495 CRC64;
                                                                                                                                                     MINOR CURLIN SUBUNIT
                                                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 111.5; DB Pred. No. 0.0058;
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                                                                                                                                                                                                                                      17; Mismatches
institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
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                                                                                                                                    POTENTIAL
                                                                             EMBL, AL627269; CAD08267.1; -.
EMBL; AE016840; AA069400.1; -.
Fimbria; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fimbriae.";
J. Bacteriol. 178:662-667(1996).
-!- FUNCTION: CURLIN IS THE STRI
                                                                                                                                                                     151 AA; 16254 MW;
                                                                                                                                                                                                     14.7%;
30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
                                                                                                                                                                                                                                       36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURLIN MONOMERS.
SIMILARITY: BELONGS
                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                       Query Match
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                                                                                                                                                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGGNNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Lessmanna donovan...;

Mol. Biochem. Parasitol. 48:173-184(1991).

I. FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala-Tyre | Leu-Lys-Lys-Lys-Lys-Lope...

COFACTOR: Binds 1 zinc ion per subunit (By similarity).

SUBCELLULAR LOCATION: Attached to the membrane by a GP1-anchor.

SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leishmania donovani.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=LV9;
MEDINE=92107220; PubMed=1762629;
MEDINE=9210720; Button L.L., McMaster R.W.;
Webb J.R., Button L.L., McMaster R.W.;
"Heterogeneity of the genes encoding the major surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                      ; DB 1; Length 151; .0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST---
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                               COFC5430E6DD361D CRC64;
                                                                                                                                                               EMBL, AJ002301; CAA05316.1; -.
EMBL, AE008749; AAL20073.1; -.
EMBL, U43280, AAC43598.1; -.
SLYGENE; SG10609; CSGB.
Simbria; Signal; Complete proteome.
Fimbria; Signal; Complete proteome.
CHAIN.
22 151 MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    590 AA
                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 111.5;
30.5%; Pred. No. 0.00
iive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                 16182 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M60048; AAA29244.1; -. HSSP; P08148; 11ML.
                                                                                                                                                                                                                                                                                                                                                                                                             36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Leishmania donovani
Mol. Biochem. Parasitol
                                                                                                                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEIDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Query Match
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ID GP63_LE
AC P23223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDAR--- 64
"Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishmania donovani chagasi promastigotes to an infectious form.";

" Biol. Chem. 267:1888-1895(1992).

" FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

- CATALVITC ACTIVITY: Preference for hydrophobic residues at P1 and P1 and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

- CORACTOR: Binds 1 zinc ion per subunit (By similarity).

- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

- SMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION PEPILDE.
LEISHMANGLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
BY SIMILARITY.
SINC (CATALYTIC) (BY SIMILARITY).
SINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase_M8.
Pfam; PF01457; Peptidase M8: 1.
PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprocease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 KDFDVPVINSSTAVAKAREQYGCDTLEYLEIEDQGGAGSAGSHIKM 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KSETTITQSGYGNGADV-------GQGADNSTIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.3%; Score 101; DB 1;
llarity 30.2%; Pred. No. 0.23;
Conservative 12; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M80672; AAA29238.1; -.
EMBL; M28527; AAA29235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A44951; A44951.
HSSP; P08148; 1LML.
MEROPS; M08.001; -.
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1656 AA;
               Query Match
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Matches 42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   OMPB RICJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=YH;
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                                                                                                                                                                                                   MEDINE=93149206; PubMed=8426614; Medina-Acosta E., Karess R.B., Russell D.G.; Medina-Acosta E., Karess R.B., Russell D.G.; Medina-Acosta E., Karess R.B., Russell D.G.; Medina-Acosta E., Karess R.B., Russell D.G.; Medina-Acosta are developmentally regulated."; Mol. Biochem. Parasitol. 57:31-46(1993).
-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala-Tyr-|-Leu-Lys-Lys-...
-!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- DEVELOPMENTAL STAGE: Expressed in both the promastigote and the
                                                                                                                         Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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FE448DDC78C10B0A CRC64;
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SIMILARITY: Belongs to peptidase family M8.
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                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN=MNYC/BZ/62/M379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S19916; S19916.
HSSP; P08148; 1LML.
MEROPS; M08.001; -.
                                                                                                              Leishmania mexicana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Eugler
NCBI_TaxID=5665;
                                                                            endopeptidase)
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ACT SITE
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                                                                                                                                                                                                                                             66 SETTITOSGYGNGADVGOGADN-STIELTQNGFRNNA--TIDQWNAKNSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                              297 NVSVITSSTVVAKAREQYGCNSLEYLEIEDQGGAGSAGSHIKMRNAKDELMAPAASAGYY 356
                                                                                                                                                                   241 AVGVINIPAANIASRYDQLVTRVVTHEMAHAVGFSGTF----FGAVGIVQEVPHLRRKDF
                                                                                                                            AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity)
-!- SUBCELLIAR LOCATION: Cell wall. This bacterium is covered by a S layer with hexagonal symmetry.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uchiyamä T.; "Sequencing of the gene encoding the protein {\tt rOmp\ B} of Rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia japonica.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 kDa SURFACE-EXPOSED PROTEIN
                    Length 646;
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                                                                          Indels
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W.
                    Score 99.5; DB 1;
Pred. No. 0.33;
13.1%; Sco...
30.8%; Pred. No. ...
've 15; Mismatches
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InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfan; PF03797; Autotransporter; I.
IIGRPAMs; TIGR01414; autotrans_barl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            006653;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq
16-OCT-2001 (Rel. 40, Last ann
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CHAIN
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                        123 AALVNOTASD 132
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                            547
                                                                                    ---TLTLGGANIISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQTGVVDASS 602
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VAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 IVVSGSALAGVY-DQLVTRVVTHEMAHASGPDSTLSTYQYGSANAALALQSDARKSETTI
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                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=KUIN-3;

PREAIN=KUIN-3;

MISDLINES-4564407; PubMed=7764866;

Michigami Y., Watabe S., Abe K., Obata H., Arai S.;

"Cloning and sequencing of an ice nucleation active gene of Erwinia
                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pantoea.
                                                                                                                  QWNAKNSDI -- TVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                   SIMILARITY: Belongs to the bacterial ice nucleation protein
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                                                        SETTITOSG----YGNGADVGQGADNSTIELTQNGFRNNATID-
                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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JOMAIN 162 993
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PROSITE; PS00314; ICE_NUCLEATION; 34
                                                                                                                                                                                                                                                                                                                           Pantoea ananas (Erwinia uredovora)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR000258; Ice nucleatn. Pfam; PF00818; Ice_nucleation; 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103378 MW;
                                                                                                                                                                                                                                                                                               ce nucleation protein inaU.
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HSSP; P06620; 1INA.
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                                 209 V-AGYGSTQTAGEESSQMA----GYGSTQT----GWKGSDLTAG-YGSTGTAGDDSSL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91009116; PubMed=2145267; Schneider P., Rerguson M.A.J., McConville M.J., Mehlert A., Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Homans S. M., Bordier C.; "Structure of the glycosyl-phosphatidylinositol membrane anchor of the Leishmania major promastigote surface protease."; J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                               01-AUG-1986 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (RC 3.4.24.36) (Gell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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MEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                 Button L.L., McMaster W.R.; "Molecular cloning of the major surface antigen of leishmania."; J. Exp. Med. 167:724-729(1988).
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MEDLINE=95406217; PubMed=7675788;
Schlagenhauf E., Etges R., Metcalf P.;
"Crystallization and preliminary X-ray diffraction studies of
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                                                                                                                                                                                   602 AA
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                                                                                                257 IAGYGSTÓTÁGEDSSLT--AGYGSTOTÁOK 284
                                                                  126 V----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE MEDLINE-88154764; PubMed=3346625;
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J. Exp. Med. 171:589-589(1990).
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                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                      Leishmania major.
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P08148; P15906;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pantoea.
NCBI_TaxID=549;
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Pred. No. 0.56;
3; Mismatches 9;
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P16239;

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O1-APR-1990 (Rel. 14, Created)

16-OCT-2001 (Rel. 14, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

ICe nucleation protein.
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Best Local Similarity 59.5%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 V-AGYGSTQTAGEESSQMA-----GYGSTQT----GMKGSDLTAG-YGSTGTA-----G 251
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                       nucleation activity.";
FEBS Lett. 258:297-300(1989).
-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate
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-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
                                                                                       crystallization in supercooled water.
-: SUBCELLULAR LOCATION: Outer membrane (By similarity).
-: DOWAIN: CONTAINS MANY IMPREFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-: SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
those of Pseudomonas species and regions required for ice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIMES; PR0033/; LCENVOLEATION; 49.
PROSITE; PS00314; ICE NUCLEATION; 49.
Ice nucleation; Repeat; Outer membrane.
DOMAIN

OCTAPEPTIDE PERIODICITY.
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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29.3%; Pred. No. 2.1;
ive 20; Mismatches
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Mol. Gen. Genet. 223:163-166(1990).
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InterPro; IPR000258; Ice nucleatn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00818; Ice_nucleation; 69.
PRINTS; PR00327; ICENUCLEATN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADSSLI---AGYGSTQTAGE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=X568;
MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonadaceae; Xanthomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807053
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ID _ICEN_XANCT
AC P18127;
                                                                                                                                                                                                                                             family
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DSTL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 TQSGYGNGADVGQGADNSTIELTQNGFRNWATIDQWNAKNSDITVGQYG----GNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 V-AGYGSTQTAGEESSQMA-----GYGSTQT----GMKGSDLTAG-YGSTGTAGDDSSL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                            -!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLULIAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS 126 INFERENCY REPEATS OF A CONSENSUS OCTAPERTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERINFOSED.
-!- MISCELLANEOUS: A STRUCTURAL OF SYMMETRY RELATED TO THAT OF ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 IVVSGSALAGVY-DQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-90092494; PubMed-2599095; Abe K., Watabe S., Emori Y., Watanbe M., Arai S.; "An ice nucleation active gene of Erwinia ananas. Sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBL_TaxID=553;
                                                                                                    Warren G.J., Corotto L.V.; "The consensus sequence of ice nucleation proteins from Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                              herbicola, Pseudomonas fluorescens and Pseudomonas syringae.";
Gene 85:239-242(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.6%; Score 95.5; DB 1; Length 1258; 28.7%; Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 1217 OCTAPEPTIDE PERIODICITY.
1258 AA; 125084 MW; 590E8A130077FBD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 V-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 IAGYGSTOTAGEDSSLT--AGYGSTOTAQK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS00314, ICE NUCLEATION, 45.
Ice nucleation, Repeat, Outer membrane.
DOMAIN 162 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000258; Ice nucleatn. Pfam; PF00818; Ice nucleation; 65. PRINTS; PR00327; ICENUCLEATN.
                                                                        MEDLINE=90152370; PubMed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M26382; AAA24823.1; -.
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Best Local Similarity
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ICEA_PANAN

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Gaps

33;

Indels

Length 1322;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 ADNSTIE---LTQN-GFRNNATI----DQWNAKNSDITVGQYG----GNNAALV---- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGN-----GADV-----GQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANBOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE. SIMILARITY: Belongs to the bacterial ice nucleation protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%; Score 93.5; DB 1; Length 1567; 29.9%; Pred. No. 3; Live 26; Mismatches 30; Indels 45;
                                                                                                                                                                                                                                                                                                        EMBL; X52970; CAA37140.1; -.
HSSP; P06620; INA.
InterPro: IPRO00258; Ice_nucleatn.
Pfam; PF00818; Ice nucleation; 81.
PRINTS; PR00327; ICENUCLEATION, 57.
ICE nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 WW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1169 TOTAGYNSILT--TGYGSTQTAQE 1190
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August 2, 2004, 14:39:17; Search time 29.7 Seconds (without alignments) 1604.150 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
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1: SP_archea!*

2: Sp_bacteria.*

3: Sp_fungi:*

4: Sp_human:*

5: Sp_inverser:*

6: Sp_mammal:*

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9: Sp_phage:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	033802 salmonella	Q7x243 citrobacter	Q7x240 citrobacter	Q8cw63 escherichia	Q7x237 enterobacte	Q54069 salmonella	Q8eih4 shewanella	Q8cw64 escherichia	Q83ru7 shigella fl	Q7uczl shigella fl	Q89ji6 bradyrhizob	Q89ji3 bradyrhizob	Q8eih3 shewanella	Q89j14 bradyrhizob	Q7x244 citrobacter	Q89ji5 bradyrhizob
SUMMARIES			D.	033802	Q7X243	Q7X240	Q8CW63	Q7X237	Q54069	Q8EIH4	Q8CW64	Q83RU7	Q7UCZ1	910680	Q89J13	QSEIH3	Q89J14	Q7X244	Q89JI5
			B	0	N	N	16	Ŋ	~	16	16	16	16	16	16	16	16	C)	16
			Match Length DB	152	150	149	152	150	16	502	160	160	151	153	171	139	130	151	154
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ALIGNMENTS

RESULT 033802 ID 0	0LT 1 802 033802	PRELIMINARY;	PRT;	152	2 AA.	
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급급	01-DEC-2001	(Tremberel.	us, mast s 19, Last a	equenc	sequence update) annotation update)	
88	AgfA protein	n (Fragment).				
S O	Salmonella	Acra. Salmonella typhimurium.				
ပ္ပ	Bacteria, E	Bacteria, Proteobacteria, Gammaproteobacteria,	Gammapro	teobac	steria; Enterobacteriales;	
ပ္ပ	Enterobácteriaceae;	riaceae; Salmo	Salmonella.			
ŏ	NCBI_TaxID=602;	:602;				
Z.						
КP	SEQUENCE FR	FROM N.A.				
KX.	MEDLINE=98(MEDLINE=98053981; PubMed=9393832;	-9393832;		1	
RA:	Sukupolvi	Sukupolvi S.S., Lorentz R.G., Gordon J.I.,	R.G., Gord	on J.I	I., Bian Z., Pfeifer J.D.,	
Z.	Normark S. J	S.J., Rhen M.;			•	
RT	"Expression	n of thin, aggr	regative f	imbria	le promotes inters	
RT	Salmonella	Salmonella typhimurium SR-11 with mouse	R-11 with	monse	small intestinal epithelial	
RI	cells.";					
RL	Infect. Immun.	ശ	325(1997).			
絽	EMBL; AJ000514;	CAA	1;			
FT	NON_TER	_				
Š	SEQUENCE	AA;	15401 MW; 9DA	7DADC2	9DA7DADC2364B006 CRC64;	
õ	Query Match	85.7%;		Score 649;	DB 2; Length 152;	
ΜŽ	Best Local Similarity Matches 134; Conser	Υat	4	No. 1 smatch	Pred. No. 1.1e-44; ; Mismatches 13; Indels 0; Gaps	0;
ð	₩-	TLLKVAAFAAIVVSC	SALAGVYDQ	LVTRV	MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ	09 0
g	- E	TLKVAAFAAIVVSG	SAVAGVVPQ	WGGGGN	MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ	09 0
δ	61 51	ARKSETTTTQSGYC	SNGADVGOGA	DNSTIE	SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGGYGG	3 120
qq	61 SI		 BNGADVGQGA	DNSTIE		3 120

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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(TrEMBLrel. 25, C (TrEMBLrel. 25, I (TremBLrel. 25, I

01-OCT-2003 01-OCT-2003

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Citrobacter sp. Fec2

Curlin-csgA protein.

PRELIMINARY;

Q7X243 Q7X243;

RESULT 2

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59 SDARKSDVTITQHGRGNGAVVGQGADDSTISLKQTGFQNSATIDQWNAKNADISVTQFGG 118
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGN--HHGGGSNYGPDSSLSIYQYGSNNSANALQ 58
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MBDLINE=22380234; PubMed=12471157;
WBICHINE=22380234; PubMed=12471157;
WBICH RA., BURLAID V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
MayMew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnanberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli O6.
Bacteria; Protecbacteria; Gammaprotecbacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCEL_TaxID=217992;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 AA; 15064 MW; 3BA57F34C1240E83 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
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STRAIN=Fec39;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
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01-WAR-2003 (TrEMBLrel. 23, Last
01-WAR-2003 (TrEMBLrel. 23, Last
Major curlin subunit precursor.
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SEQUENCE 152 AA;
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STRAIN=Fec2;
STRAIN=Fec2;
Sodaj X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Finbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.", Infect. Immun. 72:4151-4158 (2003).
EMBL; AJS15700; ASD56672.1; --
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD566751; -.
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
NCBI_TaxID=213763;
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Enterobacteriaceae; Citrobacter.
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01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,

Curlin-csgA protein.

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CSGA. Citrobacter

[1] -SEQUENCE FROM N.A. STRAIN=Fec4; NCBI_TaxID=546;

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A Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Reidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherry S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., A Madugu K., Person J.D., Umayam L.A., White O., Wolf A.M., A Wamathevan J., Weidman J., Ingraim M., Lee K., Berry K., Lee C., A Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., A Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Genome: sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."; 123(2002).

B. Embi, Abolissiz; AANS3941.1; -.
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.6%; Score 133; DB 16; Length 502; 29.6%; Pred. No. 0.013; ive 21; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 120; DB 16; Length 160;
llarity 28.7%; Pred. No. 0.036;
Conservative 17; Mismatches 67; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome. SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 AA; 16963 MW; 49F68448D979B986 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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nes 37; Conserv
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                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=70863;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHA--SGPDSTLSIYQYGSANAALA 58
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).
EMBL, AJ515702; CAD56678.1; -. SEQUENCE ISO AA, 15112 MW, 5D8BB2D872DF15F3 CRC64;
                                                                                                                                                                                                                          Gaps
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Enterobacteriaceae; Salmonella.
NCBI_TaxID=592;
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                                                                                                                                  DB 2; Length 150;
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STRAIN=SE30;
Cox J.M., Eglezos S., Woolcock J.B.;
wirulnorce of Salmonella enteritidis in chickens correla
colony morphology and expression of SERT7 finbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Q8EIH4,
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                  60.0%; Score 454.5; DB 2;
62.1%; Pred. No. 4.6e-29;
iive 24; Mismatches 29;
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Pred. No. 3.1e-20;
2; Mismatches 0;
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nes 67; Conservative
                                                                                                                                                                                               Local Similarity 62.1
nes 95, Conservative
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01-NOV-1996
01-DEC-2001
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Matches 37; Conserv
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CsGB OR BLL5297.
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Matches
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          69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
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                                 IIGQAĞTNNSAQLRQĞGSKLLTVVAQEĞSSNRAKIDQTGDYNL-AYIDQAĞSANDASISQ
                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441 (2002).
EMBL; AE015131; AAN42658.1; -.
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                                                                                                                                                                                                                                                                                                      STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.9%; Score 120; DB 16; Length 160; 28.7%; Pred. No. 0.036;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Minor curlin subunit precursor, similar ro CsgA.
CSGB OR SF1035.
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Last annotation update)
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                                                                                                                                               160 AA
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
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                                                         129 TASDSSVMVRQVGFGNNATANQY 151
                                                                               116 GAYGNTAMIIQKGSGNKANITQY 138
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Enterobacteriaceae; Shigella.
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01-0CT-2003 (TYENBLYE1, 2
01-0CT-2003 (TYENBLYE1, 2
01-0CT-2003 (TYENBLYE1, 2
Minor curlin subunit,
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                                                                                                                                              PRELIMINARY;
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es 41, Conserv
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SEQUENCE 160 AA;
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                                                                                                                                                                                                                                                                      NCBI_TaxID=623;
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13
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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DNA Res. 9:189-197(2002).
BMBL; APO059554; BAC50562.1; -.
Complete proteome.
SEQUENCE 153 AA; 15991 MW; 4CE71DBAC375145B CRC64;
                                      Α.,
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling J Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella flexneri serctype 2a strain 2457T."; Infect. Immun. 71:2775-2786 (2003).
EMBL, AEO16991; Aph16542.1; -. SEQUENCE 151 AA, 15868 MW; 5D5D266B964014A0 CRC64;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Last annotation update)
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27.0%; Pred. No. 0.046;
... M'ematches 56;
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                                                                                                                                                                                                                                                                                             15.7%; Score 118.5; DB ilarity 31.6%; Pred. No. 0.045; Conservative 13; Mismatches
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nes 41; Conservative
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IELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                     91 VQLLQVGAQNKASIT-----QIGNDNLVQLNQLGS-GNFSIQQIADGAAISIT 137
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  VVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST
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DNA Res: 9:189-197(2002).
EMBL; APO05954; BAC50564.1; -.
Complete proteome.
SEQUENCE 130 AA; 12699 MW; ACFB2D66A48D260F CRC64;
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Enterobacteriaceae, Citrobacter,
NCBI_TaxID=213763;
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotat
Nucleation component of curlin monomers
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SEQUENCE FROM N.A.
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Bl15299 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Wandupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Muller J., Khouri H., Gl.J., Utterback T.R., McDonald L.B., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                          STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Raneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DAA Res 9.189-197(2002).
EMBL; AP005954; BAC50565.1; -.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales,
Alteromonadaceae, Shewanella.
NCBI_TaxID=70863,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 171;
                                                                                    Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 AA; 17448 MW; 995DB08C01498381 CRC64;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
  24, Last sequence update)
24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.3%; Score 116; DB 16; 37.5%; Pred. No. 0.083;
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EMBL; AE015532; AAN53942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minor curlin subunit CsgB, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MR-1;
MEDLINB=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 37.5 nes 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 27.0
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01-JUN-2003 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel.
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SEQUENCE 139 AA;
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                                                  CsgA protein.
CSGA OR BLL5300.
                                                                                                                                                            NCBI_TaxID=375;
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01-MAR-2003
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Matches
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Indels

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51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQGADNSTIELTQNGFR----- 98
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74 EGGSNRAKVDQSGAYNF-AYIAQSGHSNDASISQSNYGNTAMIQKGSGNKANITQY 129
                                                                                                                                                                                     Query Match
Best Local Similarity 27.4%; Pred. No. 0.29;
Matches 32; Conservative 20; Mismatches 48; Indels 17; Gaps
STRAIN=Fec2;
Zogai X., Bokranz W., Nimtz M., Romling U.;
Zogai X., Bokranz W., Nimtz M., Romling U.;
Encoduction of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72.4151-4158(2003).
EMBL, A515700; CAD566711;
ERML, A515700; CAD566711;
ERQUENCE 151 AA; 16158 MW; BD00AF57E1400704 CRC64;
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:35:42 ; Search time 44.9 Seconds (without alignments)
950.215 Million cell updates/sec
Title:
Berfect score: 780
Sequence:
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aabb6349 AgfA::PT3 Aar74625 AgfA::PT3 Aaw38570 Salmonell Aaw38570 Salmonell Aabb6353 AgfA::PT3 Aabb6354 AgfA::PT3 Aabb6346 AgfA::PT3 Aabb6342 AgfA::PT3 Aabb6354 AgfA::PT3 Aabb6351 AgfA::PT3 Aabb6351 AgfA::PT3 Aabb6351 AgfA::PT3 Aabb6351 AgfA::PT3 Aabb6351 AgfA::PT3 Aabb6351 B: coli C Aar62761 B: coli C Aar62761 B: coli C Aar62761 B: coli C Aar62761 AgfA::BT3 Aabb6351 B: coli C Aar52664 Fibronect Aar52664 Fibronect Aar52663 Salmonell Aabs6321 Salmonell Aabs6321 Salmonell Aabs6328 Salmonell Aabs6328 Salmonell Aabs6328 Salmonell
SUMMARIES	AAB3 6349 AAR74625 AAR336341 AAR336346 AAB36350 AAB36346 AAB36346 AAB36354 AAB36354 AAB36354 AAB36354 AAB36351 AAB36351 AAB36351 AAB36318 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663 AAR52663
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Score	C
Result No.	111111111111111111111111111111111111111

Aab36339 Salmonell	Aab36320 Salmonell	Aab36322 Salmonell	Aab36327 Salmonell	Aab36337 Salmonell	Abr82644 E. coli c	Aab36344 Escherich	Sal		Abb66342 Drosophil	Abr82645 E. coli c	Aab36323 Salmonell	Aab36336 Salmonell	Aab36328 Salmonell	Abr82647 E. coli c	Abb66343 Drosophil	Abul7075 Protein e	Aab36331 Escherich	Ada33477 Acinetoba	Aag66008 F. necrop
3 AAB36339	3 AAB36320	3 AAB36322	3 AAB36327	3 AAB36337	7 ABR82644	3 AAB36344	3 AAB36342	7 ABR82649	4 ABB66342	7 ABR82645	3 AAB36323	3 AAB36336	3 AAB36328	7 ABR82647	4 ABB66343	6 ABU17075	3 AAB36331	6 ADA33477	5 AAG66008
22	22	22	22	22	24	151	151	56	262	56	19	19	19	24	287	974	23	975	580
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RESULT 1

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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antiquen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                               AgfA::PŤ3#4 amino acid sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 136; 139pp; English.
                                                                                                                                                                     vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Collison SK,
              AAB36349 standard; protein; 151 AA
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                                                                               (first entry)
                                                                                                                                                                                                    Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC64625.
                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                     WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
                                                                               26-FEB-2001
                                                                                                                                                                                                                                                                                                         12-0CT-2000.
                                                                                                                                                                                                                                        Synthetic.
                                              AAB36349;
AAB36349
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copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign animo acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogensicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                         Length 151;
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                                                                                                                                                                                                                                                                                                                      100.0%; Score 780; DB 3;
100.0%; Pred. No. 1.7e-67;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNOTASDSSVMVRQVGFGNNATANOY
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 151; Conserv
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                                                                                                                                                                                                                                                                                        Sequence 151 AA
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26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR74625;
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(KING/)
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The Salmonella AgfA protein and DNA are used in vaccine and genetic

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                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                     9
immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                 9
                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                      Length 151;
                                                                                                                  88.6%; Score 691; DB 2;
90.7%; Pred. No. 6.8e-59;
iive 3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36341 standard; protein; 151
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                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672631/65.
                                                                                                                                     Best Local Similarity
Matches 137; Conserv
                                                                               Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC64617
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                                                                                                                    Query Match
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SDARKSETTITQSGYGNGADVGQGADNSTIELIQNGFRNNATIDQWNAKNSDITVGQYGG 120
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  used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (I) use of thin aggregative fimbriae (SET17/TAF) nucleation depended assembly system of strains of Salmonella. Bscherichia coll and Enterobacteriacese for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmoneila, agfA, chromosomal gene replacement, fimbrin; epitope, vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                       Score 686; DB 2;
Pred. No. 2.1e-58;
3; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                            87.9%;
90.1%;
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Best Local Similarity 90.1
Matches 136; Conservative
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N-PSDB; AAC64629.
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                                                                                                                                                                                                                              Sequence 151 AA;
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWARNSDITVGQYGG 120
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful foe eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to $500,000 copies/Cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                      Score 691; DB 3;
Pred. No. 6.8e-59;
3; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                      88.6%;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 90.7 es 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-309886/28.
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Misc-difference
                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1994;
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directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segment of foreign amino acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the coll setul for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit for carrier fimbrial subunit for directing an immune response important for directing an immune response important for directing an immune response important for directing an immune response important for dimbriae are easy and against the inserted epitope, and hybrid fimbriae are easy and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
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                                                                                                                                                                                                                                                                                                                                   inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 675; DB 3; Le
Pred. No. 2.4e-57;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.9%;
Matches 136; Conservative
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N-PSDB; AAC64626.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA concerning the monodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbrine (SEPI)/TAP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and addances for the production of fimbriae comprising recombinant C AgfA, CsA and AgfA-homologue fimbrin submits, respectively; (2) directing recombination of a recombinant gene composition species; (3) directing recombination of a recombinant gene composition species; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, copy of that general are placement segment or segments of foreign amino acid polymer comprising separating a replacement segment or segments of foreign amino correction containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or copy acid in the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful costiciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial submit protein are usually strong immunogens, which may be important for directing an immune response cagainst the inserted epitope, and hybrid fimbriae are easy and given in conspensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 ----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
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protein useful for eliciting immune response in animal
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Pred. No. 3.3e-52;
0; Mismatches 0
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                                           Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immune response; immunogen.
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Best Local Similarity 73.6
Matches 128; Conservative
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Salmonella enteritidis.

Escherichia coli.

Synthetic.

WO200060102-A2

12-OCT-2000

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directing recombination of a recombinant gene into the chromosome of the homologus species, a recombinant gene into the chromosome of the homologus species, replacing the native comprising that gene and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an animo acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or coli sequence or sequences grown on a Salmonella, E. coli or coli sequence or sequence in an animal. In a fimbrial presentation system the heterologus antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens; which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and in the presentive is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SETI//TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
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                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequation encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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the exemplification of the present invention
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                                                                                                                                                             Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 136; 139pp; English.
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                                                                                                                                                             Collison SK,
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99US-0127888P.
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                                                                            (UYVI-) UNIV VICTORIA.
                                                                                                                                                             Doran JL,
                                                                                                                                                                                                                                     WPI; 2000-672631/65.
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05-APR-1999;
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                                                                                                                                                             White AP,
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbried (SPEPI/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of Enterobacteriaceae for the production of fimbriae comprising recombinant of AgrA, CGSA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombination of a recombinant gene into the chromosome of the homologus species, replacing the native comprising separating an aminologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. Coli or Enterobacteriaceae host cell, from the host cell and introducing the coliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to coliciting an immune response in an animal in a fimbrial presentation system the heterologous antigens are presented in high numbers (up to conding, the carrier finbrial subunit protein are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are usually strong immunogens, the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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80.8%; Pred. No. 2.4e-51;
ive 7; Mismatches 22; Indels
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                                                                                                                                                                                             05-APR-2000; 2000WO-CA000356.
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Best Local Similarity 80.8
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                  Doran JL,
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N-PSDB; AAC64622.
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back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                               AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                   vaccine; immune response; immunogen
                    AAB36347 standard; protein; 151 AA.
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                                                                                                        (first entry)
                                                                                                                                                                                                                                                       Salmonella enteritidis.
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N-PSDB; AAC64623.
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                Escherichia coli
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                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
 Length 151;
                                   Indels
78.3%; Score 611; DB 3;
81.5%; Pred. No. 3.8e-51;
iive 6; Mismatches 22,
                                   Conservative
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a replacement segment of segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for every consist of the bushing are presented in high numbers (1) the consist of the bushing are presented in high numbers (1) the consist of the bushing an election or presented in high numbers (1) the consist of the bushing an election of the presented in high numbers (1) the consist of the bushing an election of the presented of the presented on the bushing the consist of the bushing an election which is useful for a system the heterologous antigens are presented in high numbers (1) the consist of the bushing an election of the presented of the plant of the bushing and the consist of the bushing and presented of the plant of the bushing and presented of the plant of the consist of the bushing and presented of the plant of the consist of the bushing and presented of the plant of the consist of the consist of the consist of the consist o
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                           121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                             121 NNAALVNOTASDSSVMVROVGFGNNATANOY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
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                                                                                                                                                                                                                                                     RESULT 10
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26-FEB-2001
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                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                       Gaps
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                                                                       ..
                                                Length 151;
                                                                     Indels
                                                                       22;
                                               Score 608; DB 3;
Pred. No. 7.4e-51;
                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
the exemplification of the present invention
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                                                                     5; Mismatches
                                                                                                                                                                                       NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                           HEMAHANOTASDSSVMVROVGFGNNATANOY
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                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                      protein; 151 AA
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                                               77.9%;
82.1%;
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                                                          3est Local Similarity 82.1
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis
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                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                        Sequence 151 AA;
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Pred. No. 3.5e-50;
4; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response; immunogen.
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Best Local Similarity 80.8%;
Matches 122; Conservative
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N-PSDB; AAC64631
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cc (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterbacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coll or acid sequence or sequences grown on a Salmonella, E. coll or acid sequence or sequences grown on a Salmonella, E. coll or acid sequence or sequences grown on a Salmonella, E. coll or acid sequence or sequences in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TMFP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, a recombinant gene back into the chromosome of the homologous species, replacing the native comprising separating are annoacid polymer comprising a replacement segment or segments of foreign annino acid sequence or sequences grown on a Salmonella, B. coli or acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for unexpension of recombinant protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein possesses both the immunogens, which may be important for directing an immune response in manimal. The present sequence is given in the exemplification of the present invention
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Pred. No. 5.5e-50;
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                                                                                                                                                                           Disclosure; Page 139; 139pp; English
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Best Local Similarity 81.5
Matches 123; Conservative
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Plasma protein; immune response; antibacterial; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2, 2004, 14:48:25
                                                                                                                                                                                   30-JAN-2003; 2003WO-EP000943.
                                                                                                                                                                                                                              31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                                                          (HANS-) HANSA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                      Olsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             completed: August
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-646136/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ACF36153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                            WO200306446-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 44.9 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103;
                                                                                                                                                                                                                                                                                                                        Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequent of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbries (SERT)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of Enterobacteriaceae for the production of fimbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sare usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong an immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and incompanient the inserted epitope, and hybrid fimbriae are easy and incompanient in the present invention in exemple in exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.1%; Score 523; DB 3; I
68.9%; Pred. No. 1.2e-42;
cive 20; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                       Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli CsgA subunit 15 kDa protein
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                                                                                                                                       Collison SK,
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  05-APR-2000; 2000WO-CA000356.
                                              99US-0127888P.
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                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                       Doran JL,
                                                                                                                                                                              WPI; 2000-672631/65.
N-PSDB; AAC64619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
                                              05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-DEC-2003
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Matches 104;
                                                                                                                                       White AP,
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABRESGE4. ABR82GE4.-9. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, salmonella or Shigalla infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                           New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVBAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.4%; Score 518; DB 7; Length 151;
68.2%; Pred. No. 3.8e-42;
Live 20; Mismatches 28; Indels
Herwald H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GNGAAVDOTASNSSVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 41-42; 42pp; English
Wikstroem M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.2%; F1
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Query Match
Best Local Similarity 90.1
Matches 136; Conservative
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Sequence 1, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 204, App
Sequence 199, App
Sequence 199, App
Sequence 2643, App
Sequence 2643, App
Sequence 2643, App
Sequence 2643, App
Sequence 2643, App
Sequence 2643, App
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Sequence 57, Appl
Sequence 4,64, Ap
Sequence 2, Appli
Sequence 2, Appli
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4, Appli
4, Appli
33, Appl
                                                            August 2, 2004, 14:40:48 ; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13,
Sequence 2, 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                             1 MKLLKVAAFAAIVVSGSALA......bssvmvrqvgFGNNATANQY
                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-233-788A-57
US-08-233-788A-57
US-08-254-573-2
US-08-172-379-4
US-08-172-379-4
US-08-172-372-1
US-08-172-372-1
US-09-336-417A-5
US-09-336-417A-5
US-09-336-199
US-09-075-55-204
US-09-075-55-204
US-09-072-596-199
US-09-072-596-199
US-09-072-596-199
US-09-072-596-199
US-09-072-596-199
US-09-072-586-24
US-09-072-586-24
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US-09-08-286-24
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                                                                                                                                                                                389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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                                          OM protein
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Sequence 16,
Sequence 14,
Sequence 42,
Sequence 26,
Sequence 4,
Sequence 4, P
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               Sequence
Sequence
Sequence
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                       RESULT 1
US-08-233-7884-59
i Sequence 59, Application US/08233788A
i Bearent No. 5635617
i GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
ITILE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCE: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
ADDRESSE: Seed and Berry
ADDRESSE: Seed and Berry
ATREET: 0300 Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTRY: U.S.A.
ITILE OF UNIVERENCE OF SALMONELLA
MEDIUM TYPE: Floppy disk
OCMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OCMPUTER: Datentin Release #1.0, Version #1.25
COMPUTER: Datentin Release #1.0, Version #1.25
COMPUTER: C-APR-1994
FILLING DATE: 26-APR-1994
FILLING DATE: 26-APR-1994
FILLING DATE: 26-APR-1994
FILLING DATE: 30-ANDRES: 35-570
REFERENCE/DOCKET NUMBER: 35-570
REFERENCE/DOCKET NUMBER: 35-570
REFERENCE/DOCKET NUMBER: 35-3030
TELEPRAN: (206) 622-4930
TELEPRAN: 17-2830 SEEDAMBERRY
INFORMATION (NUMBER: 37-2830
TELEPRAN: 17-2830 SEEDAMBERRY
INFORMATION (NUMBER: 35-3031
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TELEPRAN: 17-2830 SEEDAMBERRY
INFORMATION OF 39: SEEDAMBERRY
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US-09-268-347-47
US-09-268-347-47
US-09-268-347-36
US-08-276-852-34
US-08-322-710A-16
US-08-387-874-16
US-08-899-576-34
US-08-899-576-34
US-08-999-577-34
US-08-999-577-34
US-08-999-578-34
US-08-999-578-34
US-08-989-578-34
US-08-989-578-34
US-08-989-578-34
US-08-989-578-34
US-08-988-34-16
US-08-988-38-16
US-08-98-888-38-34
US-08-485-880A-26
US-08-485-880A-26
US-08-485-880A-26
                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 151 amino acids
amino acid
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    US-08-233-788A-59
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  LENGTH:
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1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ

Sequence Sequence

87.9%; Score 686; DB 1; Length 151; 90.1%; Pred. No. 2.2e-62; ive 3; Mismatches 12; Indels

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Query Match
Best Local Similarity
Matches 35; Conserv
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                                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                    61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Coluthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
ATITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.9%; Score 506; DB 1; Length 120; Best Local Similarity 87.5%; Pred. No. 3.4e-44; Matches 98; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Or COLUMNIES OF SEQUENCES: 61
CORRESPONDERS: 61
CORRESPONDERS: 61
CORRESPONDERS: 63
STATE: GagO Columbia Center, 701 Fifth Avenue CITY: Seattle Statule Center, 701 Fifth Avenue CITY: Seattle Mashington COMPUTR: U.S.A.
IIP: 98104-7092
COMPUTR: IBM PC COMPATIBLE FORM: PC-DOS/MS-DOS SOFTEM: PREPABLE FORM: PC-DOS/MS-DOS SOFTEM: PREPABLICATION DATA: PSEATH OF SYSTEM: PC-DOS/MS-DOS SOFTEM: 26-APR-1994
CLASSIFICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
REFERENCE/COMPUTATION INFORMATION: TELEPHONE: (206) 682-6031
TELEPHONE: (206) 682-6031
TELEPHONE: (206) 682-6031
TELEPHONE: COSO SEEDANBERRY
INFORMATION POR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
                                                                                                                                                 121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                             121 NNPALVNÓTASDSSVMVRQVGFGNNATANQY 151
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8.09-328-352-4764
; Sequence 4764, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               US-08-233-788A-57; Sequence 57, Application US/08233788A; Patent No. 5635617; GENERAL INFORMATION:
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPEBRNCE: GTC99-03PB CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                               64 RKSETTITQS-----GYGNGADVGQGADNSTIELTQNGF-----RNNATIDQWNAKNS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | : | | : | | : 352 NTAPTITISNIVNDNDIIDNGNSGGTGSGSGNGSGGLLNGAASGNGEHNYGIGNGDDV 411
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                                                                                                                                                                                                                                                                                                                    36; Gaps
                                                                                                                                                                                                                                                                       11.8%; Score 92; DB 4; Length 975; ilarity 23.8%; Pred. No. 0.75; Conservative 24; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KANBOJ, Rajender
APPLICANT: KANBOJ, Rajender
APPLICANT: BLIOTT, Candace
APPLICANT: NUTT, Stephen
TITLE OF INVENTION: AMPA-BINDING HUMAN Glurl RECEPTORS
UNMERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                          15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDYDQLVTRVVTHEM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DITSPITGIENFSGNSFSLIGNSSSSS 438
                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08254573
Patent No. 5610032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAK: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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250 VIGEQLVNYIDIIPAKIMQQM------KNSDARDHIRVDWKRPKYISALIYDGVKVM 300
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358 KGRRTNYTLHVIEMKHDSIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTILED 417
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                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hoeger, Thomas
APPLICANT: Hoeger, Andreas
APPLICANT: Gerrer, Sylvin
APPLICANT: Gerrer, Sylvin
APPLICANT: Gerrer, Sylvin
APPLICANT: Lemaire, Hans-Georg
TITLE OF INVENTION: Subunits of Glutamate Receptors, Their
TITLE OF INVENTION: Preparation and Their Use
CORRESPONDENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 22.6%; Pred. No. 1.1;
Matches 45; Conservative 26; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDILUM TYPE: Diskette-3.5 inch, 720 Kb storage COMPUTER: PIBM AT-compatible, 80286 processor OPERATING SYSTEM: MS-DOS version 6.0 SOFFWARE: Worderfect version 5.1 CURRENT; SPELICATION DATA:
APPLICATION NUMBER: US/08/687,379 FILING DATE: 05-A0461996
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
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Sequence 1, Application US/08172332

Patent No. 6313279

GENERAL INFORMATION:

APPLICANT: Burnett, J. Paul

APPLICANT: Mayne, Nancy G
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                                                                                                                                                                                                                                                                                                                                   Sequence 4% Application US/08687379 Patent No. $5756697
                                                                                                                                                     418 PYVMLKK-----NANQF 429
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TOPOLÒGY: linear
MOLECULE TYPE: protein
US-08-687-379-4
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USA
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Patent No. 575697

GENERAL INFORMATION:

APPLICANT: Hooger, Thomas

APPLICANT: Bach, Alfred

APPLICANT: Bach, Alfred

APPLICANT: Lemaire, Sylvia

APPLICANT: Lemaire, Sylvia

APPLICANT: Lemaire, Subunits of Glutamate Receptors, Title OF INVENTION: Subunits of Glutamate Receptors, Title OF INVENTION: Preparation and Their Use

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Keil & Weinkauf
                                                                                                                                              72;
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                                                                                   DB 1; Length 906;
                                                                                                                                              56; Indels
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COMPUTER EADABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 720 Kb storage COMPUTER: IBM AT-compatible, 80286 processor OPERATION SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,379
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
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CLASSI
                                                                               Query Match
11.5%; Score 90; DB 1
Best Local Similarity 22.6%; Pred. No. 1.1;
Matches 45; Conservative 26; Mismatches
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1101 Connecticut Avenue
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Best Local Similarity 22.69
Matches 45; Conservative
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CITY: Washington
STATE: D.C.
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                    US-08-254-573-2
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US-08-687-379-2
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Sequence 3, Application US/08864038A Patent No. 6001592
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 906 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mie-prefecture
                                                                                       ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-216-326-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 NGFRNNAT --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Isshind
CITY: Tsu-city
STATE: Mie-pref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RY: JAPAN
514-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-864-038A-3
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 KGRKTNYTLHVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILED 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AEAPQSLRRQ----RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --IDQWNAKNSDI---TVGQYGGNNAALVNQT----ASD 132
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APPLICANT: Snyder, Yvonne M
APPLICANT: Sharp, Robert L
TITLE OF INVENTION: HUMAN GLUTAMATE RECEPTOR AND RELATED DNA
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lillv n --
STREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 90; DB 4; Length 906; 22.6%; Pred. No. 1.1; tive 26; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ELIOTT, Candace
APPLICANT: ELIOTT, Candace
APPLICANT: NUTT, Stephen
TITLE OF INVENTION: APPA-BINDING HUMAN GLURI RECEPTORS
NUMBER OF SQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: $3000 K Street N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/172,332
FILING DATE: 2-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/879,688
FILING DATE: May 1, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AHALQSDARKSETTITQSGYGNGADV------GOGAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Foley & Lardner
: 3000 K Street N.W., Suite 500
Washington, D.C.
                                                                                                                                                    STREET: Lilly Patent Division/JPL STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-216-326-2
; Sequence 2, Application US/08216326
; Patent No. 6406868
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 SSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Leeds, James P.
REGISTRATION NUMBER: 35241
REFERENCE/DOCKET NUMBER: X-I
TELECOMMUNICATION INFORMATION:
TELECHONE: 317-276-1667
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 906 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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Best Local Similarity 22.6
Matches 45, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: KUNIO NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 AHALQSDARKSETTITQSGYGNGADV-----GQGAD----
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPACTION
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,326
FILING DATE: 23 MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,611
FILING DATE: 10-UM-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Diskette, 3.50 inch, 1.44 MB storage
IBM Compatible
:YSTEM: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.5%; Score 90; DB 4
Best Local Similarity 22.6%; Pred. No. 1.1;
Matches 45; Conservative 26; Mismatches
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28 GGGNHNGGGNSS---GPDYDQLVTRVVTHEMAHALQSDARKSETII----TQSGYGNGAD 80
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STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                             NNAALV----NQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                           189 NNSTVAGGSHNQATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Cailly States
ZIP: $90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OBERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
RILING DATE: 19910813
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 907 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 9103330318
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (619)535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Conservative
                                                                                            VGQG-----ADNSTI
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Best Local Similarity
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TELEFAX: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               419 LIKSSASASASASASASAG----GGGGGGNGGGNGGGGG-------GG 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-09-336-447A-5
Sequence 5, Application US/09336447A
Batent No. 6310190
GBNERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: APBL, CHRISTOPH
APPLICANT: MACIVER, ISOBEL
APPLICANT: MACIVER, ISOBEL
APPLICANT: PISKE, MICHAEL J.
APPLICANT: PREDENBURG, ROSS A.
TITLE OF INVENTION: USPAI AND USPAZ ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
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25.6%; Pred. No. 1.5;
tive 11; Mismatches 59; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 84; DB 4; Length 892; illarity 26.8%; Pred. No. 4.3; Conservative 17; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGALAAALAAAGAGGGLGGGGGGALAAALAAAGAGGGGFGGLGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 YGGNNAALVNQTASDSS------VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 LGGGSAAAAAAAAAAGGGGRALRRALRRQMRGGGSAAA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | NAME/KEY: peptide | Lo 738 | LOCATION: from 1 to 738 | LOCATION METHOD: E (by experiment) US-08-864-0388-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                           FILING DATE: MAY 28, 1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: JS-July-1996
ATTORNEY/AGBMT INFORMATION:
NAME: C. BULCE Hamburg
REGISTRATION NUMBER: 22,389
REGISTRATION NUMBER: P-5610
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUS (212)986-2340
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: J38
                                               US/08/864,038A
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TYPE: mino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.6%
Matches 41; Conservative
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: May 28, 1
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Best Local Similarity
Matches 41; Conserv
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31ò Q---RIDISRRGNAGDCLANPAVFWGĞGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL 366 367 HVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTILEDPYVMLKK-- 424 75 GGKDNBAKGNYSTVGGGDYNBAKGNYST--VGGGSSNTAKGEKSTIGGGDTNDANGTYST 132 -ELTQNGFRNNATIDQWNAKNSDITVGQYG---G 120 133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATG 188 250 VIGFQLVNYIDIIPARIMQQMRISDSRDHIRVDWKRPKYTSALIYDGVKVMAEAFQSLRR -----IDQWNAKNSDI---TVGQYGGNNAALVNQT----ASDSSVMVRQVG 6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEMAHALQSDAR 65 KSETTITQSGYGNGADV-----GQGAD------NSTIELTQNGFRNNAT-Gaps 54; US-07-718-575-2; Sequence 2; Application US/07718575; Patent No.: 520257; Patent No.: 520257; Patent No.: 520257; Patent No.: 520257; Patent No.: 520257; Patent No.: 520257; Patent No.: 520257; Patent No.: 520257; Patent No.: 520257; Patent No.: 5202677; Patent Ph.D., James R., APPLICANT: Bettler Ph.D., Michael NWN APPLICANT: Bettler Ph.D., Jan E., TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND TITLE OF INVENTION: METHODS; NUMBER OF SEQUENCES: 14; CORRESPONDENCE ADDRESS: 10.8%; Score 84; DB 1; Length 907; 22.6%; Pred. No. 4.4; tive 24; Mismatches 69; Indels

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65 KSETTITQSGYGNGADV-----GQGAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA,
APPLICATION NUMBER: 08/013,767
FILING DATE: 04-FEB-1993
APPLICATION NUMBER: 07/118,575
FILING DATE: 21-UN-1991
APPLICATION NUMBER: PCT/US90/06153
FILING DATE: 25-0CT-1990
APPLICATION NUMBER: 07/428,116
FILING DATE: 27-0CT-1980
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9866
                                                        ; Sequence 2, Application US/08486269A; Patent No. 5945509; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Reiter, Stephen E
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 907 amino acids
amino acid
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TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                             92121
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                    RESULT 13
US-08-486-269A-2
                                                                                                                                                                                                                                                                                                                                                                                    STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 KSETTITQSGYGNGADV------GQGAD-----NSTIELTQNGFRNNAT- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 Q---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --IDQWNAKNSDI---TVGQYGGNNAALVNOT-----ASDSSVMVRQVG 141
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10.8%; Score 84; DB 1; Length 907;
Best Local Similarity 22.6%; Pred. No. 4.4;
Matches 43; Conservative 24; Mismatches 69; Indels
                                                                                                                                                                                                          APPLICANT: Heinemann Ph.D., Stephen F.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Bettler Ph.D., Bernhard NWN
APPLICANT: Jensen Ph.D., Jan E.
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TOWNBESONDENCE: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 So. Flower St., Suite 2000 CITY: Los Angeles STATE: California COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION 530
PRICR APPLICATION DATE:
APPLICATION NUMBER: US/08/013,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
                                                                                                                                            Sequence 2, Application US/08481206
Patent No. 5739291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 9103330318
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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(619) 535-8949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                        ----NANOF 429
142 FGNNATANOY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 Q---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: ALL, CURE.
OPERATING STEM: DOS
SOFTWARE: FASISEQ for Windows DEMONSTRATION Version 2.0D
SOFTWARE: PAPLICATION DATA:
APPLICATION WINSER: US/08/486,269A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.8%; Score 84; DB 2; Length 907; 22.6%; Pred. No. 4.4; tive 24; Mismatches 69; Indels
APPLICANT: Heinemann, Stephen F.
APPLICANT: Boulter, James R.
APPLICANT: Boulter, Michael
APPLICANT: Heilmann, Michael
APPLICANT: Bettler, Bernhard
APPLICANT: Gensen, Jan E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS
TITLE OF INVENTION: AND METHODS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600 CITY: San Diego
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 FGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNSGNYNTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
                   APPLICANT: Twardzik, Daniel R. APPLICANT: Twardzik, Daniel R. APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. Taricant. Hendricher Compound C. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350 CORRESPONDENCE ADDRESSES: SED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 84; DB 4; Length 943; Pred. No. 4.7; 9; Mismatches 41; Indels
                                                                                                                                                                                                                                                                   STATE: Washington
COUNTRY: USA
ZIP: 198104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J: 31,392
REBRENCEY/DOCKET NUMBER: 31,392
REBRENCEY/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 199:
SEQUENCE CHRACTERISTICS:
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHRACTERISTICS:
LENGTH: GARACTERISTICS:
LENGTH: 943 amino acids
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Best Local Similarity 25.2%;
Matches 31; Conservative
                                                                                                                                                                                                                             CITY: Seattle
STATE: Washington
Vedvick,
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                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Dillon, Davin C.

ITILE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241

CORRESPONDENCE ADDRESS:

ADDRESSES: SEED and BERRY LLP

STREET: G300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Dam PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

APPLICATION NUMBER: US/09/056,556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-072-596-199
Sequence 199, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
(206) 622-4900
TELEFAX: (206) 682-6910
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
STRANDENNESS:
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.2'
Matches 31; Conservative
                                                      ----NANOF 429
     142 FGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-056-556-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

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2: /cgn2_6/prodata/2/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/PCT_NEW PUB.pep:*

4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/prodata/2/pubpaa/US07_NEW PUB.pep:*

6: /cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*

7/cgn2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*

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18: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 4, Appli	ď	Sequence 2, Appli	Sequence 20638, A	Seguence 44999, A	Sequence 4, Appli	Sequence 146, App	Sequence 7, Appli	Sequence 2, Appli	Sequence 998, App	Sequence 203972,	Seguence 37715, A	Seguence 114193,	Seguence 232271,
ΩΙ	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-282-122A-44999	US-10-647-057-4	US-09-793-306-146	US-10-233-449-7	US-10-251-661-2	US-10-408-765A-998	US-10-424-599-203972	US-10-425-114-37715	US-10-437-963-114193	US-10-424-599-232271
	12	12	12	12	15	12	12	o	12	14	16	12	12	16	12
% Query Match Length DB	151	151	131	131	445	974	580	597	906	906	1448	204	244	253	283
% Query Match	66.7	66.7	56.9	56.9	13.9	11.9	11.7	11.7	11.5	11.5	11.4	11.3	11.3	11.3	11.3
Score	520	520	444	444	108.5		91.5	91	90	90	89	88.5	88.5	88.5	88.5
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	2 US-10-282-122A-	2 US-10-282-122A-6779	2 US-10-425-114-4601	6 US-10-475-970-1	US-09-810-264-28	2 US-10-282-122A-648	5 US-10-369-493-12833	6 US-10-437-963-1187	2 US-10-424-599-16889	0 US-09-952-267-5	US-09-996-634-131	0 US-09-997-182-13	0 US-09-997-1	4 US-10-193-002-19	4 US-10-084-843-20	US-10-282-122A-4977	2 US-10-282-1	US-09-996-194-16	2 US-10-164-9	2 US-10-282-122A-	0 US-09-952-267-13	4 US-10-238-C	0 US-09-820-843A-21	US-09-976-297-	US-09-801-368-1	2 US-10-282-122A-7632	2 US-10-282-12	US-09-797-862-33	0-045-674-594	2 US-10-282-122A-5	
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ALIGNMENTS

, Sequence 4; Application US/09741873B , Publication No. US20020081722A1 ; GENERAL INFORMATION:

US-09-741-873B-4

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APPLICANT Olsen, Arne
APPLICANT Olsen, Arne
APPLICANT Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT PILING DATE: 2003-04-04
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR PRIOR APPLICATION NUMBER: US 07/790,846
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
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ORGANISM: Escherichia coli
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Best Local Similarity 68.28
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-741-873B-4
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US-92-741-85-24
US-92-741-85-24
Sequence 2, Application US/09741873B
Fublication No. US20040096965A9
Fublication No. US20040096965A9
Fublication No. US20040096965A9
Fublication No. US20040096965A9
Fublication No. US2004004
FITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERBENCE: 012889-084
CURRENT FILING DATE: 01289-084
CURRENT FILING DATE: 1998-05-06
FRIOR APPLICATION NUMBER: US 08/978,878
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-06
FRIOR FILING DATE: 1999-05-04 07/89,437
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR FILING DATE: 1992-11-03
FRIOR FILING DATE: 1992-11-03
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.0
SOFTWARE: Patentin Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRXNSEWTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.9%; Score 444; DB 12; Best Local Similarity 65.6%; Pred. No. 1.2e-37; Matches 86; Conservative 19; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
                          PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
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PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-01-28
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NUMBER: PRIOR FILING DATE: 1994-10-05
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       SE 8801723-1
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US-09-741-873B-2
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TTILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TTILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TTILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 1098-05-04
FRIOR PELING DATE: 1998-05-04
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR APPLICATION NUMBER: US 07/789,846
FRIOR APPLICATION NUMBER: US 07/790,846
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR PILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1994-10-28
FRIOR FILING DATE: 1994-10-58
FRIOR FILING DATE: 1994-10-58
FRIOR FILING DATE: 1994-10-58
FRIOR FILING DATE: 1994-10-58
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                                                                                                                61 SDARKSETTITQSGYGNGADVGQGADNSTIELFQNGFRNNATIDQWNAKNSDITVGQYGG 120
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Publication No. US20020081722A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-096
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
1 MKLLKVAAIAAIVFSGSAVAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ 60
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                                                                                                                                                                                                                                                    121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin version.3.0 SEQ ID NO 4 LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Escherichia coli
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US-09-741-873B-2
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Sequence 4; Application US/10647057
Publication No. USS0040047871A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KNASAS STATE UNIVERSITY RESEARCH FOUNDATION
APPLICANT: STEWART, GEORGE
APPLICANT: GENERALA, T.
APPLICANT: CHENGAPPA, M. SANJERV
APPLICANT: CHENGAPPA, M. SANJERV
APPLICANT: CHENGAPPA, M. THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION THEREOF
CURRENT APPLICATION NUMBER: US/10/647,057
CURRENT APPLICATION NUMBER: US/10/647,057
CURRENT FILING DATE: 2003-08-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                    APPLICANT: Xu, H.

JITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITTA. 034
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-66
PRIOR FILING DATE: 2000-09-06
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PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR PILING DATE: 2001-127
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11.9%; Score 93; DB 12; Length 974;
Best Local Similarity 24.5%; Pred. No. 1.5;
Matches 36; Conservative 23; Mismatches 52; Indels
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                                                            Carr, Grant
Yamamoto, Robert
                                                                                                                                                                              Forsyth, R.
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Fublication No. US20030233675A1

GENERAL IRPORMATION:

APPLICANT: Glater, Steven C.

APPLICANT: Glater, Steven C.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 ----VKQSGNSNSVGRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                                                                                                                                                                                                                                                                                 81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
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                                                                                                                                                                              GVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGAD 80
                                                                                                                                                                                                                                                                               1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
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                                                      26; Indels
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Pred. No. 1.2e-37; 9; Mismatches 26
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COTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
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Sequence 44999, Application US/10282122A
Publication No. US20040029129A1
GENERAL INPORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Rari
APPLICANT: Ohlsen, Rari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Best Local Similarity 65.6%; Pr
Matches 86; Conservative 19;
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Best Local Similarity
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Careix, Midnel
APPLICANT: Ovendale, Pamela
APPLICANT: Jon, Shyian
APPLICANT: Cores, Midnel
APPLICANT: Cores, Midnel
APPLICANT: Cores, Midnel
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: Of Tuberculosis
FILE REFERENCE: 104058-008740US
CURRENT APPLICATION NUMBER: US 60/185,037
FRIOR APPLICATION NUMBER: US 60/185,037
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR FILING DATE: 2000-02-25
PRIOR PRILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 DNSTIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 399 GNAGD -- TNTGFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGN--AGNQS-----VGFG 449
                                                                                                                                                                                                                                                                                      ---- DVGOGADNSTIELTONGFRN 99
                                                                                                                                                                                           -----GGGNSSGPDYDQLVTRVVTHEMAH
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            100 NATIDQWNAKNSDITVGQYGGNNAAL---VNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His
US-09-793-306-146
                                                                                             Query Match
11.7%; Score 91.5; DB 12; Length 580;
Best Local Similarity 23.1%; Pred. No. 1.1;
Matches 40; Conservative 18; Mismatches 56; Indels 59
                                                                                                                                                                                                                                                                                                                                303 AKHVNVAKSSTVVVNAASGASKDASGMGSGAWDSNDTAKVDKGRSADSNV---
                                                                                                                                                                                                                                       257 KKAKKKGAVVNAASVAGIDKSAGGVAAVNIVKNKKASGSNKAGD-----
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                                                                                                                                                                                                                                                                                   ALQSDARKSETTITQ-----SGYGNGA--
                                                                                                                                                                                        5 KVAAFAAIVVSGSALAGVVPQWGGGGNHN-
; TYPE: PRT
; ORGANISM: Fusobacterium necrophorum
US-10-647-057-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 146, Application US/09793306
Patent No. US20020098200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-793-306-146
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LENGTH: 597
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RESULT 9
US-10-233-449-7
Sequence 7, Application US/10233449
; Publication No. US20030211040A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 VIGFQLVNYIDTIPAKIMQQW------KNSDARDHIRVDWKRPKYISALIYDGVKVM 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AEAFOSLRRO----RIDISRRGNAGBCLANPAVPWGGGIDIQRALQQVRFEGLTGNVQFNE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --IDQWNAKNSDI---TVGQYGGNNAALVNQT----ASD 132
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                    APPLICANT: Repaske, David
APPLICANT: Repaske, David
TILE ON INVENTION: PHOSPHODIESTERASE ACTIVITY AND REGULATION OF
TILLE OF INVENTION: PHOSPHODIESTERASE
TILLE OF INVENTION: 1B-MEDIATED SIGNALING IN BRAIN
FILE REPRENCE: 11181-010-999
CURRENT APPLICATION NUMBER: US/10/233,449
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 60/316,320
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alberini.
TITLE OF INVENTION: Methods and Compositions for Regulating
TITLE OF INVENTION: Methods Consolidation
TITLE OF INVENTION: Memory Consolidation
FILE REFERENCE: 3499.1001.003
CURRENT APPLICATION NUMBER: US/10/251,661
CURRENT FILING DATE: 2002-09-03
FRIOR APPLICATION NUMBER: 60/133,614
FRIOR APPLICATION NUMBER: FCT/US01/10661
FRIOR PRILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
LENGTH: 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 906; 2.8;
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11.5%; Score 90; DB 14; Length 90
Best Local Similarity 22.6%; Pred. No. 2.8;
Matches 45; Conservative 26; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 90; DB 22.6%; Pred. No. 2.8; ive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10251661; Publication No. US20030166555A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 SSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
APPLICANT: Greengard, Paul
APPLICANT: Repaske, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-251-661-2
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
'-hes 45; Conserva
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 906
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Sequence 37715, Application US/10425114
; Sequence 37715, Application US/20040034888A1
; Sequence 37715, Application No. US20040034888A1
; Dublication No. US20040034888A1
; APPLICANT: Inu, Jingdong
; APPLICANT: Thu, Jingdong
; APPLICANT: Tabaska Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                       81 VGQGADNSTIELTQNGFRNNATIDQMNAKNSDIT------VGQYGGNNAALVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 ----YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------NAAN--YVSGMFGGNNH--VNE 122
                                                                                                                                                                                                                                               106 GRVP-W-GGNSHERGGYSDG------SGWGQGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GGGGNHNGGGNSSGPDY------DQLVTRVVTHEMAHALQSDARKSETTITQSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 GGGGNNNNNNNBGTNYFATSSAPSLFSNSVNASALSHMSATALLQKAAQMGATTSNGGT
                                                                                                                                                                                                 GVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGAD
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                                                                                                                                                        61;
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                                                                                                            Score 88.5; DB 12; Length 204; Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 244;
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                                                                                                                                                     30; Indels
                     FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT3847_26213C.1.pep
US-10-424-599-203972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: LIB3170-053-G12_FLI.pep
US-10-425-114-37715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.3%; Score 88.5; DB 12; 22.9%; Pred. No. 0.76; ive 21; Mismatches 48;
                                                                                                     11.3%; Score vo 0.61; 25.7%; Pred. No. 0.61; rive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 114193, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Rovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 ASLLKSFGSASSSSGGGGSKLV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 QSNSNLQDLMNSFAVGGNSS 142
                                                                                                                                                                                                                                                                                                                                                                                      132 DSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GWGKNAT 189
                                                                                                            Query Match
Best Local Similarity 25.7%
Matches 35, Conservative
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ORGANISM: Glycine max
ORGANISM: Glycine max
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Best Local Similarity
Matches 32; Conserva
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US-10-437-963-114193
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 KGRRTNYTLHVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTILED 417
                                             301 AEAFQSLRRQ----RÍDISRRGNAGDCLANPAVPWGQGIDIQRALQQVAFEGLTGNVQFNE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 NGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTIT-QSGYGNGADVGQGADNSTIE 91
  --NSTIELTQ 94
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                                                                                                                                                                                                                                                                                                                                 Sequence 998, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Glosh, Sounitra S.
APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Glosh, Steven W.
APPLICANT: Glosh, Steven W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Steven W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660084.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 TLKPGPQQN-----WASKPQDNNVSNWGG--AASVKQTGT 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 LTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTAS 131
    AHALQSDARKSETTITQSGYGNGADV------GQGAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AAIVVSGSALAGVV-----PQWG----
                                                                                                                                                                                                                                418 PYVMLKK-----NANOF 429
                                                                                                                                                                                  133 SSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.4%;
24.4%;
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Best Local Similarity 24.43
Matches 39; Conservative
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ORGANISM: Homo sapiens
US-10-408-765A-998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-203972
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LENGTH: 1448
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5321) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 114193
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23221, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GGGGNNNNNNNEGTNYFATSSAPSLFSNSVNASALSHMSATALLQXAAQMGATTSNGGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 -----YGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGGNNAALVN- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 DYDQLVTRVVTHEMAHALQSDARKSETTITQSGY----GNGADVGQGADNSTIELTQNGF 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.3%; Score 88.5; DB 16; Length 253; Best Local Similarity 26.6%; Pred. No. 0.8; Matches 38; Conservative 14; Mismatches 48; Indels 43.
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US-10-424-599-232271
                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_17908C.1.pep
US-10-437-963-114193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LKVAA--FAAIVVSGSALAGVVPQWG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 RNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 YGYAGSSSAGGSGAGAGAGQAGG 190
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  Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                          ORGANISM: Oryza sativa FEATURE:
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US-10-424-599-232271
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LENGTH: 283
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Search completed: August 2, 2004, 15:36:11 Job time : 37.8 secs

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Sequence 22, Appl
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Sequence 34, Appl
Sequence 5834, Ap
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25818, A
25818, A
                       Sequence 5, An
Sequence 57, An
Sequence 26,
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Sequence 16,
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 151
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Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
19 US-09-543-407-18

US-09-543-407-15

19 US-09-543-407-26

19 US-09-543-407-26

19 US-09-543-407-16

19 US-09-543-407-112

19 US-09-543-407-114

19 US-09-543-407-14

19 US-09-543-407-14

19 US-09-543-407-24

10 US-09-543-407-24

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10 US-09-543-407-30

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US-09-543-407-6
US-09-614-1508-25818
US-09-614-1508-25818
US-60-191-637-25957
US-0101-637-25957
US-10-191-637-25957
US-10-191-637-25957
US-10-191-637-25957
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US-60-446-775-358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 18, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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1308
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         RESULT 1
US-09-543-407-18
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116
108:5
108:5
107:5
106:5
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276
250.5
175
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                                                                  2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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780
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
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(ggn2_6/ptodata/2/paa/PCTUS_COMB.ppp:*
(ggn2_6/ptodata/2/paa/US06_COMB.ppp:*
(ggn2_6/ptodata/2/paa/US08_COMB.ppp:*
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                             6019581 seqs, 976053577 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Minimum DB seq Maximum DB seq

Database

Scoring table:

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Score

Result

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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTRARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

86.5%; Score 675; DB 19; Length 151;
Best Local Similarity 81.9%; Pred. No. 7.3e-64;
Matches 136; Conservative 0; Mismatches 0; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                               CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: El POPPY disk
COMPUTER: El PR PC COMPATIBLE
COMPUTER: El PR PC COMPATIBLE
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/23,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KING, JOSHUA
REFERENCE/DOCKET NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
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Pred. No. 4.8e-65;
3; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAONE: (206) 622-4900
TELEFAX: (206) 682-631
TELEX: 3723836 SEBDANBERY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.9%;
ilarity 90.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 151 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-233-642A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 136; Conserv
                                  COUNTRY: U.S.A. ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-543-407-26
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                                                                                                                                                                                                                                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGONHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
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                                                                                                                                Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASLESC for Windows Version 4.0
SEQ ID NOS: 59
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US-08-233-642A-57

Sequence 57, Application US/08233642A

GENERAL INFORMATION:

APPLICANT: Calinson, S. Karen
APPLICANT: Clouthier, Sharon C.

APPLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-

TITLE OF INVENTION: BASED VACCINES

NUMBER OF SEQUENCES: 58

NUMBER OF SEQUENCES: 58

NUMBER OF SEQUENCES: 58

STREEF: Seed and Berry

STREEF: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
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                                                                 Length 151;
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                                                          100.0%; Score 780; DB 19;
100.0%; Pred. No. 3.7e-75;
tive 0; Mismatches 0;
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Pred. No. 1.4e-65;
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Best Local Similarity 90.7%;
Matches 137; Conservative
                                                                                                                            Matches 151; Conservative
                                                              Query Match
Best Local Similarity
US-09-543-407-18
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                                                LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGCGNSSGPDSTLSIYQYGSANAALALQ 60
----- 42
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Callisson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
SUPPREST FILING DATE: 2000-04-05
SUPPREST FILE RESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                            APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
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                                                                                                                                                                  106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                              106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Pred. No. 3.6e-58;
0; Mismatches 0;
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GENERAL INFORMATION:
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Best Local Similarity 73.6<sup>5</sup>
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                              APPLICANT: White, Aaron P.
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US-09-543-407-16
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LENGTH: 151
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                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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APPLICANT White, Aaron P.
APPLICANT Colinaen, S. Karen
APPLICANT Colinaen, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REPRESENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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                                                                                                                                                                                                                         40;
                          FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                      Length 151;
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                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                 79.2%; Score 618; DB 19;
llarity 76.6%; Pred. No. 9.8e-58;
Conservative 0; Mismatches 0;
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78.6%; Score 613; DB 19;
Best Local Similarity 80.8%; Pred. No. 3.4e-57;
Matches 122; Conservative 7; Mismatches 22;
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM; Artificial Sequence
                                                                                                                                                                                                 Best Local Similarity
Matches 131, Conserv
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US-09-543-407-14
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US-09-543-407-12
                                                                                                                         US-09-543-407-16
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
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US-09-543-407-31
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APPLICANT: Collinson, S. Karen, J. APPLICANT: ADVINCENT: RAY, William W. J. TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES; FILE REPREBRENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
INVER: PRI
TYPE: PRI
ORCHANT: 151
TYPE: PRI
ORCHANT: ORCHANT: 151
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Aaron F.
APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESNITATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543.407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.3%; Score 611; DB 19; Length 151; Best Local Similarity 81.5%; Pred. No. 5.5e-57; Matches 123; Conservative 6; Mismatches 22; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.9%; Score 608; DB 19; Length 151; Best Local Similarity 82.1%; Pred. No. 1.2e-56; Matches 124; Conservative 5; Mismatches 22; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNQTASDSSVMVRQVGFGNNATANOY 151
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US-09-543-407-24
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LENGTH: 151
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61 VGQGADNSTIELTQNGFRNNATIDQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQV 120
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: COLINSON S. Karen
APPLICANT: COLINSON S. Karen
APPLICANT: BASSIEM W.
ITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
ITLE REFERENCE: 92003.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE PRESENTATION OF WINDOWS Version 4.0
SEQ ID NO 31
LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GVVPQWGGGGGNHNGGGRSGPDSTLSIYQYGSANAALALQSDARKSETTIIQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGAD
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JAPPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REPERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-64-05

NUMBER OF SEQ ID NOS: 59

SOUTHWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 131;
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Best Local Similarity 89.3%; Pred. No. 2.6e-56;
Matches 117; Conservative 3; Mismatches 11;
                                         121 NNAALVNOTASDSSVMVROVGFGNNATANOY
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; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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; OTHER INFORM
US-09-543-407-30
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US-09-543-407-7
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                                                                                           SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASISEQ for Windows Version 4.0
LENGTH: 151
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CURRENT APPLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SSOFTWARE: PASSEG for Windows Version 4.0
LENGTH: 151
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76.9%; Score 600; DB 19;
Best Local Similarity 81.5%; Pred. No. 8.4e-56;
Matches 123; Conservative 5; Mismatches 23;
                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                      121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
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; Sequence 30, Application US/09543407
; GENERAL INFORMATION:
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GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: NORMARK. Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVERTION RIBRONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REPERENCE: 012889-081
CURRENT FILING DATE: 1997-11-26
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                             1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGHGGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT COllinson, S. Karen
APPLICANT (COLLINSON, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTERQ for Windows Version 4.0
Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                  Length 151;
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                                                                                                                                           Query Match
76.8%; Score 599; DB 19;
Best Local Similarity 81.5%; Pred. No. 1.1e-55;
Matches 123; Conservative 5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.1%; Score 523; DB 19; 68.9%; Pred. No. 1.6e-47;
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Best Local Similarity
OTHER INFORMATION:
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Best Local Similarity 68.2%; Pred. No. 3.4e-47;
Matches 103; Conservative 21; Mismatches 27; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-05
EARLIER FILING DATE: 1994-01-05
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PAPENTANIN NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PAPENTIN VEY: 2.0
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; ORGANISM: Escherichia coli
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Search completed: August 2, 2004, 15:26:43 Job time : 167.9 secs

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Sequence 7906, Ap
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'Ggn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
'Ggn2_6/ptodata/2/paa/US08 NEW COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-170-205E-16659
PCT-US04-09988-9
US-60-56-6341-11622
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US-60-579-062-7906
US-09-952-2678-5
US-10-872-768-5
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GENERAL INFORMATION:
APPLICANT Normark's Staffan
APPLICANT Olsen, Arne
TITLE OF INVENTION: Fibrenectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084.
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
FRIOR PRIOR PAPLICATION NUMBER: SE 8801723-1
FRIOR FILING DATE: 1998-05-06
FRIOR FILING DATE: 1998-05-04
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
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FRIOR FILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-01-28
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FRIOR FILING DATE: 1994-01-05
FRIOR FILING DATE: PATENTIN VUMBER: US 08/318,519
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FRIOR FILING DATE: PATENTIN VERSION 3.0
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Sequence 22, App
Sequence 22, App
Sequence 30662,
Sequence 7905, Ap
Sequence 300390,
Sequence 317, App
Sequence 311, App
Sequence 36, App
Sequence 282, App
Sequence 26, Appl
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US-10-723-981-14
US-10-723-981-15
US-10-723-981-15
US-10-045-674A-521
US-10-045-674A-521
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US-10-579-062-7905
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ORGANISM: Escherichia coli
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Matches 103; Conservative
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SQUENCE 16659, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PREFEIT OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES OF SECULIARIES
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-KNSDARDHTRVDWKRPKYTSALTYDGVKVM 313
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PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/465,568
PRIOR FILING DATE: 2003-04-24
                                                                                            56 AHALQSDARKSETTITQSGYGNGADV-
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         263 VTGFQLVNYTDTIPAKIMQQW--
                                                                                                                                                                                                                                                                                                                                                                                                                                              133 SSVMVRQVGFGNNATANQY 151
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US-10-170-205E-16659
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT ADAPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 3413
LENGTH: 852
                                                                                                                                                    GENERAL INFURGATION:
GENERAL INFURGATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1999-05-04
PRIOR PILING DATE: 1999-05-04
PRIOR PELING DATE: 1991-11-06
PRIOR PAPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1991-11-06
PRIOR PELING DATE: 1991-11-06
PRIOR PELING DATE: 1991-11-06
PRIOR PELING DATE: 1994-10-28
PRIOR PELING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VORTER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
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65.6%; Pred. No. 1.5e-32;
iive 19; Mismatches 26;
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                                                                                       Sequence 2, Application US/09741873C GENERAL INFORMATION:
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Matches 86; Conservative
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US-09-741-873C-2
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US-10-170-205E-3413
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Best Local
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                                                                                                                                                                                                                                                                                                                                        Length 1905;
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                                                                                                                                                                                                                                                                                                                                                                               47; Indels
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
ATILE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 11622
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Best Local Similarity 24.4%; Pred. No. 23;
Matches 39; Conservative 18; Mismatches 47
                                                                                                                                                                                                                                               ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7525307CD1
PCT-US04-09388-9
PRIOR APPLICATION NUMBER: US 60/476,135
PRIOR FILING DATE: 2003-06-04
PRIOR PPLICATION NUMBER: US 60/476,583
PRIOR FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PERL PROGRAM
SEQ ID NO 9
LENGTH: 1905
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Sequence 7906, Application US/60565632
GENERAL INFORMATION:
PAPLICANT: Monsanto Technology, LLC
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US-60-556-841-11622
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Kovalic, David K.
Larosa, Thomas J.
                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Best Local Similarity
Matches 40; Conserv
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US-60-556-841-11622
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APPLICANT:
APPLICANT:
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ORGANISM:
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21(53403)B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 7906
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; LOCATION: (810)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-565-632-9906
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; Pred. No. 17; 
17; Mismatches 47; Indels
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APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Roberts, James K
Lu, Maolong
Munyikwa, Tichifa R.
Roberts, James K.
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ORGANISM: Diabrotica virgifera
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Best Local Similarity 24.7%
Matches 40; Conservative
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CURRENT APPLICATION NUMBER: US/10/872,768
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Moraxella catarrhalis US-10-872-768-5
                             10.8%;
26.8%;
                                                                                                                                                                                81 VGQG-----ADNSTI--
                             Query Match
Best Local Similarity 26.88
Matches 41, Conservative
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Best Local Similarity
Matches 41; Conserv
JS-09-952-267B-5
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SEQ ID NO 5
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                                                                                                                                                                                                                                                     Sequence 312468, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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 -----AKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNSTIELTQNGFRN------NATIDQWNAKN-----SDITVGQYGGNNAAL 125
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APPLICANT: AEBI, CHRISTOPH
APPLICANT: AEBI, CHRISTOPH
APPLICANT: ACORE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TILLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT FILING DATE: 2001-00-12
PRIOR FILING DATE: 1999-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 295;
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                                                                                                                             ASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                             464 DNGAAAENTGNADPAQGNDNGAAAENSGNENGIAAENNANAD 505
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                                                      ---FRNNATIDOWN---
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US-10-425-115-312468
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27.1%; Pred. No. 6;
:ive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 312468
LENGTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Moraxella catarrhalis
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                                                      82 GQGADNSTIELTQNG-
360 GNENGTAAGNNANPD-
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 5
LENGTH: 892
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                                                                                                                           121 NNAALVNQT
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US-10-425-115-312468
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US-09-952-267B-5
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75 GGKDNEAKGNYSTVGGGDYNBAKGNYST--VGGGSSNTAKGEKSTIGGGDTNDANGTYST 132
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                                                                                                                                                                                                                                                                                                      133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQAIG 188
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                                                                40; Gaps
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US-10-872-768-5
GEQUENCE 5, Application US/10872768
GEOGRAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ACBI, CHRISTOPH
APPLICANT: COPE, LESILE D.
APPLICANT: RISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALLS
FILE REFERENCE: AMCY:024
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GRNERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LEGLIE D.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: SERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/10/872,769
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                                                                Indels
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                                                                55;
; Score 84; DB 5; 
; Pred. No. 27; 
17; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                 189 NNSTVAGGSHNQATGEGSF---AAGVENKANAN 218
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llarity 26.8%; Pred. No. 27;
Conservative 17; Mismatches 55
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DB
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29.2%; Pred. No. 12,
110, 20; Mismatches
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    Plueckthun, Andreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 415 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: 280: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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US-09-952-267B-13
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                                                                                                                                                                                                                                                                                                                                                                75 GGKDNEAKGNYSTVGGGDÝNEAKGNYST - VGGGSSNTÁKGEKSTÍGGGDÍNDANGTYST 132
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Wu, Weil-Osterfeld, Karina C.
APPLICANT: Wu, Weil-Osterfeld, Karina C.
APPLICANT: Wu, Weil-Osterfeld, Maino Acid Sequences from Xenorhabdus TITLE OF INVENTION: And Uses thereof
FILE REFERENCE: 38-21 (53444) A CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 14985
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                                                                                                                                                                                                                                       6; Length 892;
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10.8%; Score 84; DB Best Local Similarity 26.8%; Pred. No. 27;
Matches 41; Conservative 17; Mismatches
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SSCTWARE: Patentin Ver: 2.1
SEQ ID NO 5
LENGTH: 892
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GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-872-769-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1070 KTDKLVVNGSTSGTTQ 1085
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ORGANISM: Xenorhabdus bovienii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-60-579-902-6263
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250 GGGSEGGGSGGGGSGSGDFDYEKMANANKGAMTENADENALÓSDAKGKLDSVATDYGAAID 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 GGG--GNHNGGGNSSGP-DYDQLVT----RVVTHEMAHALQSDAR-KSETTITQSGYGNG 78
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Sequence 13. Application US/09952267B

SENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABEL C.
APPLICANT: COPE, LESLIE D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT APPLICATION NUMBER: US/09/336,447
PRIOR PFILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                 c/o Fish & Neave
                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER I IBM PC COMPATIBLE

COMPUTER I IBM PC COMPATIBLE

COMPATING SYSTEM: PC-DOS/MS-DOS

COFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

RAPPLICATION DATA:

RAPPLICATION DATA:

RELING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
TITLE OF INVENTION: Profession (Poly) peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
FILING DATE: 18-RB-1995
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
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| SOFTWARE: Patentin Ver. 2.1
| SEG ID NO 13
| LENGTH: 873
| TYPE: PRT | 10.7%; Score 83.5; DB 5; Length 873; US-09-952-2678-13 | 10.7%; Score 83.5; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 5; Length 873; DB 66; Length 873; DB 66; Length 873; DB 66; Length 873; DB 66; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 873; Length 87
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Search completed: August 2, 2004, 15:29:52 Job time: 17.8 secs

us-09-543-407-18.rpr

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GenCore version 5.1.6
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n - pro	Section of MKI.I.KYZaBFaIIV/SGSaI.a		
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283366 seqs, 96191526 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	fimbrin protein ag	major curlin chain	curlin protein csg	curlin major subun	გ.	cnjB protein - Tet	curlin nucleator p	urlin	curlin minor chain	fimbrin protein ag	nucleation compone	conserved hypothet	_	probable PPE prote	hypothetical prote	hypothetical prote	protein C05B5.3 [i	leishmanolysin (EC	hypothetical glyci	probable PPE prote	leishmanolysin (EC	glutamate receptor	glutamate receptor	ep		pr	olysi	e recep	probable PPE prote
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DB	2	N	N	N	~	N	N	~	N	~	~	~	N	~	N	7	~	Н	N	7	н	N	~	7	N	~	N	~	73
	151																												
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-binding pr	protein - r	ice nucleation pro	_	듼	ч	hypothetical glyci	C05B5.3 protein (c	Di O	ū	probable RTX famil		leishmanolysin (EC	hypothetical prote	chorion E2 protein	leishmanolysin (EC
	816356	•	T21956	T20847	B71360	F70971	S43574	F70825	五70969	B85547	F90696	C42049	T26667	A25473	S19916
CJ (~	~													
1028	1213	1567	407	409	495	588	364	645	3716	5188	5291	638	586	633	646
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87.5	r~	~	87	98	98	85.5	(n (00	.00 .01	:00 :21	82	9 8	84:5	84	84	84
	31		33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

•	RESULT 1 JC6039 fimbrin r	RESULT 1 UC6039 Fimbrin nrotéin adfa premirsor - Salmonella enteritidis
	C;Species	ion 31-De
	C, Accessi R, Colline	C. Accession: UC6039, PC6015; A44898 R. Collinson, S. K.; Clouthier, S. C.; Doran, J. L.; Banser, P. A.; Kay, W.W.
	J. Bacter	
	A; Referen	
	A; Molecul	Afaccession: Guevas Modecule type: Jan Ab A pacidise: 1-151 CON.
	A, Cross-1	A. Cross-reference: GB: U43280; NID: 91184712; PIDN: AAC43599.1; PID: 91184714
	A;Molecule t	A;ACCESSION: FCSUIS A:AMOlecule type: protein A:Desidne: 21.52 / CO2.
	A, Experim	mental source: strain 27655-3b
	A;Note: 1	A;Note: the authors translated the codon ACG for residue 44 as Ile R:Collinson.'S.K.: Emodv. L.: Muller, K.H.; Trust, T.J.; Kav, W.W.
	J. Bacter	
	A;Title:	Purification and characterization of thin, aggregative fimbriae from Salmonell
	A; Contents:	ts: 27655
	A;Access:	A,Accession: 3A44898
	A; Status	A;Status: pyellminary A:Miacuia tyne: nrotein
	A;Residue	
	A; Note:	A.Note: sequence extracted from NCBI backbone (NCBIP:45936)
	A;Generics: A;Gene: aqfA	cs: aofà
	C; Function:	
	A; Descri	A;Description: major component of thin aggregative fimbriae A:Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
	C, Keyword	
	F;1-20/Dx F;21-151,	F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>
	Query Match Best Local: Matches 13	Ouery Match Best Local:Similarity 90.7%; Pred. No. 9.7e-53; Matches 137; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
	è	DEPUNDED FOR TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION OF TAXABLE SELECTION
	ž 8	MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
	ò	61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
	Дþ	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
	ò	121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151

csgł

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curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C;Species: Escherichia coli (C;Date: 18-Uul-2001 #text_change 18-Uul-2001 C;Date: 18-Uul-2001 #text_change 18-Uul-2001 C;Caccession: D90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DA, Reference number: A99629; MUDD:21156231; PMID:11258796 A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Status: Preliminary A;Residues: 1-152 <HAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Description: major component of wild-type curli, interaction between CsgA and CsgB tri
A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kninogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
transcriptional repression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:gl3360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A,Gene: ECs1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S34559
A;Molecule type: DNA
A;Residues: 1-13, 'RQRDSGWLW' <OLS3>
A;Experimental source: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
A;Title: The RpoS sigma factor relieves H-NS-mediated t:
A;Reference number: S31202; MUID:93211294; PMID:8459772
A;Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.1%; Score 523; DB 2;
68.9%; Pred. No. 3.1e-38;
iive 20; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.3%; Score 501.5; DB 2
67.1%; Pred. No. 2.3e-36;
iive 21; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 21-42;44-50 <CLS2>
R;Olsen, A.N.; Armqvist, A.M.
submitted to the EMBL Data Library, October 1992
A;Reference number: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                        A,Molecule type: DNA
A,Residues: 1-6,'V',8-151 <OLS1>
A,Cross-references: EMBL:L04979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Matches 104; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: csgA
A,Map position: 23.15
C,Function:
                                                                                                                                                                                                                        A;Accession: S34560
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Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   임
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NyAlternate names: csgA protein; major curlin protein
C;Species: Bacherichia coli major curlin protein
C;Species: Bacherichia coli major curlin protein
C;Species: Bacherichia coli coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli della coli dell
                                                                                                                                                          major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Typen

C;Species: Salmonella enterica subsp. enterica serovar Typen

A;Note: this species has also been called Salmonella typen

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AI0635

R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaca, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Itile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUD:21534947; PMID:11677608

A;Actus: preliminary

A;Molecule Cype: DNA

A;Residues: 1-151 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176

C;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 691; DB 2;
Pred. No. 9.7e-53;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 90.7%;
Matches 137; Conservative
121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-151 <BLAT>
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278
A;Experimental source: strain K-12, substrain MG1655
A,Cross-references: EMBL:X06462
C,Genetics:
A,Genetics:
C,Genetics:
A,Genetic code: SGC5
A,Introns: 85/3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 777/3; 2,136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 777/3; 2,136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 777/3; 2,1451-1454/Region: glycine-rich
E,1451-1464/Region: zinc finger CCHC motif
E,1530-1514/Region: zinc finger CCHC motif
E,1551-1568/Region: zinc finger CCHC motif
E,1551-1568/Region: zinc finger CCHC motif
E,1602-1615/Region: zinc finger CCHC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWGGGGNHINGG---GNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1640 OFGGGGNSNGGOSWGTSSGSDWN-------COSNVOES-TITSSGGWGS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.5%; Pred. No. 0.11;
Matches 39; Conservative 22; Mismatches 27; Indels 4
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A; Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551

A; Recession: H8566

A; Status: preliminary

A; Residues: DNA

A; Residues: 1-152 < STO>

A; Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z16

A; Genetics: A; Genetics: Strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C,Species: Escherichia coli
C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
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R;Martindale, D.W.; Taylor, F.M.
Nucleic, Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A,Reference number: $03650; MUID:88189811; PMID:3357771
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A,Molecule type: DNA
A,Residues: 1-1748 <TAX-A
A,Residues: 1-1748 <TAX-A
A,Residues: 1-1748 <TAX-A
A,Cross-references: EMBL:L03710; NID:g161751; PID:g161752
R;Taylor, F.M.; Martindale, D.W.
Nucleac Acids Res. 21, 4610-4614, 1993
A,Fitle: Retroviral-type zinc fingers and glycine-rich repeats in a protein encoded 3
A,Reference number: S42135; MUID:94051569; PMID:8233798
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C;Species: Tetrahymena thermophila
C;Date: 19-Mar.1997 #sequence revision 18-Jul-1997 #text_change 07-Dec-1999
C;Accession: S42136; S42135; S03650
R;Taylor, F;M.; Martindale, D.W.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 501.5; DB 2
Pred. No. 2.3e-36;
1; Mismatches 28
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A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <WAR>
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67.1%;
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Best Local
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Cjaccession: AH635
Rjearkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleation component of curlin monomers [imported] - Salmonella enterica subsp. enterica Cippecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                     fimbrin protein agfB precursor - Salmonella enteritidis
C.Species: Salmonella enteritidis
C.Accession: J-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C.Accession: JC6040
R.Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
B. Bacteriol. 178, 662-667, 1996
A.Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Description: minor component of thin aggregative fimbriae
A,Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-151 <PAR>
A,Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:gl6502314; GSPDB:GN00176
C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IATATINYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQEGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A;Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IELTQNGFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 NNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Reywords: fimbria
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-151/Product: fimbrin protein agfB #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 106.5; DB 30.7%; Pred. No. 0.029; iive 17; Mismatches 4
       151
   130 ASDSSVMVRQVGFGNNATANQY
                                              | :: |: | | | | | | | | | AYGNTAMIIQKGSGNKANITQY
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Best Local Similarity 30.7
Matches 35; Conservative
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Best Local Similarity
Matches 35; Conserv
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A; Residues: 1-151 <COL>
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                                                                         108
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A.Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A.Reference number: A88480; MUID:21074935; PMID:11206551
A.Accession: G8566
A.Status: preliminary
A.Reference undary
A.Resedius: 1-151 <870>
A.Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UMGP:216
A.Accession: GSPGE
A.Status: Preliminary
A.Resedius: 1-151 <870>
A.Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UMGP:216
A.Status: Preliminary
A.Resedius: C.Special Source: Strain 0157:H7, substrain ED1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minor curlin subunit precursor C8gB [imported] - Escherichia coli (strain O157:H7, subst Cispecies: Bscherichia coli (Species: Bscherichia coli (Species: Bscherichia coli (Species: Bscherichia coli (Species: 18-011-2001 #sequence_revision 18-011-2001 #text_change 18-011-2001 C;Accession: C90806 R;Hayashi, T.;Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA, Res. 8, 11-22, 2001 A;File: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: C90806 A;Accession: 
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                                                                                                                                                           70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC81419
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Pred. No. 0.024;
9; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 107.5; DB 2;
Pred. No. 0.024;
Pred. No. 0.024;
); Mismatches 43;
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ilarity 35.4%;
Conservative
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Best Local Similarity 35.4%;
Matches 29; Conservative
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Best Local Similarity 35.4%;
Matches 29; Conservative
Similarity
29; Conserv
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Matches 2
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: F70675
R;Cole S.T.; Erosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, ...
R;Cole S.T.; Brosch, R.; Parkhill, M.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Accession: F70675
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C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: AB143
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Erage, G.; Giller, W.; Scraft, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Ahathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A;Cross-references: GB:Z82098; GB:AL123456; NID:g3261664; PIDN:CAB05045.1; PID:e280737;
A;Experimental source: strain H37Rv
C;Genetics:
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A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference humber: AB2577; MUD:21608550; PMID:11743193
A; Accession: AB3143
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A; Cosserve Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrier Carrie
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50 VVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK 109
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                                                                                                                                                                                                                                  97 -----GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ
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12.0%; Score 93.5; DE
Best Local Similarity 27.1%; Pred. No. 1.8;
Matches 38; Conservative 16; Mismatches
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell (arap, F.; Romero, P.; Zanag, S.)

Science 294, 2317-2323, 2001

A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Recerence number: AB2577; MulD:21608550; PMID:11743193

A;Status: preliminary

A;Accession: AD3143

A;Status: preliminary

A;Accession: AD3143

A;Experimental source: strain C58 (Dupont)

A;Experimental source: strain C58 (Dupont)

A;Map position: linear chromosome
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C)Species: Agrobacterium_tumefaciens
C)Species: Agrobacterium_tumefaciens
C)Accession: H98144
R)Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Goience 294, 2323-2328, 2001
A)Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A, Accession: H98144
A, Status: preliminary
                                                                                                                                                                                                                                                                   conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain CS C,Species: Agrobacterium tumefaciens C,Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A;Cross-references: GB:AE007870; PIDN:AAK88682.1; PID:g15158413; GSPDB:GN00170 C;Genetics:
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12.2%; Score 95.5; DB 2; Length 145;
Best Local Similarity 24.2%; Pred. No. 0.25;
Matches 39; Conservative 22; Mismatches 57; Indels 43
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Best Local Similarity 24.2%; Pred. No. 0.25;
Matches 39; Conservative 22; Mismatches 57;
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A,Gene: AGR L_228
A,Map position: linear chromosome
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-!- FUNCTION: CURLIN IS THE STRUCTURE SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE=91310566; PubMed=1677357;
COllinson S.K., Emcody L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
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SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=9401373; PubMed=810466.
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA, the Structural gene for thin, aggregative fimbriae.";
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SPECIES-S.enteritidis; STRAIN=27655-3B;
MEDLINE-96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
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Collinacon S.K., Emcedy L., Trust T.J., Kay W.W.;

Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).

-!- FUNCTION: CURLIN 1S THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
STRAIN-K12 / W3110;
STRAIN-S93211294; PubMed=8459772;
Olsen A., Arngvist A.;
"The RpoS sigma factor relieves H-NS-mediated transcriptional "The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding curli
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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MEDLINE=93023873; PubMed=1357528;
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MEDLINE=97061202; PubMed=8905232;
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Mol. Microbiol. 7:523-536(1993).
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                                      (Rel. 24, Created)
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
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STRAIN=K12 / MC4100;
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                                                                                                                                                                                         NCBI_TaxID=562;
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FIBRONECTIN.
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CSGB ECOLI
P39828;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
28-FEE-2003 (Rel. 41, Last sequence update)
28-FEE-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coll 0157:H7.
Escherichia; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=1120551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grobeck E.J., Davis N.W., Linh S., Dimalante E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Walch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0157:H7 / ATCC 43895, MEDLINE=21218556; PubMed=11319125; Uhlich G.A., Keen J.E., Elder R.O.; associated with variations in the csgD promoter associated with variations in expression in certain strains of Escherichia coli 0157:H7.", Appl. Environ. Microbiol. 67:2367-2370 (2001).
                                                                                                                                                                                                                                                          Score 523; DB 1; Length 151;
Pred. No. 1.7e-38;
0; Mismatches 27; Indels
                                                                                                                                                                                                                         A -> E (IN REF. 1).
C003470D208D395F CRC64;
                                                                                                                                                                                                                MAJOR CURLIN SUBUNIT.
 SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                           152 AA.
                                                                                                                                                                                                                                                                                 20; Mismatches
                                                                                                        151 AA; 15049 MW;
                                                                                                                                                                                                                                                            67.1%;
68.9%;
                                                                                                                                                                                                                                                                     Best Local Similarity 68.9
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=83334;
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21
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSGA_ECO57
Q93U24;
                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                        SEQUENCE
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CSGA_ECO57
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PEDGINE TOTAL N. S. STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STR
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STRAIN=K12 / MC4100;
MEDLINE=56414468; PubMed=8817489;
Hammar M., Anguist A., Bian Z., Olsen A., Normark S.;
Hammar M., Anguist A., Bian S., Olsen A., Normark S.;
Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHAL
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria, Proteobbacteria, Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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MAJOR CURLIN SUBUNIT.
; EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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EMBL, AE005315; AAG55788.1; -.
EMBL, AP002054; BAB34843.1; -.
PIR, D90806; D90806.
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Best Local Similarity 67.1%;
Marches 102; Conservative
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EMBL; AE000205; AAC74125.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OLSTHI / KIMD 0509952;
MEDLINE-2115631; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic Escherichia coli "Complete genome sequence of enterchemorrhagic Escherichia coli Ols7.HT and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                    Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        **Ranguist A., Olsen A., Normark S.,
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the mucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CURLIN IS THE STRUCTUMAL SUBUNIT OF THE CURLI. CURLI AR
COLLED SURFACE STRUCTUMES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIRENDECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                          SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
MEDLINE=97426617; bubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.E.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21074935, PubMed=11206551,
Berna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Gorbbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=0157:H7 / EDL933 / ATCC 700927;
K-12.";
Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                    MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12;
MEDLINE-95157246; PubMed-7854117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                     Shao Y.;
                                                                                                                                                                                                                                                                                                               STRAIN=K12;
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                     Mau B.,
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EMBL; X90754; CAA62281.1; -.

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                                                                                                                                                                                                                                                                                                            70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                           49 IGQAĞINNSAQLRQĞGSKLLAVVAQEGSSNRAKIDQTGDYNL-AYIDQAĞSANDASISQG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
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                                                                                                                                                                                                                                   13.8%; Score 107.5; DB 1; Length 151; 35.4%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                          1 21 POTENTIAL.
22 151 MINOR CURLIN SUBUNIT.
151 AA, 15882 MW, B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSCWT.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CC-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA.
                                                                                                                                                                                                                                                                        9; Mismatches
           EMBL, D90741; BAA338311; --
EMBL, AP005315; AA655787.1; --
EMBL, AP005254; BAB34842.1; --
FIR, C90806; C90806.
FIR, S70787; S70787;
FIR, S70787; S70787.
FIR, S70787; S70787.
                                                                                                                                                                                                                                                                                                                                                                                  130 ASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                       | :: |: | | | | | | | | | | | | | AYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:848-852(2001)
                                                                                                                                                                                                                                                Local Similarity
es 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SALTI
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
CSGB_SALTI
                                                                                                                                                                                                                                                                        Jatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSGB
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Query Match
Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKO3 CAEEL
P34291;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                              55 MAHALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQNGFR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.19phimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Floraca L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURLI ARE
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MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fimbriae.";
J. Bacteriol. 178:662-667(1996).
J. Bacteriol. 178:662-667(1996).
J. Bacteriol. CURLI IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARCOLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 NRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                                                                 19;
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                                                                                                                                                                                                                                                                                  13.7%; Score 106.5; DB 1; Length 151; 30.7%; Pred. No. 0.015; Live 17; Mismatches 43; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGRED OR STM1143.
Salmonella typhimurium, and
Salmonella enteritidis.
                                                                               or send and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                   35; Conservative
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Matches 35; Conserv
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                                                                                                                                                                                                                                                                                       Query Match
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ID CSGB (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --IELTQNGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 NNATIDOWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 106.5; DB 1; Length 151; 30.7%; Pred. No. 0.015; ive 17; Mismatches 43; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 92; DB 1; Length 401; larity 23.2%; Pred. No. 0.8; Conservative 19; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRANIE-Brisch 17;
Mortimore B.J.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Durbin R.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 43.5 kDa protein C05B5.3 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 151 MINOR CURLIN SUBUNIT.
151 AA; 16182 MW; COFC5430E6DD361D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 401 AA; 43472 MW; C99DF259EF6C8B55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 MAHALQSDARKSE----TTITQSGYGNGADVGQ-GADNST---
                                                                                                                                                                                                                                                          EMBL, AJ002301, CAA05316.1; -.
EMBL, AE008749; AAL20073.1; -.
EMBL, U43280; AAC43598.1; -.
PIR, JC66040; JC66040.
StyGene, SG10609; CSGB.
Fimbria, Signal; Complete protecome.
SIGNAL.
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WormPep; C05B5.3; CE17369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.73
Matches 35, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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3 LLKVAAFAAIVVSGSALAGVV 30 LQQYRAYAGCSSSGCVFATIV 49 RVVTHE	Oy 133 SSWWRQVGFCNNATANQ 150 Db 198 NOVNGPTSGFSNQTSNQ 215 RESULT 8 OMPB_RICJA TO OMPB_RICJA TO OMPS_S; DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 10-MAY-2000 (Rel. 39, Last sequence update) DT 10-CT-2001 (Rel. 40, Last annotation update) DE COTT-2001 (Rel. 40, Last annotation update) DE COTT-2001 (Rel. 40, Last annotation update) E Sexes protein B precursor (168 kDa surface-layer protein) DE (Surface protein anishen) (Cell surface antigen 5) (Sacas) (Fromps) E (Nomp B) (Contains: 120 kDa surface-exposed protein (Surface protein		This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation. Ct the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial C entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch). DR EMBL, AB003681; BAA20138.1; - DR INTERPRO; IPR006315; Autotransporter. DR INTERPRO; IPR006315; Autotransporter. DR PROSTOR AUTOTRANSPORTER.	DR TIGREAMS; TIGRO1414; autocrans_barl; 2. KW Antigen; S-layer; Cell wall. FT CHAIN 1338 1556 BETA PEPTIDE. FT CHAIN 1339 1656 A3; 168097 MW; 3132A69C9DD5999F CRC64; Query Match Dest Local Similarity 26.2%; Pred. No. 4; Matches 45; Conservative 19; Mismatches 52; Indels 56; Gaps 9;
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                                                                                                       104
                                                                                                                                                              602
                                                 ----LANDATK 547
6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whether structure and the genes encoding the major surface glycoprotein of Leishmania donovani.";
Heterogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.";

-1. Elschmania donovani.";

-1. FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-1. CATALVIIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is P1' and basic residues at P2 and P3'. A codel nonapeptide is clavaved at -Ala-Tyr-1-Leu-Lys-Lys-.

-1. Cataved at -Ala-Tyr-1-Leu-Lys-Lys-.

-1. COPACTOR: Binds 1 zinc ion per subunit (By similarity).

-1. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-1. SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEISHMANDLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CAPALYTIC) (BY SIMILARITY).
ZINC (CAPALYTIC) (BY SIMILARITY).
ZINC (CAPALYTIC) (BY SIMILARITY).
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                                                                                                                                                        548 ---TLTLGGANIISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQTGVVDASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
KEL_TaxID=5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 34.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                               105 QWNAKNSDI--TVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                  Therepro, IPR006025; Pept M. Zn. BS.
InterPro; IPR001577; Peptidase_M8.
PEAN; PR00782, LEMMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Call adhesion; GPT-anchor; Lipoprotein.
SIGNAL.
                               66 SETTITQSG----YGNGADVGQGADNSTIELTQNGFRNNATID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                          590 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
TRAIN=LV9;
HEDLINE=92107220; PubMed=1762629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MBL; M60048; AAA29244.1; -.
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TEROPS; MO8.001;
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Mol. Biol. Evol. 10:127-139(1993).

-!- FUNCTION: Essential for biological clock functions. Determines the period length of circadian and ultradian rhythms; an increase in PER dosage leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythmicaty of locomotor activity, eclosion behavior, and for the rhythmic component of the male courtship song that originates in the thoracton nervous system. The biological cycle depends on the rhythmic formation and nuclear localization of the TIM-PER complex. Light induces the degradation of the TIM-PER complex. Light induces the degradation of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity).

-!- SUBUNIT: Forms heterodimer with timeless (TIM); the complex then transcroates into the nucleus (By similarity).
                                                                                                                                                                                                                                                                                                 241 YDÓLVÍRVVÍHEMAHALGESVVFFRDARILESISNVRHKDFDVPVINSSTAVAKAREQYG 300
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                                                                                                                                                                                                                                Gaps
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MEDLINE=97357421; PubMed=9214747;
Gleason J.M., Powell J.R.;
Gleason d.M., Powell j.R.;
Interspecific and intraspecific comparisons of the period locus in the Drosophila willistoria sibling species.";
Mol. Biol. Evol. 14:741-753(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peixoto A.A., Campesan S., Costa R.H., Kyriacou C.P.; "Molecular evolution of a repetitive region within the per gene of
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GPI-anchor amidated asparagine (By
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NCBI_TaxID=7260,
                                                                                                                                                                                              Length 590;
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                                                                                                                                                           OFB315D299659F58 CRC64;
                                                                                                                                                                                                                              39;
                                                                                                                                                                                          11.7%; Score 91.5; DB 1; 30.5%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PER DROWI STANDARD; PRT; 1093 AA. 003297; 018421; 018422; P91721; P91722; 01-0CT-1993 (Rel. 27, Created) 15-0UL-1998 (Rel. 36, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Period circadian protein (Fragment).
                                                                                                                                                                                                                            12; Mismatches
                                                                                                                                            similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                            352 LGFYQADFS-KAEEMPWGRNA 371
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MEDLINE=93196482; PubMed=8450754;
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Mol. Biol. E
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S -> F (IN STRAIN 0811.4).
G -> V (IN STRAIN 0811.4).
G -> A (IN STRAIN MANAUS 2).
G -> A (IN STRAIN MANAUS 2).
MISSING (IN STRAIN PORTO ALEGRE 3).
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SUBCELLULAR LOCATION: Nuclear at specific periods of the day.
                    SUPERILORAR INCATION: NUCLEAR AND SECURITY: Contains 1 PASSABLE STRING ACCOUNTING THE SECURITY SUCCESSION ADOUT ONE hour before translocation into the nucleus. Interaction with Tim is required for indebar localization (By similarity).

FOR INCERT STABLIZATION (BY SIMILARITY).

FIRE STABLIZITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABLIZITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER MISCELLANDON THE SECURITY. OF PER MONOMER AND IN THE FORMATION OF HETERODIMER MISCELLANDONS: THE SECURICE SHOWN IS THAT OF STRAIN ATLIXCO. SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains. SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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MISSING (IN STRAINS GUADELOUPE, MANAUS
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GUANA).
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InterPro; IPR00014; PAS_domain.
Pfam; PR00989; PAS; 2.
SWART; SM00091; PAS; 2.
PROSITE; PS50112; PAS; 2.
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EMBL, U51056, AAB41361.1)
EMBL, U51059, AAB41362.1,
EMBL, U51059, AAB41363.1,
EMBL, U51059, AAB41365.1,
EMBL, U51060, AAB41365.1,
EMBL, U51061, AAB41365.1,
EMBL, U51062, AAB41367.1,
EMBL, U51062, AAB41369.1,
EMBL, U51066, AAB41369.1,
EMBL, U51066, AAB41370.1,
EMBL, U51066, AAB41372.1,
EMBL, U51069, AAB41372.1,
EMBL, U51069, AAB41372.1,
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EMBL, U51069, AAB41373.1,
EMBL, U51069, AAB41373.1,
EMBL, U51069, AAB41373.1,
EMBL, U51069, AAB41375.1,
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EMBL; L06342; AAA28765.
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Structure 6:1035-1046(1998).

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at "Ala-Tyr-|-Leu-Lys-Lys-.
                                                                                                                                                                                 27 GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95406217; PubMed=7679788; Schlagenhauf E., Etges R., Metcalf P.; "Crystallization and preliminary X-ray diffraction studies of leishmanolysin, the major surface metalloproteinase from Leishmania
                                                                                                                                                                                                                                                                                                                                                GP63_LEIMA STANDARD, PRT, 602 AA. P08148, P15906, 01-AWG-1998 (Rel. 08, Created) 01-ARP-1990 (Rel. 14, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease) (Major surface glycoprotein) (GP63 protein) (Promastigote surface
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Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
 MISSING (IN STRAINS MANAUS 4, PORTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Button L.L., McMaster W.R., "Molecular cloning of the major surface antigen of leishmania."; J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Homans S.W., Bordier C., "Structure of the glycosyl-phosphatidylinositol membrane anchor
                                                                                                                     11.7%; Score 91; DB 1; Length 1093; 26.1%; Pred. No. 3.1; ive 8; Mismatches 46; Indels
                                                                                          115896 MW; AB6DE050267EC187 CRC64;
                                                             A -> T (IN STRAIN 0811.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Leishmania major promastigote surface protease.";
J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                                                            87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                         -----SCSGLGGNGNVGSGNGNNSQPSTNQY 796
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J. Exp. Med. 171:589-589(1990).
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COPACTOR: Binds 1 zinc ion per subunit.
SUBCELULIAR LOCATION: Attached to the membrane by a GPI-anchor.
PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED, UNBRANCHED 1-0-ALKYL CHAIN (MAINLY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-0-ACYL CHAINS (C12:0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL). N-LINKED (GLCNAC. . .) (POTENTIAL). GPI-anchor amidated asparagine.
                                                                                                                              C14:0, C16:0, AND C18:0).
SIMILARITY: Belongs to peptidase family M8.
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ZINC (CATALYTIC).
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CDTLEYLEVEDQGGAGSAGSHIKM 337

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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE PROM N.A.

MEDLINE=91352027; PubMed=1652753;

A Chen X.N., Hood L.E.;

Puckettic., Gomez C.M., Korenberg J.R., Tung H., Meier T.J.,

A Chen X.N., Hood L.E.;

Interpretate receptor genes.";

In Proc. Nail. Acad Sci. U.S.A. 88:7557-7561(1991).

I. Proc. Nail. Acad Sci. U.S.A. 88:7557-7561(1991).

I. Proc. Nail. Acad Sci. U.S.A. 88:7557-7561(1991).

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I. Proc. Nail. Acad Sci. U.S.A. 88:7557-7561(1991).
                                                                                                                                                                                                                                    MEDINE=92159065; PubMed=1311100; Sun W., Ferrer-Montiel A.V., Schinder A.F., McPherson J.P., Strans G.A., Montal M.; Evans G.A., Montal M.; Evans G.A., Montal M.; Income and functional expression of human brain glutamate receptors."; Proc. Natl. Acad. Sci. U.S.A. 89:1443-1447(1992).
                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Glutamate receptor 1 precursor (GluR-1) (GluR-A) (GluR-KI) (Glutamate receptor ionotropic, AMPA 1).
GRIAL OR GLURI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P42261-2; Sequence=VSP_000092, VSP_000093, VSP_000094, VSP_000096; VSP_000096, TISSUE SPECIFICITY: Widely expressed in brain.
MISCELLANBOUS: This receptor binds AMPA (quisqualate) > glutamate
                                                                                                                                                                         Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalià; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                              TISSUE=Hippocampus;
MEDLINE=2232975; PubMed=1320959;
Potter M.C., Spillantinh M.G., Carter N.P.;
The human glutamate receptor cDNA Glubl: cloning, sequencing, expression and localization to chromosome 5.";
DNA Seq: 2:211-218(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                         906 AA
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IsoId=P42261-1; Sequence=Displayed;
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EMBL; M64752; AAA58613.1;
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PIR; S25852; S25852.
HSSP; P19491; 1GR2.
                                                                                                                                                                 (Human)
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                                                                                                                                                                 Homo sapiens
                                                            HUMAN
                                  RESULT 12
GLR1_HUMAN
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6; Mismatches
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  This, 125.49;

R GO; GO: 0005886; C:plasma membrane; TAS.

R GO; GO: 0005866; F:glutamate receptor activity; TAS.

R GO; GO: 0001527; F: kainate selective glutamate receptor activity; TAS.

R GO; GO: 0007126; F:sglutamate selective glutamate receptor activity; TAS.

R GO; GO: 0007126; F:sglmal transduction; TAS.

R InterPro; IPR001329; NF receptor.

R InterPro; IPR001320; R-channel_pore.

R InterPro; IPR001508; NMDA_receptor.

R InterPro; IPR001311; SBS/glu_receptor.

R Pfam; PF01094; ANF_receptor.

R Pfam; PF01094; PRPed; Ind.

R Receptor, Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 KGRRINYTLHVIEMKHDSIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILED 417
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Fransmembrane; Alternative splicing.

SIGNAL 1 8 POTENTIAL.

CHAIN 19 906 GLUTAMATE RECEPTOR 1.

POMAIN 19 536 EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stenos J., Walker D.,

"The rickettsial outer membrane protein A and B genes of Rickettsia
"The rickettsial outer group.";

submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: THE 120 KDB SURFACE-EXPOSED FROTEIN IS A MAJOR.

STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by a S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
-!- By similarity)
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S
-!- SUBCELLULAR LOCATION Symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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G -> S (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).

I -> V (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

C -> S (IN REF. 3).

E -> S (IN REF. 3).

C -> S (IN REF. 3).

G -> S (IN REF. 3).

H -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 33-1649 FROM N.A.
SEQUENCE OF 33-1649 FROM N.A.
MEDLINE=20395643; PubMed=10395649;
ROUX V., Raoult D.;
Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rompB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                      "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001)
                                                                                                                                                                                             MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGRFAMS; TIGRO1414; autorrans_barl; 2.
Antigen; S-layer; Cell wall; Complete proteome.
CHAIN 1334 32 kDa SURRACE-EXPOSED PROTEIN.
CHAIN 1335 1655 32 kDa BETA PEPTIDE.
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E -> D (IN REF. 3).

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H -> R (IN REF. 3).

W, E49E19377D5FCE37 CRC64;
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EMBL; AFL23721, AAF34124.1; --
EMBL; AF123726; AAF34129.1; --
EMBL; AF149110; AAD39533.1; --
PIR; E97885; E97835
InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
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                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Malish 7;
                                                              NCBI_TaxID=781;
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                                                                                                                       552 GGANIIGANGGTINFQANGGTIKLTST--QNNIVVDFDLAIATDQTGVVDASSLTNAQTL 609
                                                                            ------LANDATK---TLTL 551
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                          Gaps
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SEQUENCE FROM N.A.
MEDLINE-92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
VCBI_TaxID=44271;
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01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 34.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks
Arg-Gly-Asp sequence.";
Mol. Biochem. Parasitol. 39:267-274(1990).
                          45;
DB 1; Length 1655;
                                                                                                       SGY----GNGADVGQGADNSTIELTQNGFRNNATID-------
                                                                                                                                                            DIT--VGOYGGNNAAL-----VNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                          90;
                                                                              LVGGALAAGTITLDGSATITGDIGNAGGAAALQGIT
11.3%; Score 88.5; D 25.2%; Pred. No. 8.1; ive 17; Mismatches
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InterPro; IPRO0157; Peptidase_MB.
Pfam; PFO1457; Peptidase_MB: 1
PRINTS; PRO0782; LSHMANOÏYSIN.
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EMBL; M28527; AAA29235.1; -.
PIR; A44951; A44951.
                          Conservative
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               Local Similarity
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MEDLINE=91293102; PubMed=1712294;

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Eukaryota, Metazoa, Arthropoda; Hoxapoda; Insecta; Pterygota;
Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Behydroidaa; Drosophilidae; Drosophila.
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PROSITE; PS00142; ZINC PROTEASE; 1.

Hydrolase, Metalloprotease; Glycoprotein; Metal-binding;
Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
SIGNAL
39
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01-0CT-1996 (Rel. 34, Created)
10-CCT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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MEDLINE=95021209; PubMed=7935398;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                 DR EMBL, U11383; AAB66216.1; -..

DR EMBL, U11383; AAB66216.1; -..

DR EMBL, X5977.2; CAB3621.1; ALT_SEQ.

PIR; A56038; A56038.

DR TRANSPRAC; TO0669; ...

DR TRANSPRAC; TO0669; ...

R PYBASE PEROUNG3028; OVO.

R INTERPRO; IPR007087; Znf C2H2.

R PROSITE; PS00028; Znr C2H2; 3.

R ROSITE; PS0157; Znr FINGER C2H2_1; 3.

R PROSITE; PS0157; Znr FINGER C2H2_1; 3.

R PROSITE; PS0157; Znr FINGER C2H2_2; 3.

M Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein; T DOWANT.

T DOWANT.
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11; Mismatches 58; Indels 47;
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2, 2004, 14:49:29

Search completed: August Job time : 5.3 secs

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August 2, 2004, 14:39:17; Search time 29.7 Seconds (without alignments) 1604:150 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	033802 salmonella Q7x243 citrobacter	VXZ40 CitioDaccei Q28cw63 escherichia	Q1xz3/ encerobacce Q54069 salmonella	Q9s3j5 escherichia Q94821 tetrahymena	Q8eih4 shewanella Q7x244 citrobacter	Q89ji3 bradyrhizob O7uczi shiqella fl	Q8cw64 escherichia	Q83ru7 shigella fl	Q89ck5 bradyrhizob	Q9s3j8 escherichia
SUMMARIES	033802 Q7X243	Q1X240 Q8CW63	Q/AZ3/ Q54069	Q9S3J5 Q94821	Q8EIH4 Q7X244	Q89JI3 O7UCZ1	Q8CW64	Q83RU7	Q89CK5	Q9S3J8
DB	1000	7 7 6	7 (7	04 N	16	16	16	16	16	C)
% Query Match Length DB	152	4 LD L	76	29 1748	502	171	160	160	1209	91
% Query Match	87.4	0.00	4.6 4.8 7.8	15.6	14.5	13.8	13.8	13.8	13.7	13.5
Score	593.5	44 0 0 0 4 0 0 0 0 0 0 0 0	428.5 303	122	113	108	107.5	107.5	106.5	105.5
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	Q9vix5 drosophila	ĽΩ		_		Q98ln6 rhizobium l		Q7x241 citrobacter	mycoplas	3	ro:	7	Q7v8s5 prochloroco	Q8eyy9 leptospira	σ			Q8xsd6 ralstonia s	Q89ji6 bradyrhizob	093397 cyprinus ca		m	Q9vix6 drosophila	P71868 mycobacteri	α	н		Q8ev92 mycoplasma
.0 154 16	.9 26	.8 179 2	.7 130 16	.6 157 16	.6 362 16	.6 3659 16	.5 151	.5 152 2	.4 368 16	.4 1422 16	.4 2035 2	.4 2039 16	.4 1765	.3 490 16	.2 145 16	.2 1613 2	.2 3501 16	.2 3552 16	.1 15	.1 348 13	.1 480 16	.0 139 16	.0 287 5	.0 582 1	.0 582 16	.0 1615 2	.9 141 16	.8 353 1
101/5 1	8 101 1	1 001 6	0 99 1	1 98 1	2 98 1	98 1	4 97.5 1	5 9775 1	6 97 1	7 97 1	8 97 1	9 97 1	96.5 1	1 96 1	95:5	95:5	95.5	95:5	94:5 1	94.5	94 1	93:5 1	93.5	1 93.	93.5	93.5 1	93 1	-σ
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ALIGNMENTS

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01-OCT-2003 (01-OCT-2003 (01-OCT-2003 (

PRELIMINARY;

Q7X243 Q7X243;

RESULT 2

27X243

121

g

Enterobacteriaceae; Citrobacter,

SEQUENCE FROM N.A.

Citrobacter sp. Fec2 Curlin-csgA protein.

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SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG 120
                                                                                                                               SDARKSDVTITOHGRGNGAVVGOGADDSTISLKOTGFQNSATIDOWNAKNADISVTOFGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
      MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAQ
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STRAIN=O6:HI / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MELOR R.A. Burlad V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhwa G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhwa H.I.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
EMBL; AE016759; AAN79779.1; -.
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STRAIN=Fec39;
Zogaj X., Bokranz W., Nimtz M., Romling
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Zogal X., Boxanz W., Nimtz M., Romling U.;
Zogal X., Boxanz W., Nimtz M., Romling U.;
Zogal X., Boxanz W., Nimtz M., Romling U.;
Zogal X., Boxanz W., Nimtz M., Romling U.;
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515700; CAD56672.1;
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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ZOGAJ X., Bokranz W., Nimtz M., Romling U.;
ZOGAJ X., Bokranz W., Nimtz M., Romling U.;
ZOGAJ X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515701; CAD56675.1;
SEMBL; AJ515701; CAD56675.1;
SEMBL; AJ515701; CAD56675.1;
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Enterobacteriaceae, Citrobacter.
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NNAALVNQTASDSSVMVRQVGFGNNAPANQY 151
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72-4151-4158(2003).

EMBL, AJS15702; CADS66781; -- SEQUENCE 150 AA; 15112 MW; 5D8BS2D872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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                                                                                                                                                                                                                                       33;
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 303; DB 2; Length 76; Pred. No. 6.6e-17;
                                                                                                                                                                     21; Indels
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fregment).
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                                                                                                                             DB 2;
                                                                                                                         54.9%; Score 428.5; DB 2
55.1%; Pred. No. 1.8e-26;
7ative 21; Mismatches 21
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                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQ--WGGGGNH
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                                                                                                                                                                     92; Conservative
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SEQUENCE FROM N.A.

TRANSPOSON=Insertion sequence 1S1;

MEDLINE=99314153; PubMed=10386375;

La Regione R.M., Collighan R.J., Woodward M.J.;

La Regione R.M., Collighan R.J., Woodward M.J.;

"Non-curliation of Escherichia coli 078:K80 isolates associated with

IS1 inserti on in csgB and reduced persistence in poultry infection.";

FPMS Microbiol. Lett. 175:247-253(1999).

NON_TER. 29 29
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Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Hymenostomatida,
Tetrahymenina, Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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MEDLINES BASISSHIP, PubMed=1357771;
Martindale D.W., Taylor F.W.;
"Multiple introns in a conjugation-specific gene from Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q94821 PPRELIMINARY, PRT, 1748 AA. (994821, P92145, P92145, P92145, P92145, P92145, P92145, P92145, P92145, P92145, P92145, P92141, Q94820, O1-FEB-1997 (TYEMBLYEL) 02, Created) (TYEMBLYEL) 02, Last sequence update) 01-CT-2003 (TYEMBLYEL) 25, Last annotation update)
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MEDLINE=94001569; PubMed=8233798;
MEDLINE=94001569; PubMed=8233798;
Taylor F.M., Martindale D.W.;
"Retroviral-type zinc fingers and glycine-rich repeats in a Lectroviral-type zinc fingers and glycine-rich melosis.";
encoded by cnjB, a Tetrahymena gene active during meiosis.";
Nucleic, Acids cas. 21.4610-4614(1993)
EMBL; X06462; CAB37323.1;
EMBL; X0646136; S42136;
PIR; S42136; S42136
HSSP; P05888; 1AAPF.
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                                                                                                                                                                                                                                                                                                             Score 122; DB 2; Length 29;
Pred. No. 0.0042;
1; Mismatches 2; Indels
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56 I -> N (IN REF. 1).
199624 MW; 0B03F210104008A3 CRC64;
                                                                                                                                                                                                                                                               29 AA; 2789 MW; E290DFC07ABBB243 CRC64;
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Nucleic Acids Res. 16:2189-2201(1988)
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GO: GO:0003676; F:mucleic acid bi:
InterPor; JPR001878; ZH_CCHC.

Fram, PF00098; ZH-CCHC; 7.

PRINTS, PR00339; C2HCZNFINGER.

SMART; SM0343; ZnF C2HC; 7.

CONFLICT 251 ZF.

CONFLICT 255 ZF.

CONFLICT 256 Z56 I ->
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[ Similarity 89.7%;
26; Conservative
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Best Local Similarity
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                               Conservative
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les 29; Conserv
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Q7UCZ1
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                                                                                                                                                                                                                                                                                                                                                                           MEDILINE-22297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Elsen J.A., Seshadri R., ward N., Methe B., Clayton R.A.,
Mayer T., Tsapin A., Soctu J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Feterson J.D., Umayam L.A., White O., Wolf A.M.,
Wamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
Genome sequence of the dissimilatory metal ion-reducing bacterium
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Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
1681 -SGSGNQ----TGGGWGSN---DNQQQQNENTGGGGWGSSNS---NQTNNESS---
                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
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502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                               01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nucleation component of curlin monomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.5%; Score 113; DB 16; I 26.0%; Pred. No. 0.64; ive 20; Mismatches 58;
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EMBL; AE015532; AAN53941.1; -.
                                                                                                                                                                                                                                  Conserved hypothetical protein.
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Best Local Similarity 26. تاریخ
است 40; Conservative
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                                                                1723 WGSNNQAS 1730
                                                                                                                                                                                                                                                                   Shewanella oneidensis.
                                 149
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SEQUENCE FROM N.A.
STRAIN=Fec2;
                                 142 FGNNATAN
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Citrobacter sp.
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJS15700; CADS6671.1; -.
SEQUENCE 151 AA; 16158 MW; BD00AF57E1400704 CRC64;
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Nakamara Y., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Rawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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DNA Res. 9:189-197(2010.)
EMBL; AP005954; BACS0865.1; -.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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Local Similarity 36.6%; Pred. No. 0.44;
nes 34; Conservative 10; Mismatches 39;
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25.0%; Pred. No. 0.24;
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MEDLINE=22484998, PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watenabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                          STRAIN=301 / Serotype 2a,
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun D., Xue Y., Zhao A. Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res: 9:189-197(2002).
EMBL; AP005963; BAC53057.1; -.
                                                                                                      Bacčeria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBL_TaxID=623;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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                                                                                                                                                                                                                                                                                                                                                                                                        160 AA; 16919 MW; 50269F5268D2A32F CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Minor curlin subunit precursor, similar ro CsgA. CSGB OR SF1035.
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Last annotation update)
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Best Local Similarity 35.4*
Matches 29; Conservative
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                                                                                               Shigella flexneri.
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SEQUENCE 1209 AP
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                                SEQUENCE FROM N.A.
STRAIN-2457T / ATCC 700930 / Serotype 2a;
STRAIN-2457T / ATCC 700930 / Serotype 2a;
STRAIN-22590274; Pubmed-12704152.
Webline-2590274; Pubmed-12704152.
Webline-2590274; Pubmed-12704152.
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Rau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella liexneri serotype 2a strain 2457T.";
Infect. Immun. 71:277-2786 (2003).
EMBL; AE016981; AAP16542.1;
SEQUENCE 151 AA; 15868 MW; 5D5D266B964014A0 CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Pred. No. 0.45;
9; Mismatches 43; Indels 1;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit precursor.
CSGB OR C1305.
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Pred. No. 0.42;
9; Mismatches
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35.4%;
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Best Local Similarity
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Q83RU7;
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Recombinant acfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SETI/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                           Salmonell
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             Aab36327
Aab36337
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AAB36322
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AAG29728
AAG29727
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36350 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356
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 Salmoneila enteritidis.
Escherichia coli.
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N-PSDB; AAC64626.
 WO200060102-A2
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   AgfA sequ
Salmonell
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E. coli c
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Aab36353 AgfA::PT3
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                                                                                                               2, 2004, 14:35:42 ; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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774
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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Aab36321
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Aab36338
Abr82644
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                               1586107 segs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                  OM protein - protein search, using sw model
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ABR82651
AAR62761
AAW23569
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AAB36351
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geneseqp2003as:*
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geneseqp2004s:*
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geneseqp1990s:*
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Match Length
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Score

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Minimum DB Maximum DB

Database

Title: Perfect score:

Run on:

Seguence:

Scoring table:

Searched:

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copy of that gene, and (4) eliciting an immune response in an animal, compyrising separating an amino acid polymer comprising a recombinant Agra protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriacaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant Agra protein which is useful for the expression of recombinant Agra protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens; which may be important for directing an immune response immunogens, which may be important for directing an immune response immunogens; unsertied epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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0
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                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 151; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
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Disclosure; Page 138; 139pp; English

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbried (SEFIJ/TAF) mucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and antecting recombination of fimbried comprising recombinant GAGA. GagA and AgGA-homologue fimbrien subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgGA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid the expression of recombinant AgGA protein which is useful for useful for the expression of recombinant AgGA protein which is useful for illustrial in a fimbrial presentation system the heterologous antigens are presented in high numbers (U) to system the heterologous antigens are presented in high numbers (U) to some seconds and protein protein possesses both the immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens and involved and hybrid fimbriae are easy and immunication of the present invention represent sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.6%; Score 709; DB 3; Length 15
89.9%; Pred. No. 3.7e-64;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inexpensive to purify in large amount. The pathe exemplification of the present invention
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Best Local Similarity 89.9
Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
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26-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR74625
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(UYVI-) UNIV VICTORIA INNOVATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                                      89.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.7
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW23570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                            SDARKSETTITOSGYGNGADVGCGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG 120
                                                                                                                                                                                                                                                             SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                                immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans, (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                  nume response to Salmonella - using attenuated Salmonella constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                               Gaps
                                                                                                     Salmonella AgfA protein and DNA are used in vaccine and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene replacement; fimbrin; epitope;
                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                            Length 151;
                                                                                                                                                                                                 Indels
                                                                                                                                                                           Score 689; DB 2; L. Pred. No. 4.1e-62; 3; Mismatches 11;
  Doran JL;
                                                   Eliciting an immune response to Salmonella -
                                                                                                                                                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay WW;
 Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                                                                                                                                                                                                                                                                                                                                                                             AAB36341 standard; protein; 151 AA
                                                                                7B; 95pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                           89.0%;
nilarity 90.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
 SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVI-) UNIV VICTORIA.
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                    WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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                                                                                                                                                                                    Local Similarity
les 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC64617
                                                                                                                                                        Seguence 151 AA;
                                                                                Disclosure; Fig
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                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                             Query Match
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                                                              strains,
Kay WW,
                                                                                                                                                                                       Best Loca
Matches
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assembly system of strains of Salmonella, Escherichia coll and assembly system of strains of Salmonella, Escherichia coll and assembly system of strains of Salmonella, Escherichia coll and Enterdaceae for the production of finbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species, respectively; (2) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native comprising species, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in manner response in manner or mine, the inserted epitope, and hybrid fimbriae are easy and cinexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 689; DB 3;
Pred. No. 4.1e-62;
3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis 27655-3b agfA.
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protein useful for eliciting immune response in animal
                                             Page 138; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36349 standard; protein; 151 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SDARK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151 AA;
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                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                                              The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                       Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 684; DB 2;
Pred. No. 1.3e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36354 standard; protein; 151
                                                                                                                                                        Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.1
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran JL,
                       WPI; 1997-309886/28.
N-PSDB; AAT74142.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-672631/
N-PSDB; AAC64630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEP1/7RF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterpoatchariaceae for the production of fimbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising species, 3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an ammon acid polymer response in an animal, we protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. oli or acid sequence or sequences grown on a Salmonella, E. oli or acid sequence or sequences grown on a Salmonella, E. oli or acid sequence or sequences grown on a Salmonella, E. oli or acid sequence or the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 1000,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune seponse or animal submit proteins are usually strong animal proteins are usually strong animal proteins are usually strong animal properties are usually errors animal proteins are usually strong animal proteins are usually errors animal proteins are are usually errors animal proteins are usually are proteins are presented and are presented and are presented and are presented and are presented and are presented and are presented and are presented and are presented and are presented and are presented and are presented and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 151;
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ilarity 81.9%; Pred. No. 2.3e-59;
Conservative 0; Mismatches 0
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbries (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of Enterobacteriaces for the production of fimbriae comprising recombinant componences of the changes species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant pack to comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid segment or segments of foreign amino acid segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid segment or segments of foreign amino settle segment or segments of foreign amino settle segment or segments of foreign amino settle segment or segments of foreign amino settle segment or segments of foreign amino containing a replacement segment or segments of foreign amino settle for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for altereting an immune response against the inserted epitope, and hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are usually strong inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention present sequence is given in
                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Pred. No. 2.8e-55;
0; Mismatches 0;
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                                                                                                 Kay WW;
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                                                                                                                                                                                                                                                                                                              Disclosure, Page 136; 139pp; English.
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                                                                                                 Collison SK,
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73.6%; Pred
0; 1
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                                              (UYVI-) UNIV VICTORIA.
                                                                                              White AP, Doran JL,
                                                                                                                                            WPI; 2000-672631/65.
N-PSDB; AAC64625.
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05-APR-1999;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fambriae (SPRI) mucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AgfA, CSA, and AgfA, homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologus species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are combinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fidmbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein postesses of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                Collison SK,
                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                       99US-0127888P
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                   Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-672631/65.
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                                                                                                               WO200060102-A2.
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                                                                                                                                                           12-OCT-2000
                                                                                                                                                                                                                                                                                                                                             White AP,
                                                                  Synthetic.
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(I) use of thin aggregative fimbriae (SEIT/TARF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of AffA, CsgA and AgfA, homologue fimbrin subunits, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the seful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for the animal in an animal. In a fimbrial presentation of animune response in an animal. In a fimbrial presentation of animune response in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%; Score 611; DB 3; Length 151; 80.8%; Pred. No. 3.7e-54; ive 7; Mismatches 22; Indels
                                                                                                                                                AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                      AAB36346 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA000356.
                                                                                                       (first entry)
                                                                                                                                                                                                                                                Salmonella enteritidis.
Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-672631/65.
N-PSDB; AAC64622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                          WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-1999;
                                                                                                         26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000.
                                                               AAB36346;
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9

1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

Matches 122; Conservative

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of the gene described are:

(1) use of thin aggregative fimbriae (SETI/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and casembly system of strains of Salmonella, Escherichia coli and direction of strains of Salmonella, Escherichia coli and directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA copy of the animal in conjunction with a carrier of diluent. (1) is susful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation constaining are recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation constaining are expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation constaining are usually strong immunogenicity and adhesion proteins relevant for an efficient live constained epitope, and hybrid fimbriae are easy and immunogens, which may be important for directing an immune response constance in purify in large amount. The present sequence is given in a incompanion in a since the purify in large amount. The present sequence is given in
120
                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope; vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                          121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                         121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 136; 139pp; English.
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                                                                                                                                                                                                                                                          AAB36347 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White AP, Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC64623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
    61
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05-APR-1999;
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                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
AAB36355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                              SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                               The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CSgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant of a recombinant gene.
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                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGONHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                              gene replacement; fimbrin; epitope;
                                                                       ·;
                                              Length 151;
                                                                     22; Indels
                                              Score 609; DB 3;
Pred. No. 5.8e-54;
6; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                        AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
the exemplification of the present invention
                                                                                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison SK,
                                                                                                                                                                                                                                                                                 AAB36352 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA000356
                                              Query Match 78.7%;
Best Local Similarity 81.5%;
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888P
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC64628
                        Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200060102-A2
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                                                                                                                                                                                                                                                                                                                                                                                Salmonella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                              61
                                                                                                                                                                                                                                                                                                        AAB36352;
                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                     AAB36352
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                  in
Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copiesofcall), the hybrid fimbrin protein possesses both the immunogénicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 606; DB 3;
Pred. No. 1.2e-53;
5; Mismatches 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgfA::PÍ3#10 amino acid sequence SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36355 standard; protein; 151
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82.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 124, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
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CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterbacteriaese for the production of fimbriae comprising recombinant of Enterbacteriaese for the production of fimbriae comprising recombination of a recombination of a recombination of a recombinant gene (CC directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinate part of protein containing a replacement segment or segments of foreign amino comprising separating an amino acid polymer comprising recombinant AgfA protein containing a replacement segment or segments of foreign amino composition or sequence or sequences grown on a Salmonella, E coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrin protein see usually strong communogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response cagainst the inserted epicope, and hybrid fimbriae are easy and income constitution of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 81.5
Matches 123; Conservative
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                              Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA comparison encoded by a segment of the gene has been replaced by a segment of a foreign DNA comparison to this described are:

(1) use of thin aggregative fimbrise (SETI/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and content of the production of fimbrise compissing recombinant of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a namino acid polymer comprising a replacement segment or segments of foreign amino comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino contenting a replacement segment or segments of foreign amino contenting a replacement segment or segments of foreign amino contenting a replacement segment or segments of foreign amino cortision of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to solono copies/cell), the hybrid fimbrin protein possesses both the immunogencity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial submit proteins are usually strong immunogens, which may be important for directing an immune response in expression of the present invention requence is given in the exemplification of the present invention invention invention in the present invention in the present invention of the present invention in the present invention of the present invention in the present invention in the present invention in the present invention in the 
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Pred. No. 2.2e-50;
6; Mismatches 23
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                                                                                                                                                                                 Disclosure; Page 136; 139pp; English
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ilarity 80.8%;
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Matches 122; Conserva
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Kay WW;

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA control of the encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SPEPA/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and Entertoacteriacaea for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of a recombinant gene into the chromosome of the homologus species, replacing recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a menho acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or comprising separating an amino acid polymer comprising the main an conjunction with a carrier or dilutent. (I) is a coli section for the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the animal in conjunction with a carrier or dilutent. (I) system the heterologus antigens are presented in high numbers (up to system the heterologus antigens are presented in high numbers (up to consolicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be imprortant for directing an immune response capainst the inserted epicope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 135; 139pp; English.
                                                                                                                                                    Collison SK,
05-APR-2000; 2000WO-CA000356
                                                99US-0127888P
                                                                                                 (UYVI-) UNIV VICTORIA
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9 9 1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNFGGGGNNSGPNSELNIYQYGGGNSALALQ 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 0; Gaps Ouery Match 68.2%; Score 528; DB 3; Length 151; Best Local Similarity 68.9%; Pred. No. 1.1e-45; Matches 104; Conservative 20; Mismatches 27; Indels Sequence 151 AA; ò g

SDARKYDOLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 19 à d à

120 120

> 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

ABR82651 standard; protein; 151 ABR82651 RESULT 15 ABR82651 XEXEXEX

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(first entry) 04-DEC-2003

subunit 15 kDa protein. E. coli CsgA

The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABRESGES, ABRESGES, The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections. Plasma protein; immune response; antibacterial; vaccine; gene therapy Herwald H; Disclosure; Page 41-42; 42pp; English. Σ Wikstroem 30-JAN-2003; 2003WO-EP000943 31-JAN-2002; 2002GB-00002275 (HANS-) HANSA MEDICAL RES AB. Bjoerck L, Olsen A, WPI; 2003-646136/61. Escherichia coli. N-PSDB; ACF36153 Sequence 151 AA; WO2003064446-A2 15 kDa protein 07-AUG-2003

., Query Match 67.6%; Score 523; DB 7; Length 151; Best Local Similarity 68.2%; Pred. No. 3.46-45; Matches 103; Conservative 20; Mismatches 28; Indels SDARKYDOLVTRVVTHEMAHAGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG 120 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 -19 61 d Š ò

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Copyright (c) 1993 - 2004 Compugen Ltd.
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7087		ŗ.	Kay, William W.	aren	Clouthier, Sharon	HODS	OF SALMONELLA		erry							isk	IEM PC COMPACIBLE	SYSTEM: FC-DOS/MS-DOS	ו תמ מ	TA: TIC/00/233 7882	0 7 0	† n	N.C		35,570	 	TELECOMMUNICATION INFORMATION:	TELEPHONE: (206) 622-4900	31	BER	n	. r	3				.48	 *°
15)	James L.	lam	, K	S S	MET	5	٠ ن ن	and Berry	STREET: 6300 Columbia				;	 ≅	MEDIUM TYPE: Floppy disk	d to	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	1) e			APR-T	CLASSIFICATION: 455 ATTORNEY/AGENT INFORMATION:			REFERENCE/DOCKET NUMBER:	FORM	622-	682-6031	EDAN	FORMALION FOR SEQ ID NO.	. ביינו			ein		88.	larity 90.1%; Conservative
			W11]	nsor	o)		. o	150.0	d a	01ur		ton		5	FORM:	lob!	ر ز	 Y	inc in	CS C	7 0 0 V	4	THOR!	Tochila	NUMBER:	E	NI	(90			7 100	CHARAC	acid	ar	protein			:Y erva
	175	Doran.	ay,	0111	lout	INVENTION:	OF INVENTION:	10 P	Sec	00	tle	Washington	U.S.A.	-705	ABLE		E E	S	אם היה	SE	Š ,		Z É	1	: E	OCK	OIL	Š	(206)	3723836	2 6	5 6		line				arit
- 59 cr	6356 9356 8356					INA	HV	ממט מאסקר) E E E	63	Seattle	Was		8104	READ	TYPE	 : :	n S		1144	2011	1 4 4	A CAL	K + N	ATIC	CE/L	NICA	NE.		372		5 4	amir	 بخ	TYPE	- 59		imi 7
788A		ANT	CANT	CANT	CANT	O (ئ _ا بد د	2.0	ADDRESSEE: Seed	EET:	CITY:	 IE:	COUNTRY:	σ.	TER	M E	COMPUTER:	OPERATING SYSTEM:	SOFTWARE	RRENT APPLICATION DA	1	FILLING DAIE: Ze	VOL.		REGISTRATION	EREN	OMMU	EPHO	TELEFAX:	TELEX	N PER	COENCE CHARACTERS 151	TYPE: amino	TOPOLOGY: linear	ULE	7887	tch	al Sir 136;
333-,	atent No. 5635617	APPLICANT:	APPLICANT:	APPLICANT:	APPLICANT:	TITLE OF INVENTION:	LLE	NUMBER OF SECUENCES: 0	ADD	STR	CIT	STA	500	ZIP: 98104-7092	OMPU	MED		OPE	SOF	JRRE	A L	1 6		MAN	REG	REF	BLEC	TEL	TEL		INFORMATION FOR SEC	4 Z	4 Y	TOP	MOLECULE TYPE:	233-	y Ma	Loc
US-08-233-788A-59	Sequence of Approximation of colors of patient No. 555517	N N	A	Α	A	βi	F .	ž č	í					i	ŭ				i	บ			4	\$			Ξ			Ì	N C	ó			Σ	S-08-233-788A-59	Query Match	Best Local Similarity Matches 136; Conser
dis.							٠.			٠.		٠.	٠.	٠.	٠.		٠.	٠.	•-		٠.		٠					٠.	٠.,	٠.	•-					ÛS	_	

1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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                                                                      61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INPORMATION:

APPLICANT: Doran, James L.

APPLICANT: Kay, William W.

APPLICANT: Collinson, Karen S.

APPLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

TITLE OF INVENTION: METHODS AND

CORRESPONDENCE ADDRESS:

ADDRESSES: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: 4300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STREET: U.S.A.

ZIP: 98104-702

COMPUTER: BADABLE FORM:

MEDIUM TYPE: FLOORYMAD AND

COMPUTER: BADABLE FORM:

MEDIUM TYPE: FLOORYMAD AND

CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/233,788A

FILING DATE: 26-APR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: King, JOSHMEN 35,570

REFERENCE/DOCKET NUMBER: 35,570

REFERENCE/DOCKET NUMBER: 35,570

REFERENCE/DOCKET NUMBER: 35,570

TELECOMMUNICATION INFORMATION:

NAME: King, JOSHMEN 35,570

REFERENCE/DOCKET NUMBER: 35,570

TELECOMMUNICATION INFORMATION:

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Pred. No. 9.2e-47;
3; Mismatches 11; Indels
                                                                                                                                                                                                               NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                               121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 57, Application US/08233788A Patent No. 5635617
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cch 65.1%; sl Similarity 87.5%; 98; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-233-788A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-09-252-991A-27661
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Best Local 9
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Kunio NAKASHIMA et al.
FUNTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
FENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
FENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
FENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
FENTION: TO SAID POLYPEPTIDE
                                         RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 LFAVAAL-GILFAGSTILPGELSPVGSAYAKGGNGGGNGGGHSGGKGGSHGGNLGGHSSK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LLKVAAFAAIVVSGSAL-----LSIY 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Gaps
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING:
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27661
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 GHGSATSGIASSRDSRGLSQASAISATTPGDHNSKGLSNAIGSSTKN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 QYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTON 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM COMpatible OPERATING SWEETER MINIOWS 95 SOFTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A FILING DATE: MAY 28, 1997 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1996 ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: 22,389
REFERENCE/DOCKET NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 10.8%; Score 83.5; DB 4; 1. Similarity 29.0%; Pred. No. 0.35; 31; Conservative 12; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Isshinden CITY: Tsu-city STATE: Mie-re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOW TITLE OF INVENTION: CONTITLE OF INVENTION: VECT TITLE OF INVENTION: SALISTILE OF INVENTION: TO SUMMER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mie-prefecture
: JAPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-27661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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MOLECULE TYPE: protein

Sequence 27661, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:

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279 NGTGDSG-VSALGGSGNGSGDGAGNGIASGNGEHNYGIGNG----NGDDVDITAPITGVL 333
                                                                                                                                                                                                                                                                                                                                                                                                                     75 THE-----MAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                              334 NISGNSFTLIGNSSSSSVNTAPTTTSNTVNDNDTID--NGNSGGTGSGSGNGSGDGLLNG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: No. 56679900 No. 5667990disk of No. 5667990th America, Inc. 1: 405 Lexington Avenue New York: New York
                                                                                                                                                                                                                                                                                                                             15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                         Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boominathan, Karuppan C.
AITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.1%; Score 78; DB 1
30.7%; Pred. No. 2.9;
cive 13; Mismatches
                                                                                                                                                                                                                                                                                     19; Mismatches
                                                                                                                                                                                                                                         10.3%; Score 79.5;
25.0%; Pred. No. 8;
TITLE OF INVENTION: BAUMANNII FOR DIAGNOS' FILE REFERENCE: GTC99-032BA CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 4764 LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08458023B
Patent No. 5667990
                                                                                                                                                      TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME:: Lowney Dr., Karen A.
REGIESTRATION NUMBER: 31,274
REFRENCE/DOCKET NUMBER: 4086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 AASGNGEHNYGIĞNĞN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 363 amino acids
amino acid
                                                                                                                                                                                                                                                              Best Local Similarity 25.09
Matches 34; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Berka,
                                                                                                                                                                                                US-09-328-352-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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Patent No. 6562958
GENERAL INFORMATION
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/09498520A
Patent No. 661353
GENERAL INFORMATION:
APPLICANT: Rock, Charles O
APPLICANT: Heath, Richard J
TITLE OF INVENTION: No. 661353el Enoyl Reductases and Methods of Use Thereof
FILE REFERENCE: SJ-0022
CURRENT FILIAG DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 LKAAGLKVMVVCGAVKHAVKAEQAGCDAVICQGGEGGGHTGLVGTLPLVAQAVEAVKIPV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AADEDTVRTRCYSGKPMRVKKNPYVDDWEARPGDIQPFPQQAMVSIRNGAMGGIGGQIEG 275
                                                                                                                                                                                                                                                                                                                                 419 LLKSSASASASASASASAG-----GGGGGNGGGNGGGGG------GGAGALAALAA 465
                                                                                                                                                                                                                                                                                                                                                                         ARKYDQL----VTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQY 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 GADNSTIEL-TQNG----FRNNATIDQWNAKNSDITV------GQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                     LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
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                                                                                                                                                                                                                                            Indels 47;
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                                                                                                                                                                                                Length 738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGSAAAAAAAAAAGGGGRALRRALRRQMRGGGSAAA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LKVAAFAAIVVSGSA-----LAG---VVPQWGGGGNHNG
                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                DB 3;
                                                                                                                                                                                             Query Match
10.8%; Score 83.5; Di
Best Local Similarity 27.7%; Pred. No. 2;
Matches 44; Conservative 12; Mismatches
                                                                                     NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: E (by experiment)
US-08-864-0388-3
ORIGINAL SOURCE:
ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 QTASDSSVMVRQVGFG 143
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Best Local Similarity
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US-09-498-520A-18
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US-09-128-450-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Welinder, Karen
APPLICANT: Andersen, Morten B
APPLICANT: Andersen, Morten B
APPLICANT: Andersen, Morten B
APPLICANT: Andersen, Morten B
TITLE OF INVENTION: HYDROGEN PEROXIDE STABILITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58518110 No. 5851811disk of No. 5851811th America, Inc.
STREET: New York
STREET: New York
----PDSTLSI 47
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNH---NGGGNSSG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09168406A
Patent No. 6258769
GENERAL INFORMATION:
APPLICANT: Welinder, Karen G.
APPLICANT: Andersen, Morten B.
TITLE OF INVENTION: Peroxidase Variants With Improved
TITLE OF INVENTION: Hydrogen Peroxidase Stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3769.204-US
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NAME: Harrington, James J.

REGISTRATION NUMBER: 38,711

REFERENCE/DOCKET NUMBER: 3769...

TELECOMMUNICATION INFORMATION:

TELEPAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 435 amino acide

TURENCE CHARACTERISTICS:

LENGTH: 435 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-331-515A-2; Sequence 2, Application US/08331515A; Patent No. 5851811
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STRANDEDNESS: single
TOPOLOGY: linear
US-08-331-515A-2
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US-09-168-406A-2
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89 WGQGGGTHNQWNKPSKPKTNMK--HWAGAAAAGAVVGGLGGY--MLGSAMSRPMMHFGND 144
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APPLICANT: Caughey, Byron W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE OF BY DEATH OF PROTEIN OF FOREIN APPLICATION NUMBER: US/09/128,450
CURRENT APPLICATION NUMBER: US/09/128,450
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 ADNSTIELTQNGFRNNA---TIDQWNAKNS-----DITVGQYGGNNAAL-VNQTASDSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.1%; Score 78; DB 3; Length 435;
Best Local Similarity 30.7%; Pred. No. 3.8;
Matches 35; Conservative 13; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNH---NGGGNSSG-
FILE REFERENCE: 3769.214-US
CURRENT APPLICATION NUMBER: 08/931,515
PRIOR APPLICATION NUMBER: 08/331,515
PRIOR FILING DATE: 1994-11-01
PRIOR FILING DATE: 1994-11-01
PRIOR FILING DATE: 1994-06-01
PRIOR PRIOR APPLICATION NUMBER: 0792/92
PRIOR PREDICTION DATE: 1993-06-01
PRIOR PREDICTION DATE: 1992-06-01
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 2
LENGTH: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
LOCATION: (1)...(435)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/09128450
Patent No. 6211149
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Coprinus cinereus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 25.49
Matches 32, Conservative
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TYPE: PRT
ORGANISM: Hamster sp.
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TELEPAX: (206) 682-6031
INFERMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
REGISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-861-3067
                                                                                                                                        TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
                                                                                                                                                                                                                                                                                 LENGTH: 364 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity 26.2
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               TOPOLÓGY: linear
MOLECULE TYPE: peptide
US-07-792-259-17
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STATE: Washington
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US-09-056-556-204
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US-09-056-556-204
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TITLE OF INVENTION:
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CURRENT FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,259
FILING DATE: 19911115
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: SCOTT, WATSON T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. STREET, N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: USA ZIP: 20036
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Patent No. 528638
GENERAL INFORMATION:
APPLICANT: TANAKA, YOSHIKAZU
APPLICANT: HATANKA, HARUYO
APPLICANT: HATANKA, HARUYO
APPLICANT: HATANKA, TERUO
APPLICANT: MAKATAMA, TORU
APPLICANT: SUMIDA, MOTOO
TITLE OF INVENTION: PERCOIDE GENE O
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                    Sequence 26, Application US/09823494 Patent No. 6355610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Hamster sp.
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Best Local Similarity
Matches 32; Conserv
                                     US-09-823-494-26
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US-07-792-259-17
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LENGTH: 254
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Patent No. 6350456
GENERAL INFORMATION
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: CONFOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue 39; 24; Query Match
Best Local:Similarity 30.4%; Pred. No. 3.3;
Matches 35; Conservative 13; Mismatches 28; Indels 3: 9.9%; Score 77; DB 4; Length 943; 26.2%; Pred. No. 14; ive 14; Mismatches 66; Indels

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RESULT 15

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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 20638, A
Sequence 3443, Ap
Sequence 77944, A
Sequence 7794, App
Sequence 7799, App
Sequence 48048,
Sequence 48048,
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Sequence 48048,
Sequence 28, Appl
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Sequence 28, Appl
Sequence 64573, Appl
Sequence 64573, Appl
                                                                                                                                                   August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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                                                                                                                                                                                                                                                            US-09-543-407-20
774
1 MKLLKVAAFAAIVVSGSALA.....DSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT MRW PUB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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2 US-09-741-873B-4
2 US-09-741-873B-2
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5 US-10-369-493-20638
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4 US-10-282-122A-49412
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7 US-10-282-122A-64848
8 US-09-793-306-146
8 US-10-282-122A-64573
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1 US-10-283-123A-64573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1291235 seqs, 313682936 residues
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                                                                                                     OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length
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Publication No. US2002008172241

Publication No. US2002008172241

Publication No. US2002008172241

APPLICANT NORMARTA, Staffan

APPLICANT Olsen, Arne

APPLICANT Olsen, Arne

TILLE OF INVENTION: Elbronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 8801723-1

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-06

PRIOR PRIOR PRIOR NUMBER: US 07/347,189

PRIOR PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

SOFTWARE: PARCHILL OF SECTION NUMBER: US 08/318,519

PRIOR FILING DATE: 1994-10-05

SOFTWARE: PARCHILL OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SE
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68.2%; Pred. No. 6e-46;
iive 21; Mismatches 27; Indels
4 US-10-128-714-8213

4 US-10-238-075-1119

4 US-10-085-194-16

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Best Local Similarity 68.23
Matches 103; Conservative
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             US-09-741-873B-4
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GENERAL INFORMATION: Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-03
PRIOR FILING DATE: 1991-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR PELING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2
FEATURE 111
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Best Local Similarity 64.9%; Pred. No. 5.2e-38;
Matches 85; Conservative 20; Mismatches 26;
             PRIOR FILLING DATE: 1998-05-06
PRIOR PLILING DATE: 1997-11-26
PRIOR FILLING DATE: 1997-11-26
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PRIOR FILLING DATE: 1997-11-36
PRIOR FILLING DATE: 1991-11-06
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PRIOR FILLING DATE: 1992-11-03
PRIOR FILLING DATE: 1994-01-28
PRIOR FILLING DATE: 1994-01-28
PRIOR FILLING DATE: 1994-01-28
PRIOR FILLING DATE: 1994-01-28
PRIOR FILLING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARR: Patentin version 3.0
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APPLICATION NUMBER: SE 8801723-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09741873B Publication No. US20040096965A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
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                                                                                                     Sequence 4, Application US/09741873B
Publication No. US20040096965A9
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFRENCE: 012689-08
CURRENT APPLICATION NUMBER: US/09/741,873B
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01288-0408
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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Best Local Similarity 68.2%; Pred. No. 6e-46;
Matches 103; Conservative 21; Mismatches 27;
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PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR PILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1999-11-26
PRIOR PILING DATE: 1999-11-26
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-741-873B-2
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Length 131;

Length 131; DB 12;

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us-09-543-407-20.rapb

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55 KKVLÓPELDKFEEGTGIKVKLEVVPWSDLLNRILT--ATTSGQGPDVLNIGNTWSASLQA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LOSDARKYDO------LVTRVVTHEMAHAGOGADNSTIELTON-GFRN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu, H.
INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
12.2%; Score 94.5; DB 14; Length 438;
Best Local Similarity 25.9%; Pred. No. 0.39;
Matches 37; Conservative 27; Mismatches 46; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE REPERENCE: BLITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/20,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
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PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-10-22
PRIOR PLING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
TITLE OF INVENTION: NOVEL FULINGLAND.
FILE REFERENCE: 249-226
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF:SEQ ID NOS: 15109
SQ ID NO 9343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 49412, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 NATIDOWNAKNSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 TGALLPWDAKNFD----KIGGKD 131
                                                                                                                                                                                                                                                                                         ; TYPE: PRŤ
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Daniel
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US-10-282-122A-49412
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TITLE OF I
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: DANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: 10,10,369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
                                                                                                                                                                                                              81 AGQGADNSTIELIQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GSANAALALQSDARKYDQLVTRVVTHEMAHAGQGA-----DNSTIELTQNGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 GNSNS------VGRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPS 123
                                                                                   21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAH 80
                                                                                                                   7 AAFAA-----IVVSGSALAGVVPQWGGGG-----GNSSGPDSTLSIXQY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 QWNAKN------SDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 101.5; DB 15; Length 445; 26.0%; Pred. No. 0.076; 1ve 20; Mismatches 55; Indels 53;
                                  Indels
        Best Local Similarity 64.9%; Pred. No. 5.2e-38; Matches 85; Conservative 20; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) LOCATION: (1)..(445)
) OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 20638, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9343, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION: APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHIBA, TADAYOSHI
SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.04
Matches 45; Conservative
                                                                                                                                                                                                                                                                                      141 GEGNNATANOY 151
                                                                                                                                                                                                                                                                                                                      RESULT 5
US-10-369-493-20638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-10-156-761-9343
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ORGANISM: Yersinia pestis
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                                                                                                                                                                                                                                                                                                     51 PA------DKAITLATVPAGSLASAGAVAGTSNPTDLQLSLTGCTGTATKAIARFENG 102
                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSS----GPDSTLSIYQYGSANAA 56
                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NGS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 49412
LENGTH: 186
                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                        103 PIVDQINGYLSN-TAGTAQNVEVRLLNAQMQPINV---TTGANNDITIN 147
                                                                                                                                                                                                                                                                                                                                     101 ATIDOWNAKNSDITVGOYGGNMAALVNOTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                               Length 186;
                                                                                                                                               Query Match
11.8%; Score 91; DB 12; Length 186
Best Local Similarity 29.6%; Pred. No. 0.3;
Matches 50; Conservative 17; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Deformed 77944, Application US/10282122A Geneme 77944, Application US/10282122A GENERAL INFORMATION: US20040029129A1 GENERAL INFORMATION: CARLOS APPLICANT: Malone, Cherlos APPLICANT: Malone, Cherlos APPLICANT: Malone, Cherlos APPLICANT: Carros Chiese, Rai APPLICANT: Chiese, Kari APPLICANT: Chiese, Wari APPLICANT: Trawick, John APPLICANT: Trawick, John APPLICANT: Trawick, John APPLICANT: Yamanoto, Robert APPLICANT: Yamanoto, Robert APPLICANT: Yamanoto, Robert APPLICANT: Porsyth, R.
                                                                                    TYPE: PRT
ORGANISM: Burkholderia fungorum
                                                                                                                   US-10-282-122A-49412
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-26

PRIOR PEDICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-26

PRIOR PEDICATION NUMBER: 60/207,727

PRIOR PEDICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-05-06

PRIOR PEDICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-110-27

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PRIOR PELING DATE: 2001-12-16

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PRIOR PELING DATE: 2001-02-09

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PRIOR PELING DATE: 2001-02-16

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                                                                                                                                                                 44; Gaps
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                                                                                  DB 12; Length 3705;
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11.0%; Score 85; DB 12; Length 631
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
Matches 40; Conservative 19; Mismatches 58; Indels
                                                                                                                                                                     55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1406 --- ASTNNLGASSSVALAGAGDTLSLSGFNGTFGNSVTGS 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----FGNNATAN 149
                                                                              Query Match 11.0%; Score 85; DB 1
Best Local Similarity 23.8%; Pred. No. 57;
Matches 38; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67793, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NNAALVNQTASDSSVMVRQVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Syskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-67793
US-10-282-122A-77944
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US-10-282-122A-67793
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Gaps

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52 SANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNAT-IDQWNAKN 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AFAAIVVSGSALAGVVP------QWGGGGNHN-GGGNSSGPDSTLSIYQYG 51
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
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PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR PILING DATE: 2001-12-2
PRIOR PILING DATE: 2001-12-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 QAIGSGAYSVAIGNLSSATQSGAVAMGSGAAATGVAAIGLGNNAFASGQY 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.9%; Score 84; DB 12; Length 1129;
Best Local;Similarity 27.1%; Pred. No. 16;
Matches 46; Conservative 20; Mismatches 72; Indels 3:
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APPLICANT HU, Guihua
APPLICANT Lu, Guihua
APPLICANT Lu, Guihua
TITLE OF INVENTION: Of Use
FILE REPRENCE: 1183
CURRENT APPLICATION NUMBER: US/09/810,264
CURRENT PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 43
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 278;
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Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09810264; Patent No. US20020076775A1
Patent No. INFORMATION:
APPLICANT: Crane, Virginia C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burkholderia cepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%;
20.8%;
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Famodu, Omolayo O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OKGANISM: Triticum aestivum
US-09-810-264-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Burkho
US-10-282-122A-48048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 48048
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US-09-810-264-28
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APPLICANT: I.N.S.E.R.M.
TITLE OF INVENTION: Polymucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polymucleotides and of their FILE REFERENCE: BLANDINE US/10/238,075
CURRENT APPLICATION WINBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
LENGTH: 1778
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   966 NTSFSTSLGDALLWD-----ATAGKFSAKHGINNAPSVITDVANGAVSSTSSDAINGSO 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----QSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQ--NGFRNNATIDQWNAKN 110
                                                                                                                                               55 AALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIEL-------TQNGFRNN 100
                                                                                                                                                                                                         -----APÁTPIDLLVS---PDGLRLTGRGEAGTTVNIRDAAGNLIGSGTVGADGNFNVT 207
                                    AAIVVSGSALAGVVPQW-----GGGG----NHNGGGNSSG---PDSTLSIYQYGSAN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KVAAFAAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Forsyth, R. APPLICANT: You, H. TILE OF INVENTION: 1 dentification of Essential Genes in Microorganisms TITLE REPERENCE: BLITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 29; Gaps
                                                                                     111 AGIGTAĞSAM----PTWAIAGLSLLĞVĞĞAAAAADNĞĞĞĞSSĞĞSDPDTS----
                                                                                                                                                                                                                                                                101 ATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                     DB 14; Length 1778;
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10.9%; Score 84.5; Di
Best Local Similarity 26.8%; Pred. No. 25;
Matches 40; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1020 LYGVSDYIADALGGN--AVVN---TDGSI 1043
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Publication No. US20040029129A1
GENERAL HORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Mandone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zysind, Judith
APPLICANT: Zysind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 749, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-238-075-749
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APPLICANT:
APPLICANT:
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119 GGNNAALVNQTASDSSVMVRQVGFGNN 145
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                                                                                                                                                                                                                                                 PRIOR PELICATION NUMBER: 60/111,0/8
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
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                                                Carr, Grant
Yamamoto, Robert
Forsyth, R.
Wall, Daniel
Trawick, John
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US-10-128-714-3213
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                                                                                                                                                                                         120 -HGDNEGSSGGTGACVKPVREPRLVVQTLSDIDILDDGFRWRKYGQKVVKGNPNPRSYYK 178
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                                                  SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shyian
APPLICANT: Jodes, Michael
APPLICANT: Corixa Corporation
AITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: Of Tuberculosis
                                                                                                                                                                                                                                            -- NNATIDOWNAKNS-DITVGOYGGNNAALVNQTASDSSVMV 137
                                                                                                                                                                                                                                                                        Gaps
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                                                                                        71 NSSGCAAVIAE-----DHINGSEHSGPIPENSSVIFGDDEADNGAEPEIKREKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: mTTC#3-His US-09-793-306-146
     67;
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     51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358 FGNSGNNNIGFFNSG-NNNVGFFNSGNNNFGFGNAGD
     23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 014058-008940US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR PELICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 146, Application US/09793306
Patent No. US20020092200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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       37; Conservative
                                                                                                                                                75 TH---EMAHAGQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 34; Conserv
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US-10-282-122A-64573
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LENGTH: 597
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APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 GGGNTGNSNFGFGNTGNVNFGNGNTGDTNFGSGNLGSGNIGFGNKG-----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 64573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.7%; Score 83; DB 12;
Best Local Similarity 24.5%; Pred. No. 10;
Matches 36; Conservative 15; Mismatches 52;
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70 ---VIRVVIHEMAHAGO--GADNSTIELTQNGFR-----NNATIDQ------WN:107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 TDFALRTAYHD--HTGKVPGSDTEKVAVAKKRFEQAAMVNNKIVEKLVSASDDFTMYLWD 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQL--- 69
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.7%; Score 82.5; DB 14; Length 435;
Best Local Similarity 19.6%; Pred. No. 6.6;
Matches 31; Conservative 30; Mismatches 66; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| : : || |: 388 PENSTKPIARLLGHQKEVNHVTFSPDMAXIASAGFDNH 425
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR PILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/305,890
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SEQ ID NO 3213
LENGTH: 435
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                                                                                                                                                                                                                                                                                                                       TYPE: PRT / ORGANISM: Aspergillus fumigatus US-10-128-714-3213
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
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APPLICANT: Collinson, S. Karen
APPLICANTON: PACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543.407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
19 US-09-543-407-20

19 US-09-543-407-26

19 US-09-543-407-26

19 US-09-543-407-28

19 US-09-543-407-12

19 US-09-543-407-12

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ORGANISM: Artificial Sequence
FEATURE:
           US-09-543-407-20
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LENGTH: 151
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7: cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Total number of

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Sequence:

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Scoring table:

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8854, Ap 8854, Ap 20638, A 20638, A 7657, Ap 7656, Ap 7965, Ap 7946, Ap 7946, Ap 7946, Ap

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Matches 137; Conserv
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ZIP: 98104-7092
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CITY: Seattle
STATE: Washingt
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                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REPERENCE: 920043.406
CURRENT PELLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
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                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 91.6%; Score 709; DB 19; Length 151; Best Local Similarity 89.9%; Pred. No. 3.8e-68; Matches 143; Conservative 0; Mismatches 0; Indels 1.
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                                       Query Match 100.0%; Score 774; DB 19;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
Matches 151; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/09543407 GENERAL INFORMATION:
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Order, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCES ADDRESSE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

88.4%; Score 684; DB 6; Length 151;
Best Local Similarity 90.1%; Pred. No. 1.9e-65;
Matches 136; Conservative 3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                     Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                           Score 689; DB 19;
Pred. No. 5.6e-66;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: (206) 622-4900
TELETAX: (206) 622-4900
TELETAX: 8723336 SEEDAMBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Application US/08233642A GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              , ORGANISM: Salmonella enteritidis
US-09-543-407-5
                                                                                                                                                                                                                                                              89.0%;
ilarity 90.7%;
Conservative
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RESULT 7
US-09-543-407-22
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                                                                              61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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9
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  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                            MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYOYGSANAALALQ
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BATERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.405
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DOTAIN, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: Recombinant Salmonella enteritidis 3b afgh INFORMATION: sequence containing the replacement fragment INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.5%; Score 662; DB 19; Length 151;
81.9%; Pred. No. 4.7e-63;
iive 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-18
Sequence 18, Application US/09543407
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 81.9
Matches 136; Conservative
                                                                                                                                                                                                                                                                                        -09-543-407-28
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US-09-543-407-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 NNATIDOWNAKWSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
CRGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
CTHER INFORMATION: sequence containing the replacement fragment
CTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-18
                                                                                                                                                               Score 622; DB 19; Length 151;
Pred. No. 1e-58;
0; Mismatches 0; Indels 46
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Sequence 2. Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REPERENCE: 92043.406
CURRENT APPLICATION UNMBER: US/09/543,407
CURRENT APPLICATION UNMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 619; DB 19;
Pred. No. 2.2e-58;
0; Mismatches 0;
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US-09-543-407-12
Sequence 12, Application US/09543407
GENERAL INFORMATION:
                                                                                                                                                     80.4%; Scc...73.6%; Pred 0; 1
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Best Local Similarity 74.6'
Matches 129; Conservative
                                                                                                                                                                           Query Match
Best Local Similarity 73.6
Matches 128; Conservative
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61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Exp. William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIREBOLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 131
TYEE: PRT
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GENERAL INFORMATION:
APPLICANT:
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Collinson, S. Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.3%; Score 606; DB 19; Length 151; Best Local Similarity 82.1%; Pred. No. 5.7e-57; Matches 124; Conservative 5; Mismatches 22; Indels (
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89.3%; Pred. No. 1.3e-56;
                                             121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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    121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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Best Local Similarity
                                                                                                                                                                                                   RESULT 10
US-09-543-407-24
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US-09-543-407-31
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LENGTH: 151
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYDQ 120
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                        APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043. R06
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-543-407-14
US-09-543-407-14
Sequence 14, Application US/09543407
SEQUENCE 11, Application US/09543407
SEQUENCE 11, APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.7%; Score 609; DB 19; Length 151; larity 81.5%; Pred. No. 2.7e-57; Conservative 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Collinson, S. Karen
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 123; Conserv
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LENGTH: 151
APPLICANT:
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74.2%; Score 574; DB 19;
80.8%; Pred. No. 1.7e-53;
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                                                                                                                                                        6; Mismatches
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                                                                                                                                     Best Local Similarity 80.8
Matches 122; Conservative
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Matches 104; Conservative
                ) OTHER INFORMATION:

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) OTHER INFORMATION:

US-09-543-407-16
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                                                                                   61 VGQGADNSTIELFQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 120
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Sequence 16, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BRCTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BRCTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BRCTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BRCTERIAL FOR HETEROLOGOUS PEPTIDE SEQUENCES

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16

LENGTH: 151
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Callinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FastsEQ for Windows Version 4.0
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Pred. No. 5.4e-56;
5; Mismatches 23;
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Best Local Similarity 81.5%;
Matches 123; Conservative
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LENGTH: 151
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61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT: NORWARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION *FIREONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DAFE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
BARLIER FILING DATE: 1998-05-06
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APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
FILE REPRENCE: 920043.40
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PLING DATE: 2000-04-05
NUMBER OF SEQ ION WINGOWS VERSION 4.0
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Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                   Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER PILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: PATENTING DATE: 1995-06-28
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Search completed: August 2, 2004, 15:26:44 Job time : 168.9 secs

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August 2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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2. /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

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7. /cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000

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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Sequence 4, Appli	Sequence 2, Appli	Sequence 7907, Ap	•	Sequence 193207,	Sequence 7905, Ap	Sequence 7905, Ap	Sequence 7906, Ap	Sequence 7906, Ap	Seguence 7377, Ap		Sequence 320950,			Seguence 11319, A			Seguence 35514, A	Sequence 35515, A	Sequence 7973, Ap	Sequence 7973, Ap				'n	Sequence 5, Appli
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10-872-769-5 -US03-24982A-	US-10-482-706-129 US-10-425-115-242035 US-10-425-115-339993	39-490-3 50-563-8	PCT-0804-10229-38 US-60-556-841-11867 US-09-248-7964-25347	ח ו	US-60-579-062-8923 US-60-581-351-9813 PCT-US04-07096-553	US-10-425-115-343835 US-09-248-796A-22578	US-60-556-841-9640 US-10-490-953-13
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ALIGNMENTS

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US-99-741 #873C-4

US-99-741 #873C-4

Sequence 4, Application US/09741873C

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Olsen, Arne

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873C

CURRENT FILING DATE: 2000-12-22

FRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR FILING DATE: 1997-11-26

PRIOR PRILING DATE: 1997-11-06

PRIOR PELLING DATE: 1991-11-06

PRIOR PELLING DATE: 1991-11-06

PRIOR PELLING DATE: 1992-11-03

PRIOR PELLING DATE: 1994-01-08

PRIOR FILING DATE: 1994-01-08

PRIOR FILING DATE: 1994-01-08

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 11

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.0
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Best Local Similarity 68.2%; Pred. No. 8.3e-40;
Matches 103; Conservative 21; Mismatches 27; Indels
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ORGANISM Escherichia coli
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US-09-741-873C-4
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APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Shang, Bal
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REFERENCE: 38-21 (54403) C
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SEQ ID NO 7907
LENGTH: 573
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinhua
APPLICANT: Cao, Yongwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERRICE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                 241 GNENGTGAENNANADAQTDVAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD 299
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11.2%; Score 87; DB 7; Length 573;
Best Local Similarity 24.9%; Pred. No. 9.5;
Matches 42; Conservative 15; Mismatches 62; Indels
                                                                                                                                                                 62; Indels
                                                                          ; Score 87; DB
; Pred. No. 9.5;
15; Mismatches
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APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R.
APPLICANT: Roberts, James K
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US-60-579-062-7907
                                                                              11.2%;
24.9%;
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                                                                     Query Match
Best Local Similarity
Matches 42; Conserv
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US-10-425-115-193207
US-60-565-632-7907
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APPLICANT: Baum, James A

APPLICANT: Kovalic, David K.

APPLICANT: Lu, Maolong

APPLICANT: Lu, Maolong

APPLICANT: Lu, Maolong

APPLICANT: Lu, Maolong

APPLICANT: Munyikwa, Tichifa R. I.

APPLICANT: Roberts, James K.

APPLICANT: Roberts, James K.

APPLICANT: Ru, Wei

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TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT APPLICATION NUMBER: US 8601723-1
PRIOR PELLING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR PAPLICATION NUMBER: US 09/978,878
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1999-11-06
PRIOR PELLING DATE: 1999-11-06
PRIOR PELLING DATE: 1994-10-05
PRIOR PELLING DATE: 1994-10-05
PRIOR SPELING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
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57.8%; Score 447; DB 5; Length 13:
Best Local Similarity 64.9%; Pred. No. 7.1e-33;
Matches 85; Conservative 20; Mismatches 26; Indels
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                                                                 Sequence 2, Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Diabrotica virgifera
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APPLICANT: Lu, Maclong
APPLICANT: Lu, Maclong
APPLICANT: Runytkwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Weits, James K
APPLICANT: Roberts, James K
APPLICANT: Stangy, Bar
APPLICANT: Stangy, Bar
ITILE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
ITILE OF INVENTION: Compositions thereof
FILE REPERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7906, Application US/60565632

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Lavosa, Thomas J.
APPLICANT: Lavosa, Thomas J.
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Noberts, James K.
APPLICANT: Noberts, James K.
APPLICANT: APPLICANT: Munjkwa, Tichifa R. I.
APPLICANT: Munjkwa, Tichifa R. I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKYDQLVTRVVTHEMAH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; NAMBYKEY; misc feature
; LOCATION: (392)
; OTHER INFORMATION: Xaa can be any naturally occurring amino US-60-579-062-7905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 --AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
108 --AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
                                      204 AAENNGNADAAQSNDNGAAAENNTNADAQNDAAQ-GTANEANA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.0%; Score 85; DB 'Best Local Similarity 26.4%; Pred. No. 9.6; Matches 43; Conservative 12; Mismatches
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                                                                                                                                                                                 US-60-579-062-7905
; Sequence 7905, Application US/60579062
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     APPLICANT Baum, James A
APPLICANT Kovalic, David K
APPLICANT Larosa, Thomas J
APPLICANT LU, Maolong
APPLICANT Munyikwa, Tichifa R. I.
APPLICANT Roberts, James K
APPLICANT RU, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (369)...(369)
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US-60-565-632-7906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNN 122
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LOCATION: (369)...(369)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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LOCATION: (392)..(392)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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                                                                                                                                                                                                                                                                                                                  Length 147;
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                 ; CTHER INFORMATION: Clone ID: MRT4577_107790C.1.pep
US-10-425-115-193207
                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                           Query Match
11.0%; Score 85; DB 6;
Best Local Similarity 24.6%; Pred. No. 2.8;
Matches 35; Conservative 18; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 AALVNQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIPLDTGLSRAGFL--OPGTGN 146
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ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 43; Conserva
      CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 193207
LENGTH: 147
                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-60-565-632-7905
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                                                                                                                                                                                           FEATURE:
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Sequence 7636, Application US/60581351
GENERAL INFORMATION.
DEPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REPRENEURS: 38-21(53372)8
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ### 16 HHLQLNTQSINNEKGH--MSADTVDINTHQQGLNNTAGLIVAERNMILRTGELLNRQGSV 473
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                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Was will and Use there is a sequence of from the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 QLLASKSLVVSASAI------DNRQGKITSSGGDITLTTGQLDNLSGKIA----GQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TIDQWNAKNS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GGGAGGGSSVAGNGIAMTANHNQOHSAAEAAGLLAIARS------GGDLAQSGQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 ----DITVGQYG-----GNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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10.5%; Score 81.5; DB 7; Length 436;
Best Local Similarity 26.1%; Pred. No. 21;
Matches 29; Conservative 16; Mismatches 43; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 85; DB 7; Length 2663; 24.7%; Pred. No. 91;
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US-10-425-115-320950
; Sequence 320950, Application US/10425115
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US-60-581-351-7636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Xenorhabdus bovienii
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SEQ ID NO 7636
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128 RGNLLDLHSD----
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nes 42; Conserv
                                                                              RESULT 10
US-60-579-902-7377
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US-60-581-351-7636
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Matches
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TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: Compositions thereof
FILE REFERENCE: 38-21 (53403) C
CURRENT PPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 AGQGADN-STIELTQN-----GFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 AAQGTDNGAAAENTGNADPAQGNDNGAA----AENSGNENGTAAGNNA---NPDVQNDA 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKYDQLVTRVVTHEMAH
                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

// DCATTON: (810)

// OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-60-565-632-7906
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; LOCATION: (810)...(810)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-579-062-7906
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
11.0%; Score 85; DB 7; Length 841;
Best Local Similarity 30.7%; Pred. No. 23;
Matches 42; Conservative 13; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7906, Application US/60579062
GENERAL INFORMATION:
APPLICANT: Baum, James A
APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Mucyikwa, Tichifa R. I.
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 VMVRQVGFG--NNATAN 149
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                                                                                                                                                                                   ORGANISM: Diabrotica virgifera FEATURE:
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 7906
LENGTH: 841
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Best Local Similarity
Matches 42; Conserv
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US-60-579-062-7906
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242 VSLYPLAGGATQAFAKENNQKAYKETYGVSHITRHDMLQIPKQQQNEKYQVPQ---FDQS 298
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                  FRIOR APPLICATION NUMBER: US 60/340,187
PRIOR PLING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/340,187
PRIOR PLEING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 10/296,115
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2000-04-25
PRIOR PLING DATE: 2000-04-25
PRIOR PLING DATE: 2000-04-25
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PRIOR PLING DATE: 2000-01-21
PRIOR PLING DATE: 2001-01-25
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 822
CURRENT APPLICATION UNBER: US/10/389,559
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 60/365,264
PRIOR FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 60/340,187
PRIOR FILING DATE: 2001-12-12
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Goodrich, Ryle W.
Chen, Rui-hong
Wehrman, Tom
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Ma, Yunqing
Ghosh, Malabika
Xue, Aidong J.
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Best Local Similarity 22.3
Matches 27; Conservative
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Wang, Jian-rui
Zhang, Jie
Ren, Feiyan
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Wang, Dunrui
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Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-07412-1695
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Evoalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Colory Youngwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 320950
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 IRLLEERAQEAILASCRDVLRASGFRFEDAWAKVIPGSDEGVYAWVAANYALGRLGGDPN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 -LIQNGFRNNATID----QWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---YVNNG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 KTVGIIELGGASAQLTFVSDEVLPPKLSYNYTFGETTYTLYTNSFLNFGQNAAQDSFHEM 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 STLSIYOYGSANAALALOSDA-------91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVS-----GSALAGVVPQWGGG-----GNHNGGGNSSGPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 511;
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TITLE OF INVENTION: Novel Mucleic Acids and Polypeptides
FILE REFERENCE: 822CIP/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: MRT4577_55769C.1.pep
US-10-425-115-320950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 80.5; DB 6; 20.8%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(511)
POERE INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: PCT/USO4/07412
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION UNMBER: US 10/389,559
PRIOR FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 60/365,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1695, Application PC/TUS0407412
Sequence 1695, Application PC/TUS0407412
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jian-rui
APPLICANT: Zhang, Jien-rui
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Dunrui
Goodrich, Ryle W.
Chen, Rui-hong
Wehrman, Tom
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Ma, Yunqing
Ghosh, Malabika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boyle, Bryan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aidong J.
di, Vinod
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Zhao, Qing A.
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Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 TAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 TGN 302
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APPLICANT:
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APPLICANT:
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APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 TI-----DQWNAKNSDITVGQYGGNNAALV----NQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 TIKNIESAKGLDVWDSWPLQNADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDN 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 LKAAGLKVMVVCGAVKHAVKAEQAGCDAVICQGGEGGGHTGLVGTLPLVAQAVEAVKIPV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 VAAGGLHDG-----RGLA-AALALGAQG---VWMGTRFIASHEAHAGDLYRQAVVE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 GADNSTIEL-TONG----FRNNATIDOWNAKNSDITV------GQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AADEDTVRTRCYSGKPMRVKKNPYVDDWEARPGDIQPFPQQAMVSIRNGAMGGIGGQIEG 275
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                                            PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2001-01-25
PRIOR PELLING DATE: 2001-01-25
PRIOR PELLING DATE: 2001-01-25
PRIOR PELLING DATE: 2001-01-25
PRIOR PELLING DATE: 2001-01-25
PRIOR PELLING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-03
PRIOR PRIOR FILING DATE: 2000-04-03
PRIOR PELLON NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR SEQ ID NOS: 1920
SOFTWARE DE FLAGENES VERSION 6.0
SEQ ID NO 1695
LENGTH: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.3%; Score 80; DB 6; Length 581;
Best Local Similarity 22.3%; Pred. No. 41;
Matches 27; Conservative 25; Mismatches 47; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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10.3%; Score 79.5; DB 7; Length 321;
Best Local Similarity 24.5%; Pred. No. 22;
Matches 48; Conservative 15; Mismatches 64; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11319, Application US/60556841
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genee and Uses for Plant Improvement FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 11319
LENGTH: 321
APPLICATION NUMBER: PCT/US00/35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Caulobacter crescentus CB15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 A 146
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US-60-556-841-11319
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Oy 128 GTASDSSVMVRQVGFG 143

Db 276 LDAAKSCFAMGQSAGG 291

Search completed: August 2, 2004, 15:29:5
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Search completed: August 2, 2004, 15:29:53 Job time : 18.8 secs

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OM protein - protein search, using sw model

August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-543-407-20 774 1 MKLIKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: Dirl:*
2: DirZ:*
3: DirZ:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	brin prote	r.cúrlin cha	curlin protein csg	najor	cal prot	d Tru	۳.	F3F19.21 protein -	ıclea	urlin	Ä	$\overline{}$	ncleatic	atic	eishman	PPE pr	lysin	probable homeobox		isease	ice anti	fimbrin protein ag	reempon	dhesin	able adhesin	leishmanolysin (EC	eishmanolysin (E	eishmanolysin (E	rsin (E
Ţ	C603	I063	078	9080	999	4	4	9	S70787	2	9	96	7	5	S	2	4	5	2	8	35	2	8	8	18	A45621	4204	4495	1991
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% Query Match	9 .	•	68.2	S.	'n	ω.	س	ď.	12.5	ď	ά.	ď.	u,	Η.	•	ä	ä	ä	۲.	i,	Η.	•	H	ä	٠.	ä		ä	11.4
a)	69	689	a	96.	٠	05.	05.	66	9	•	è.	96	ď	91.5	91	91	06	e,	89.5	ö	89	ω	88.5	œ	ä	80	88	89	88
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	protein kinase sgg	cnjB protein - Tet	hemolysin [importe	probable secreted	probable PPE prote	hypothetical prote	probable autotrans	F7-2 fimbrial prot	ice nucleation act	ice nucleation pro	hypothetical prote	hypothetical prote	hypothetical prote	PPE		CREB-binding prote
	S35327	S42136	AI0452	T35789	E70663	E96590	AD0123	YQECF2	JC2143	JQ0188	T15502	F87494	T20847	E70946	A70762	T13828
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	575	1748	1635	438	615	891	3705	188	1034	1258	494	407	409	590	678	3190
	11.3	11.2	11.1	11.0	11.0	11.0	11.0	10.9	10.9	10.9	10.9	10.7	10.7	10.7	10.7	10.7
476.	87.5	87	8,	85 	8	.80 .E3	82	84:5	84.5	84.5	8	83	83	83	83	83
	30	31	3	93	34	35	36	3.7	38	33	0	41	42	43	44	45

ALIGNMENTS

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A; Description: major component of wild-type curli; interaction between CsgA and CsgB tri
A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C;Species: Escherichia coli (5) = 18-Jul-2001 #18-Jul-2001 #19-Jul-2001 #
     transcriptional repression of csg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 < CHMY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Cross-references: GB:EA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Cross-references: GB:EA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Genetics:
A;Genetics:
A;Genetics:
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A;Residues: 1-133, RQRDSGWLW' <0LS3>
A;Cross-references: EMBL:L04979; NID:g290424; FIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
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A;Title: The RpoS sigma factor relieves H-NS-mediated tr
A;Reference number: S31202; MUID:93211294; PMID:8459772
A;Accession: S31202
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Best Local Similarity 68.9%; Pred. No. 1.2e-37;
Matches 104; Conservative 20; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%; Score 506.5; DB 2, 67.1%; Pred. No. 7.7e-36; ive 21; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Residues: 21-42;44-50 < CLS2>
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library, October 1992
A,Reference number: 834559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-6,'V', 8-151 <OLS1>
A;Cross-references: EMBL:L04979
A;Accession: S34560
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Best Local Similarity 67.1%
Matches 102; Conservative
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CySpecies: Escherichia coli

C;Species: Escherichia coli

C;Species: Escherichia coli

C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002

C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002

C;Accession: S70788; G64846; S31202; S34560; S34559

R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.

Mol: Microbiol. 18, 661-670, 1995

A;Atter Expression of two csg operons is required for production of fibronectin- and Cc
A;Reference number: S70783; MUD:96414468; PMID:8917469

A;Reference number: S70783; MUD:96414468; PMID:8917469

A;Reference number: S70789; MUD:97141758; PIDN:CAA62262.1; PID:91147564

A;Reference number: S70784; MID:91147558; PIDN:CAA62262.1; PID:91147564

A;Residues: 1-151 cHAM.
A;Coss-references: strain R12, substrain W310

A;Rose, D.J; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUD:97426617; PMID:9278503

A;Residues: 1-151 cBLAP.
A;Residues: 1-151 cBLAP.
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Pred. No. 3.1e-51;
3; Mismatches 11;
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NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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nilarity 90.7%;
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Best Local Similarity
Matches 137; Conserv
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() Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
() Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
() Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
() Accession: C86266
() R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408 # 816-820, 2000
A. Mature 408 # 816-820, 2000
A. Mature, J.L.; J.L.; J.L.; J.L.; J.L.; S.X.; Liu, Z.A.; Lurcs, J.S.; Maiti, R.; Marziali Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A. Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A. Arithe: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A. Accession: C86266
                                                                                                                                                                                                                                                        56 ALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
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A;Molecule type: DNA
A;Residues: 1-573 <STO>
A;Cross-references: GB:AE005172; NID:g4850402; PIDN:AAD31072.1; GSPDB:GN00141
C;Genetics:
                                                                                         ----GGNHNGGGNSSGPDSTLSIYQYGSANA
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13.6%; Score 105.5; DB 2;
Best Local Similarity 23.2%; Pred. No. 0.049;
Matches 36; Conservative 27; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
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3 LLKVAAFAAIVVSGSALAGVVPQWGG---
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A; Map position: linear chromosome
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R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A.Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A.Reference number: A88480; MUID:21074935; PMID:11206551
A.Scatus: preliminary
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD343
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A.Rocession: AD3143
A.Rocession: Apeliminary
A.Molecule type: DNA
A.Rocession: A.Rocession: A.Rocession: A.Rocession: A.Rocession: A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A.Rocession: C58. A
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QSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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13.6%; Score 105.5; DB
Best Local Similarity 23.2%; Pred. No. 0.049;
Matches 36; Conservative 27; Mismatches 6
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                                                                                                                                                                                                                                                               A;Experimental source: straim coc;Genetics:
A;Gene: Atu4768
A;Map position: linear chromosome
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R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhey iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPDB:GN00145; UWGP:Z1
                                                                   C)Accession: C9806
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Gsaawara, N.; Yakomaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Accession: C9806
A;Accession: C98066
A;Status: preliminary
minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, C.Species: Escherichia coli
C.Species: Escherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECS1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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A;Molecule type: DNA
A;Residues: 1-151 <STS-
A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          curlin minor chain precursor, CsgA homolog [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.5%; Score 96.5; DB 28.1%; Pred. No. 0.29; cive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.5%; Score 96.5; DB Best Local Similarity 28.1%; Pred. No. 0.29; Matches 32; Conservative 15; Mismatches
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Matches 32; Conserv
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A;Experimental source: strain K-12, substrain MG1655
A;Genetics:
A;Genetics:
A;Map position: 23.15
A;Map position: 23.15
A;Map position: A;Map position: A;Map position: Minor component of wild-type curli; interaction between CsgA and CsgB tri A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H;Kninosen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-21/Domain: signal sequence #status predicted <SIG>F;2-151/Product: minor curlin chain #status predicted <MAT>
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                                                                                                                                             13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTR 72
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12.5%; Score 96.5; DB 2; Length 151;
Best Local Similarity 28.1%; Pred. No. 0.29;
Matches 32; Conservative 15; Mismatches 62; Indels
                                                                                                                                                                               DB 2; Length 573;
0.81;
                                                                                                    Indels
                                                                                                                                                                                                                                         73 VVTHEMAHAGOGADNSTIELTQNGFRNNA-TIDOWNAKNS
                                                                                                    24; Mismatches
                                                         12.8%; Score 99; 25.4%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                  123 AALVNOTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                              ::|:: | |:
184 NVMMNKSPTQSFVV 197
                                                                                                       34; Conservative
                                                         Query Match
Best Local Similarity
Matches 34; Conserv
                A; Map position:
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C.Species: Sinorhizobium meliloti C.Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C.Accession: B95965 R.Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9884, 2001 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endd hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) maga

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A; Modecule type: protein
A; Residues: 101, E7, 103-118, SV', 121-123 <BOU>
A; Residues: 101, E7, 103-118, SV', 121-123 <BOU>
A; Residues: 101, E7, 103-118, SV', 121-123 <BOU>
B; Experimental source: strain LEM513 
B; Schlagenhauf, E.; Erges, R.; Metcalf, P.
Submitted to the Brookhaven Protein Data Bank, March 1997
A; Reference number: A68135; PDB:11LML
A; Contents: annotation; X-ray crystallography, 1.86 angstroms, residues 100-407,412-498
A; Note: strain LRC-L119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leishmanolysin (EC 3.4.24.36) precursor [validated] - Leishmania major
N/Alternate names: promastigote surface proteinase; surface endopeptidase glycoprotein
C/Species: Leishmania major
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ice nucleation protein inaA - Erwinia ananas
C,Species: Erwinia ananas
C,Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 26-Aug-1999
C,Accession: S07053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELT
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                                                                                                                                                                                                                                                                              A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1322 <ABE>
A;Cross-references: GB:X17316; NID:g296095; PIDN:CAA35194.1; PID:g296096
C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leishmania
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A, Cross-references: GB: Y00647; NID: 99554; PIDN: CAA68673.1; PID: 99555
A, Note: this!is a review to the sequence from reference A27598
A, Note: this!is and A2759; N.R.
J. Exp. Med. 167, 724-729, 1988
A, Title: Molecular cloning of the major surface antigen of Leishmania A, Reference number: A27598; MUID: 88154764; PMID: 3346625
A, Accession: A27598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1322;
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A;Molecule type: DNA
R;Bouvier, J.; Bordier, C.; Vogel, H.; Reichelt, R.; Etges, R.
Mol. Biochem, Parasitol. 37, 235-246, 1989
A;Title: Characterization of the promastigote surface protease of
A;Reference number: A60648; MUID:90114330; PMID:2608099
A;Accession: A60648
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                                                                                                                  R;Abe, K.; Watabe, S.; Emori, Y.; Watanabe, M.; Arai, S.
FEBS Lett. 258, 297-300, 1989
A;Title: An ice nucleation active gene of Erwinia ananas.
A;Reference number: S07053; MUID:90092494; PMID:2599095
A;Accession: S07053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 11.8%; Score 91.5; DB Local.Similarity 29.1%; Pred. No. 8.9; Nes 37; Conservative 19; Mismatches
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A; Residues: 1-602 < BUT>
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                                                                                       A; Molecule Type: DNA
A; Residues: 1-2174 «KUR»
A; Residues: 1-2174 «KUR»
A; Residues: 1-2174 «KUR»
A; Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A; Experimental source: strain 1021, megaplaemid psymB
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Aluthors: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUID:21368234; PMID:11474104
C; Genetics: annotation
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inaX from Xanthomonas campestri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLTAGYGSTQTAQEGSRLTSGYGSTATSGSDSAVI----SGYGSTQTAGSESSLTAGYG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 -DQWNAKNSDITVGQYG----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STQTARKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Xanthomonas campestris
Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
Accession: S11672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 VSGSALAG-----VVPQWGG---GGNHN-----GGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGS-----ANAA----
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A;Residues: 1-1567 <2HA>
A;Cross-references: EMBL:X52970; NID:g48531; PIDN:CAA37140.1; PID:g48532
C;Superfamily: ice nucleation protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.4%; Score 96; DB 2; Length 2174; 27.0%; Pred. No. 6.5;
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C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_C;Accession: S11672
C;Accession: S11672
R;Zhao, J.; Orser, C.S.
Mol. Gen. Genet. 223, 163-166, 1990
A;Title: Conserved repetition in the ice nucleation gene
A;Reference number: S11672; MUID:91080859; PMID:2259339
A;Status: preliminary
      A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95965
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25.8%; Pred. No. 8.9;
:ive 27; Mismatches
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Best Local Similarity
Matches 46; Conserv
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                                                                       Status: preliminary
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A;Genome: plasmid
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S07053
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C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; homodimer; hydrolase; lip F;1-39/Domain: signal sequence #status predicted <SIG>, F;40-100/Domain: activation peptide #status predicted <ATP> F;40-100/Domain: activation peptide #status predicted <ATP> F;40-100/Domain: activation peptide #status predicted <ATP> F;101-577/Product: leishmanolysin #status experimental k%AMT> F;48.264,268,334/Binding site: xinc, catalytic (Cys, His, His, His) His) (inhibited) #status F;100-101/Cleavage site: Val-Val (autolytic) #status experimental F;25-142,191-230,314-386,333-455,406-425,415-489,466-510,515-565,535-558/Disulfide bond F;265/Active site: clu #status predicted (Asn) (covalent) #status experimental F;265/Active site: carbohydrate (Asn) (covalent) #status experimental F;265/Active site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form F;777/Wodified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)
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11.8%; Score 91; DB 1; Length 602;
Best Local Similarity 37.5%; Pred. No. 4;
Matches 27; Conservative 6; Mismatches 15; Indels 24; Gaps
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec Run on:

US-09-543-407-20 774 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapext 0.5

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	salmonella	es	68		P18127 xanthomonas	par	leishmani	sa]	salmonell	leishmani	leishmani	P43150 leishmania	Q9kk89 mycobacteri	escheric	pantoea	erwinia	E	P04480 citrobacter	Q44052 arthrobacte	drosc	Q05925 homo sapien	sacch	Н	Ωι	bacillus an	Ε	canlobacte	coprinu	mes	art	met	O86343 mycobacteri	
ΙD		SGA		CSGB_ECOLI	CE	CEZ	GP63 LEIMA	CSGB_SALTI		GP63_LEIDO	GP63_LEICH	GP63_LEIME	PST3 MYCAV	FMF2 ECOLI	ICEN_PANAN	ICEN ERWHE	YF48_MYCTU	CEA_CITFR	IMD_ARTGO	OVO_DROME	HMEI HUMAN	N145_YEAST	OMPB_RICJA	ICEN PSEFL	SACB_BACAM	Y442_MYCTU	HFAA_CAUCR	PER COPCI	PRIO MESAU	PER ARTRA	Z	ST3	ြင္မ
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Q06981 salmonella Q0in81 drosophila Q8vxp3 chlamydomon Q60506 cricetulus Q47112 escherichia 033479 pseudomonas P07184 drosophila	099tc9 staphylococ P39442 natronomona 099834 pentcillium 009112 mus musculu P75780 escherichia
FLIC SALMC FRU DROMB: TBCZ CHLRE PRIO CRIGR CEA7 ECOLI CCEV-PSESX CH18 DROME	ACUC_STAAM HCY NATPH PCLI PENOL DUS8_MOUSE YBIL_ECOLI
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ALIGNMENTS

us-09-543-407-20.rsp

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Major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIESES.enteritidis; STRAIN=27655-3B;
MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                 SEQUENCE FROM N.A. STRAIN=27655-3B; SPECIES=S.enteritidis; STRAIN=27655-3B; SPECIES=S.enteritidis; PubMed=8550497; Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.; Salmonella enteritidis agfBAC operon encoding thin, aggregative
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SECUESS.S. enteritidis, STRAIN=27655-3B;

MEDLINE=940137; PubMed=8104955;

Doran J.L., C3011,nson S.K., Buffian J., Sarlos G., Todd E.C.D.,

Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;

Musc C.K., Kay C.M., asser F.A., Peterkin P.I., Kay W.W.;

the structural gene for thin, aggregative fimbriae.";

J. Clin. Microbiol. 31:2263-2273(1993).
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B7DAC0D16B621359 CRC64;
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                                                                    Bacteriol. 185:2330-2337(2003).
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Matches 137; Conserv
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MEDLINE=97061202; PubMed=8905232;
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                     curlin subunit precursor
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STRAIN=K12 / MC4100;
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STRAIN=K12 / MG1655;
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-- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLIED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Anquist A., Bian Z., Olsen A., Normark S.;
Hammar M., Anquist A., Bian Z., olsen A., sorduction of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.4%; Score 506.5; DB 1; Length 152; 67.1%; Pred. No. 2.6e-37; ive 21; Mismatches 28; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AR27573; AAK5312.1; -.
EMBL, AR205315; AAK5312.1; -.
EMBL, AR005315; AAK5312.1; -.
EMBL, AR005515; AAK5312.1; -.
PIR, D90806; D90806.
PIR, H85665; H85665.
Fimbria; Signal; Complete proteome.
SIGNAL
21 152 MAJOR CURLIN SUBUNIT.
CHAIN : 1509 MW; EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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01-FBB-1995 (Rel. 31, Created)
01-0CT-1996 (Rel. 34, Last sequence up
28-FBB-2003 (Rel. 41, Last annotation of the curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammap
Enterobacteriaceae, Escherichia.
[3]
SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
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Best Local;Similarity 67.1;
Matches 102; Conservative
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NCBI TaxID=562, 83334;
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CSGB_E
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                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=2128556; PubMed=1131255;
Whitch G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli 0157:H7.";
pppl. Broviron. Microbiol. 67:2367-2370(2001).
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
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68.9%; Pred. No. 3.6e-39;
live 20; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAJOR CURLIN SUBUNIT.
A -> E (IN REF. 1).
C003470D208D395F CRC64;
    -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 104979; AAA23616.1; --
EMBL; X90754; CAA62282.1; --
EMBL; AE000205; AAC74126.1; --
EMBL; D90741; BAA58832.1; --
EMBL; D90742; BAA5840.1; --
EMBL; D70788; S70788; --
ECGGNe; EG14489; CSGA.
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NCBI_TaxID=83334;
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CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AA; 15049 MW;
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Best Local Similarity
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CONFLICT
SEQUENCE
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SIGNAL

CSGA ECO 093U24;

CSGA_ECO57 RESULT

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Gaps

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EMBL; AE000205; AAC74125.1; -...
EMBL; D90741; BAA35831.1; -...
EMBL; AE005315; AAG55787.1; -...
EMBL; AP002554; BAB34842.1; -...
PIR; C90806; C90806.
PIR; G85665; G85665.
PIR; S70787; S70787.
EcoGene; EG12621; csgB.
Finbria; Signal; Complete proteome.
SIGNAL
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HSSP; P06620; 11NA.
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Best Local Similarity 28.1<sup>†</sup>
Matches 32; Conservative
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P18127;
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"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the mucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREPERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Roberta N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Posfa J., Mayhew G.F., Evans P.S., Gregor J., Kikpattick H.A.,
Posfa J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
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STRAIN=K12;
MEDLINE=95157246; PubMed=7854117;
                                                                               Mol. Microbiol. 18:661-670(1995)
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EMBL; X90754; CAA62281.1; -.

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                                                                                      7
                                                                                                                                         16
                                                                                                               38 SSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGF 97
                                                                                                                                            21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                  SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                       98 RNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                    Xanthomonas campestris (pv. translucens).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
                                                                                      .
.
                                                          DB 1; Length 151;
                                                                                     Indels
15 AA, 15882 MW, B18D266B964014B8 CRC64;
                                                             0.097;
                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                          12.5%; Score 96.5; D 28.1%; Pred. No. 0.09 ative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00818; Ice_nucleation; 81.
PRINTS; PR00327: ICENUCLEATION; 57.
PROSITE; P800314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000258; Ice nucleatn.
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                                                                    QNGFRNNATIDQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PETRUCTURE 6:1035-1046(1998).

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-...

-!- SUBCEDINIAR LOCATION: Attached to the membrane by a GPI-anchor.

-!- FUM: THE PROSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, AND C18:0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95406217; PubMed=7675788; Schlagehhauf E., Etges R., Metcalf P.; Schlagehhauf E., Etges R., Metcalf P.; Carystallization and preliminary X-ray diffraction studies of leishmanolysin, the major surface metalloproteinase from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
MEDLINE#98416698; PubMed=9739094;
Schlagephauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase leishmanolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01.APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmaholysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDLINE=88154764; PubMed=3346625;
Butron L.L., Ordwaster W.R., Major surface antigen of leishmania.";
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferguson M.A.J., McConville M.J., Mehlert A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE 91009116; PubMed=2145267; Schneider P., Ferguson M.A.J., McConville M.J., Mehler Homans S.W., Bordier C.; "Structure of the glycosyl-phosphatidylinositol membra "Structure of the plycosyl-phosphatidylinositol membra the Leishmania major promastigote surface protease."; J. Biol: Chem. 265:16955-16964 (1990).
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                   GSTSTAGPDSSL-IAGYGSTQTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Button L.L., McMaster W.R.;
J. Exp. Med. 171:589-589(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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14,
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01-AUG-1988 (Rel.
01-APR-1990 (Rel.
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                                                                                                                      11;
                                                                                                                                                                                                                        QSDARKYDQLVT-----RVVTHEMAHAGQGADNSTIELTQNGFRNNATI------ 103
                                                                                                                                                                                                                                                                                                                                                              STLIAGYGSTQTAQEGSRLISGYGSTATSGSDSAVI----SGYGSTQTAGSESSLIAGYG 319
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                                                                                                                                                                                 14 VSGSALAG-----VVVPQWGG---GGNHN-----GGGNSSGPDSTLSIYQYGSANAALAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                             104 -DQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STQTARKGSDITAG-YGSTGTAGSDSALLAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEDURNE FROM N.A.

**REDINES 9092494; PubMed=2599095;

**REDINES9092494; PubMed=2599095;

**A be K., Watabe S., Emori Y., Watanabe M., Arai S.;

**Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;

**An ice nucleation active gene of Erwinia ananas. Sequence similarity to chose of Pseudomanas species and regions required for ice nucleation activity.";

**FINGTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

**C. I SUBCELLULAR LOCATION: Outer membrane (By similarity).

**C. I SUBCELLULAR LOCATION: Outer membrane (By similarity).

**C. I SUMILAR LIDE A-G. Y-G. S-T. Y-T.; FURTHER ON A 16-RESIDUE AND A RECIONAL 48-RESIDUE ABERDONED.

**C. I SUMILARITY: Belongs to the bacterial ice nucleation protein family.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
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                                                       Length 1567;
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W; 89B0EE24AA837039 CRC64;
                                                                                                                      Indels
152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                      56;
                                                           DB 1;
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(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                       12.0%; Score 92.5; DB 25.8%; Pred. No. 3.1; ive 27; Mismatches
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COMAIN 162 1281 OCTAPEPTID
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Pfam. PF00818; Ice_nucleation; 69.
PRINTS; PR00337; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131094 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleation protein inaA.
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Best Local Similarity 29.19
Matches 37; Conservative
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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1567 AA;
                                                                                        Local Similarity
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01-FEB-1991 (
16-OCT-2001 (
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SEQUENCE
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RESULT

membrane anchor of

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63 ARKYDQLVTRVVTHEMAHA----GQGADNSTIELTQNGFRNNATIDQWNAKNSDITV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91; DB 1; Length 602;
Pred. No. 1.4;
6; Mismatches 15; Indels
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CSGB_SALTI
D_CSGB_SALTI STANDARD; PRT; 151 AA
AC Q827M3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
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Best Local Similarity 37.5%;
Matches 27; Conservative
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602 AA;
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or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=TY2 / ATCC 700931;
STRAIN=TY2 / ATCC 700931;
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Burland V., Indu S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Rodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
J. Bacteriol. 185:2330-2337(2003).
-: FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO FENERAL STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STRUCTURE STR
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                                                                                                                                                                                                                                                                                                      Parkhill J., Bougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leacher S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of a multiple drug resistant Salmonella anterica serovar Turbi CT18."
                                                                                                                  Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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161C54326E573495 CRC64;
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Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
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; Pred. No. 0.48
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fimbria; Signal; Complete proteome
                                                                                                                                                                                                                                                                                                   MEDLINE=21534947; PubMed=11677608;
                                                                                                                     Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL627269; CAD08267.1; -.
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Nature 413:848-852(2001).
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SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=601;
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ID CSGB_SALTY
AC P55226;
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SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative finbtiae.";
"Bacteriol. 178:662-667(1996).
-!- PUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIRENDECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=S. 19phimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534946; PubMed=11677609; MCDLINE=21534946; PubMed=11677609; MCTCLIIdad M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Alii J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miler W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                       SPECIES—S. typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                      Gammaproteobacteria; Enterobacteriales;
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MINOR CURLIN SUBUNIT.
COFC5430E6DD361D CRC64;
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Pred. No. 0.48;
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EMBL, AE008749, AAL20073.1; -.
EMBL, U43280, AAC43598.1; -.
EMBL, U43280, AC64598.1; -.
Stydenc, S010609, csgB.
Fimbria, Signal; Complete proteome.
       precursor
                                                                                                                                                                               Enterobacteriaceae; Salmonella
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31.0%;
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CSGB OR AGFB OR STM1143.
Salmonella typhimurium, and
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                             NCBI_TaxID=602, 592;
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                                                                                                                                                                                                                                                           Webb J.R., Button L.L., McMaster R.W.;
"Heterrogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.",
"Heterrogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.",
"Heterrogeneity of the genes encoding the infection of macrophages in the mammalian host.
-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-leu-Lvs-Lvs-.|
-!- COFACTOR: Binds I zinc ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SIMILARITY: Belongs to peptidase family M8.
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ZINC (CATALYTIC) (BY SIMILARITY)
                                                       01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-12003 (Rel. 42, Last annotation update)
Ledshmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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InterPro; IPRO06025; Pept M Zn BS.
InterPro; IPRO01577; Peptidase_MS.
Pfam; PF01457; Peptidase M8; 1.
PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PSOTERSE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
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ACTIVATION PEPTIDE.
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ZINC (CATALYTIC)
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                             LEIDO
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Score 88; DB 1; Length 590; Pred. No. 2.5;

11.4%;

Query Match Best Local Similarity

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"Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishmania donovani chagasi promastigotes to an infectious form.";

J. Biol. Chem. 267:1888-1895(1992).

-! FUNCTION: Has an integral role during the infection of macrophages in the mammanian host.

-! CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala-Tyr-|-Leu-Lys-Lys-.

-! COPACTOR: Binds 1 zinc ion per subunit (By similarity).

-! SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-! SIMILARITY: Belongs to peptidase family M8.
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REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
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MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90205976; PubMed=2320059;
Miller R.A., Read S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Gly-Asp sequence.";
                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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InterPro; IPR01577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8. 1.
PRINTS; PF01457; Peptidase_M8. 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
SIGNAL 1.
PROPEP 40 97 ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                      599 AA.

    Biochem. Parasitol. 39:267-274(1990).

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                                                        238 ASRYDOLVTRVVTHEMAHA 256
63 ARKYDQLVTRVVTHEMAHA 81
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HSSP; P08148; 1LML.
MEROPS; M08.001; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MNYC/BZ/62/M379;

MEDLINE=93149206; PubMed=8426614;

MEDLINE=93149206; PubMed=8426614;

Medina-Acosta E., Karess R.E., Russell D.G.;

Medina-Acosta E., Karess R.E., Russell D.G.;

Structurally distinct genes for the surface protease of Leishmania mexicana are developmentally regulated.";

MOD Biochem. Parasitol. 57:31-46(1993).

I. FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1 and basic residues at P2 and P3'. A model nonapeptide is cleaved at AAA-Tr-1-Leu-Lys-Lys-Lys-

I. COFACTOR: Binds 1 zinc ion per subunit (By similarity).

I. DEVELOPMENTAL STAGE: Expressed in both the promastigote and the
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GP63-C1.
Leishmania mexicana.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5665;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
ZINC (CATALYTIC) (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GPISSIANCHOUS amidated asparagine (By GLCNAC. . .)
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                                                                                                                                                                                                                                      Score 88; DB 1; Length 599;
Pred. No. 2.6;
Mismatches 1; Indels
                                                                                                                                                                                                           746730AE8E2A2E7C CRC64;
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                                                                                                                                                                                               similarity)
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InterPro; IPR006625; Pept M Zn BS.
InterPro; IPR001577; Peptidase_M8.
Pfan; PF01457; Peptidase_M8, 1.
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                                                                                                                                                                                                             63848 MW;
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Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                               PIR; S19916; S19916.
HSSP; P08148; 1LML.
MEROPS; M08.001; -.
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SEQUENCE FROM N.A.
    endopeptidase)
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ID GP63_LEIME
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Carrolls.D., Wallace R.C., Keane J., Arbeit R.D.;
"Identification of Mycobacterium avium DNA sequences that encode
exported proteins by using phoA gene fusions.",
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required for binding-protein-mediated phosphate
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PRINTS; PRO0782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Zymogen; Signal; Cell adhesion; Miltigene family.
39
POTENTIAL.
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Bacterià; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3) (PstS-3)
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Conservative
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Best Local Similarity
Matches 45; Conserv
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Q47879;
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                                                                                                                                                                                                                                            1 MKLNRFGAVLSVLSAGALVL-----SGCGSDNNGAGAGAAGSSSSKVSCGGKKALKASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      van Die I., Bergmans H.;
"Nucleotide sequence of the gene encoding the F72 fimbrial subunit of
Nucleotide sequence of the gene encoding the F72 fimbrial subunit of
Gene 32:83-90(1984).
                                                                                                                                                                                               Gaps
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STRAIN=06:HI / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MADLAN G.F., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.D.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17024 (2002).
-I- FUNCTION: Finbriae (also called pili), polar filaments radiating from the surface of the bacterium to a length of 0.5-1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "DNA sequences of three papA genes from uropathogenic Escherichia coli strains: evidence of structural and serological conservation."; Infect. Immun. 59:3849-3858(1991).
                                                                                                         PHOSPHATE-BINDING PROTEIN 3.
N-palmatroyl Oysteine (Potential).
Schlacylglycerol cysteine (Potential).
CBOEAOAC108463EC CRC64;
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MEDLINE-92040048; PubMed=1682251;
Denich K., Blyn L.B., Craiu A., Braaten B.A., Hardy J., Low D.A.,
O'Hanley P.D.;
                                                                                                                                                                                               21;
                                    Pfam; PF01547; SBP bac 1; 1.
PROSITE; PS00013; PROXĀR_LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
                                                                                                                                                                      Length 369;
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                                                                                                                                                                                               21; Mismatches 49;
                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           21-701-1986 (Rel. 01, Created)
21-701-1986 (Rel. 01, Last sequence update)
21-701-1986 (Rel. 01, Last sequence update)
77-2 fimbrial protein precursor (F7-2 pilin).
F7-2 OR PAPA OR C3592.
Escherichia coli, and
Escherichia coli, o6.
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                                                                                                                                                                      11.2%; Score 86.5; 27.8%; Pred. No. 2;
EMBL, AF137360; AAF74819.1; -.
HSSP, P06128; 1A54.
InterPro; IPR0006137; Prok lipoprot_S.
InterPro; IPR006059; SBP_Dac_1.
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MEDLINE=85155489; PubMed=6152241;
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Enterobacteriaceae, Escherichia
NCBI_TaxID=562, 217992;
                                                                                                                                               37225 MW;
                                                                                                                                                                                               35; Conservative
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369 AA;
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Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 ---NAKNSDITVGQYGGNNAALVNQTASDSSVM------VRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
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-: SUBCELLULAR LOCATION: Outer membrane.
-:- DOWAIN: CONTAINS INTERFECT REPERTS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FUNTHER ON A 16-RESIDUB AND A REGIONAL 48-RESIDUE PRIODICITY IS SUPERINPOSED.
-:- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-:- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 ANAALALQSDA----RKYD-QLVTRVVTH-EMAHAGQGADNSTIELTQNGFRNNATIDQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 --SKLFLENDGESQPKSFDIKLINCDITNFKKAAGGGGAKTGTVSLTFSGVPSGPQSDML
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micrometers and numbering 100-300 per cell, enable bacteria to colonize the epithelium of specific host organs. SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 84.5; DB 1; Length 188; 25.0%; Pred. No. 1.4; ive 26; Mismatches 76; Indels 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROBABLE.
0EEF750CFD843157 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosci. Biotechnol. Biochem. 58:762-764 (1994)
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InterPro; IPR008966; Adhes bact.
InterPro; IPR008059; Fimbrial.
Pfam; PFf00419; Fimbrial; 1.
Fimbria, Signal; Complete proteome.
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MEDLINE-94264407; PubMed-7764866;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M12861; AAA23778.1; -.
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EMBL, D14992, BAA03636.1; -..

DR PIR, JCZ143; JCZ143.

BR HSSP; P66620; IINA.

DR PIR, JCZ02143; LCE nucleatn.

DR PIR, JCZ02143; LCE nucleatn.

DR PRINTS; PR00125; ICE NUCLEATN.

DR PRINTS; PR00127; ICENUCLEATN.

DR PRINTS; PR00124; CE NUCLEATION; 34.

FEM. CE nucleation; SPORAT.

FORM CE nucleation; SPORAT.

FORMIN 162 993 OCTAMBEPTIDE PERIODICITY.

SEQUENCE 1034 AA; 103378 MW; FA222523D333EADD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 EESSQWAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSL-IAGYGSTQTAGEDSSLTAGYGS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 ALOSDARKYDQLVTRV----VTHEMAHAGOGADNSTIELTQNGFRNNATID----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS------GPDSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.9%; Score 84.5; DB 1; Length 1034;
Best Local Similarity 26.9%; Pred. No. 9.6;
Matches 45; Conservative 17; Mismatches 66; Indels 39; Gaps
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                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Description	033802 salmonella Q7x243 citrobacter	Q7x240 citrobacter O8cw63 escherichia		Q34089 saimonella Q983j5 escherichia	089ji4 bradyrhizob	Q8ein3 shewanella Q8eih4 shewanella	Q8u6n9 agrobacteri	Q89ji6 bradyrhizob	Q9saf2 arabidopsis	Q89ji5 bradyrhizob	Q7v8s5 prochloroco	O88hg0 pseudomonas
SUMMARIES	033802 Q7X243	Q7X240 O8CW63	Q7X237	Q953U5 Q953U5	Q89J14	QBEIH3 QBEIH4	6N9N8O	911680	Q9SAF2	Q89JIS	Q7V8S5	O88HG0
DB	77	7 1 1 1	01 0	4 (1	1,6	9 1	16	16	10	16	16	16
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q ŏ 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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Q?uczl shigella fl Q8cw64 escherichia Q83ru7 shigella fl Q82ru8 rhizobium m Q8efu3 shewanella Q82m56 streptomyce Q25275 leishmania Q89cx5 bradyrhizob Q89sy8 escherichia Q7x244 citrobacter Q4394 leishmania Q7x244 citrobacteri Q88833 shewanella Q7ulc5 mycobacteri Q80m16 mycobacteri Q80m16 mycobacteri Q8m19 leishmania Q80r73 bradyrhizob Q8n121 neurospora Q7x244 citrobacter Q7x244 citrobacter Q7x24 citrobacter Q7x274 leishmania Q8m19 leishmania Q8x07 bradyrhizob Q8m10 rhodopirell Q8x01 streptococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx6 synechococc Q1xx7 synechococc Q1xx7 synechococc Q1xx7 synechococc	ALIGNMENTS RY; PRT; 152 AA. 1. 05, Created) 1. 19, Last annotation update) 1. 19, Last annotation update) 1. 19, Last annotation update) m. ria; Gammaproteobacteria; Enterobacteriales; almonella. Med=9393832; dggregative fimbriae promotes interaction of m SR-11 with mouse small intestinal epithelial 0.5325(1997). 151.1; 5401 MW; 9DA7DADC2364B006 CRC64; 87.9%; Score 680; DB 2; Length 152; 87.9%; Score 680; DB 2; Length 152; 87.9%; Pred: No. 2.38-48; ive 4; Mismatches 12; Indels 0; Gaps 0; VVSGSALAGVVPQMGGGNHNGGGNSSGPDSTLSITYQYGSANAALALQ 60
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61 SDARKYDQLVIRVVIHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SITAIN=06:HI / CFT073 / ATCC 700928;
STRAIN=06:HI / CFT073 / ATCC 700928;
STRAIN=288834; PubMed=12471157;
WEDLINE=2388234; PubMed=12471157;
Welch R.A., Buckles E.L., Liou S.R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; Perna N.T., Stroud D., Strough W.D., Perna N.T., Donnenberg M.S., Blattner F.R.; Perna N.T., Conput Structure revealed by the complete genome sequence of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=217992;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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Last annotation update)
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67.1%; Pred. No. 7.1e-34;
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Best Local Similarity 67.1%; Pred. No. 7.1e
Matches 102; Conservative 20; Mismatches
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                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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SEQUENCE 152 AA;
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
EMBL; AJS15701; CADS66751; -. SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                Citrobacter sp. Fec2.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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                                                                                                                                                            Last sequence update)
Last annotation update)
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78.8%; Pred. No. 2.3e-40;
ive 10; Mismatches 21;
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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es 119; Conservative
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   NCBI_TaxID=562;
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Q8EIH3
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).

EMBL, AJ515702; CAD56678.1; -. SEQUENCE ISO AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBL_TaxID=592;
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Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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"Virulence of Salmonella enteritidis in chickens correlates with
"Virulence of Salmonella enteritidis in chickens correlates with
colony morphology and expression of SEF17 finbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U53207; AAA98671.1; -.
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                                                                                                                                                                                                                                                                                    34; Indels
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Last sequence update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fragment).
                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                             55.6%; Score 430.5; DB 2
58.9%; Pred. No. 6.9e-28;
rative 27; Mismatches 34
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Q54069;
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01-NOV-1996 (TrEMBLrel. 01, C, 01-NOV-1996 (TrEMBLrel. 01, L, 01-DEC-2001 (TrEMBLrel. 19, L, SEF17 fimbrin (Fragment).
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                                                                                                                                                                                                                                                                                    89; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LKVAAFAAIVVSGSALAGVVPQWGGG-----GNHNGG-----GNSSGPDSTLSIYQYGS 52
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                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada Tabata S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                            Score 122; DB 2; Length 29;
Pred. No. 0.0019;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Indels
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SEQUENCE 130 AA; 12699 MW; ACFB2D66A48D260F CRC64;
                                                                                                                                                                         29 AA; 2789 MW; E290DFC07ABBB243 CRC64;
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Last annotation update)
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%; Score 115; DB 16; 25.9%; Pred. No. 0.046; tive 27; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
SEQUENCE FROM N.A.
TRANSPOSON=Insertion sequence IS1;
                                                                                                                                                                                                              Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23,
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B115299 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Heidelberg U.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,
Read T.D., Eisen J.A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Uttersback T.R., MoDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 110; DB 16; Length 139; 28.3%; Pred. No. 0.13; ive 18; Mismatches 34; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 NISLVTÓIGT-NNEVQLLÓVGAQNKÁSITÓIGNDNLVQLNÓLGSGN 122
                                                                                                                                                                                                                                                                                                                                        139 AA; 14811 MW; 41EC1CFA76957920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1 protein; Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit CsgB, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 AA
                                                                                                                                                                                                                                                                                  Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Biotechnol. 20:1118-1123 (2002).
EMBL; AE015532; AAN53941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                         STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                  EMBL; AE015532; AAN53942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                      Shewanella oneidensis.";
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                                        Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                                           Complete proteome.
SEQUENCE 139 AA;
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Matches 30; Conserv
                                                                                                           SEQUENCE FROM N.A.
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                                                                                NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                             $00866;
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SEQUENCE 50
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                                                                                                                                                                         222
                                                                                                                                                                                                                                                                                        23 NSVDIÝQKGDNHTGFVYALAGSENDISMEQEGSNNTÁYLSMTTGDDNTVDITQDGDSNTV 282
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                                                                                                                    --GNHNG-----SGNS----SGBD
                                                                                                                                                                      163 AVFRVEGDNNDGDIKQYGNNNQAGLIALDLSANVGNNNDVSVEQIGNNNFGAAKGIAGND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-2160856; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.
                                                          31;
                                                                                                                                                                                                                                                                                                                                               100 -NATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 145;
Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium. NCFI_TaxID=176299;
                                                          Indels
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145 AA; 14984 MW; DEDC870E1713D51A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4768
ATU4768 OR AGR L 228.
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%; Score 105.5; DE 23.2%; Pred. No. 0.32;
13.8%; Score 106.5; D 23.1%; Pred. No. 1.2; cive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                    10 AAIVVSGSALAGVVPQWGGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 294:2317-2323(2001).
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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Best Local &
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73 VVTHEMAHAGOGADNSTIELTQNGFRNNA-TIDQWNAKNS------DITVGQYGGNN 122
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NGUJENCE TO CARLE TO TRIPP M., Palm C.J., Jones T., Wu T.,

NGUJEN M., Southwick A., Tripp M., Chang C.H., Dale J.M.,

Deng J.M., Hayashizaki Y., Hauan V.W., Lee J.M., Ishida J., Kamiya A.,

Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,

Satou M., Sehim P., Tang C.C., Toroumi M., Wong C., Wu H.C.,

Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,

Davis R.W.,

Submitted (DEC-2002) Lo the EMBL/GenBank/DDBJ databases.
P., Walker M.,
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Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kaniya A., Kawai
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Bakurail T., Satoun M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Bcker J., Theologis A., Davis R.W.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P. Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; "Arabidopsis thaliana chromosome 1 BAC F3F19 sequence."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 573;
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                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ databases.
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EMBL; A7062557; AAD31072.1; --
EMBL; A7062557; AAD32605.1; --
EMBL; B7062557; AAD32605.1; --
EMBL; B7062567; AAD30935.1; --
EMBL; B706266; C86266.
GO; GO: 0003676; F: nucleic acid binding; IEA.
InterPro; IPR00076; F: nucleic acid binding; IEA.
InterPro; IPR00076; F: nucleic acid binding; IEA.
INTERPRO; IPR00076; F: nucleic acid binding; IEA.
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INTERPRO; IPR00076; F: nucleic acid binding; IEA.
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5.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 99;
Pred. No.
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NCBI_TaxID=375;
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25.4%;
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Bll5298 protein.
                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
Theologis A.;
Submitted (MAY-1999)
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SEQUENCE FROM N.A.
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           ALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
F3F19.21 protein (Hypothetidal protein).
F3F19.21 OR ATIG13190, F3F19.21 OR ATIG13190.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP065954; BAC50562.1; -...
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                          55; Indels
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(TremBlrel. 24, Last sequence update)
(TremBlrel. 24, Last annotation update)
                                                                                                                                                                                                                           GOFGSNHTTILTODGNGNIAAGVOVGRGCSANVSO 131
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CSGB OR BLL5297.
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01-JUN-2003
01-JUN-2003
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                                                                                                                                                                                                                                                                     3; Gaps
             MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zhiser B.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
Nature 424:1042-1047(2003).
EMBL; BX572095; CABZ0431:1; -.
Complete protecome.
SEQUENCE 1765 AA, 187603 MW; 817CE4F5007580CD CRC64;
                                                                                                    "Complete genomic sequence of nitrogen-fixing symbiotic bacterium tradyrhicobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005954; BAC50563.1; -.
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                                                                                                                                                                                                                             Query Match 12.7%; Score 98.5; DB 16; Length 154; Best Local Similarity 36.8%; Pred. No. 1.3; Matches 25; Conservative 12; Mismatches 28; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hemolysin-type calcium-binding region:RTX N-terminal domain.
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12.6%; Score 97.5; DB 16;
Best Local Similarity 28.7%; Pred. No. 31;
Matches 41; Conservative 21; Mismatches 50;
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SEQUENCE FROM N.A.
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NCBI_TaxID=74547;
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Search completed: August 2, 2004, 14:54:39 Job time : 30.7 secs

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2, 2004, 14:35:42; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A Geneseq 29Jan04:*

1: geneseq11980s:*

2: geneseq11990s:*

4: geneseq12000s:*

5: geneseq12001s:*

6: geneseq12001s:*

7: geneseq12003bs:*

8: geneseq12003bs:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Description	1	27	Aab36354 AgfA::PT3	Aar74625 AgfA segu	41	3570	Aab36355 AgfA::PT3	50	3352	46	Aab36347 AgfA::PT3	Aab36353 AgfA::PT3	σ	Aab36348 AgfA::PT3	43	Abr82651 E. coli C	Aar62761 AgfA sequ	Aaw23569 Salmonell	64 Fibr	663 FN	Aab36316 Salmonell	Sa	25 Sal	Sal	Aab36320 Salmonell	
SUMMARIES		AAB36351	AAB36354	AAR74625	AAB36341	AAW23570	AAB36355	AAB36350	AAB36352	AAB36346	AAB36347	AAB36353	AAB36349	AAB36348	AAB36343	ABR82651	AAR62761	AAW23569	AAR52664	AAR52663	AAB36316	AAB36318	AAB36325	AAB36339	AAB36320	ABR82644
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ALIGNMENTS

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. The present invention describes a recombinant agfA gene (1) where a segment, of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFT/TAF) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native Salmonejla; agfA; chromosomal gene replacement; fimbrin; epitope; AgfA::Pṛ3#6 amino acid sequence SEQ ID NO:22. Kay WW; Disclosure; Page 137; 139pp; English. vaccine; immune response; immunogen. Collison SK, AAB36351 standard, protein, 151 AA. 05-APR-2000; 2000WO-CA000356. (first entry) Salmonella enteritidis. (UYVI-) UNIV VICTORIA. Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64627. Escherichia coli WO200060102-A2. 05-APR-1999; 26-FEB-2001 12-OCT-2000. Synthetic. White AP, AAB36351, RESULT 1 AAB36351

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copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens(city and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response immunogens, in inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Pred. No. 9.5e-68;
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100.0%; Pred. No. 9.5
ive 0; Mismatches
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Best Local Similarity 100.
Matches 151; Conservative
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N-PSDB; AAC64630
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epiteppe or antigen. Also described are:

(I) use of thin aggregative finbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Encombinations of Salmonella, Escherichia coli and AgfA, CoBA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence esponse in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to coliciting an immune response in an animal. In a fimbrial presentation system the carrier fimbrial submit protein possesses both the immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response against the inserted epitops, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
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91.8%; Score 712; DB 3;
Best Local Similarity 91.1%; Pred. No. 1.7e-61;
Matches 144; Conservative 0; Mismatches 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 151 AA;
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26-JUN-1995
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CC assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and contract assembly system of strains of Salmonella, Escherichia coli and Salmonella and Salmonella, Escherichia coli and directing recombination scheroly; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene comprising separating an eminon acid polymer comprising separating an amino acid polymer comprising a recombinant of comprising separating an amino acid polymer comprising a recombinant of protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or consequity for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunosencity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunosencity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit protein are usually strong immunosensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 682; DB 3;
Pred. No. 1.4e-58;
2; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
/note= "Encoded by GCC"
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Best Local Similarity 90.7
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1994;
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29-SEP-1997
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AAW23570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                     immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                        nune response to Salmonella - using attenuated Salmonella constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                   Salmonella AgfA protein and DNA are used in vaccine and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                    Score 682; DB 2; Length 151;
Pred. No. 1.4e-58;
2; Mismatches 12; Indels
                      Doran JL;
                                                                                                                             Eliciting an immune response to Salmonella -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                    Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                                          7B; 95pp; English.
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Matches 137; Conservative
                      SK,
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N-PSDB; AAC64617.
                                                             WPI; 1994-358275/44.
                    Collinson
                                                                                                                                                                                                                                                                                                                                              Sequence 151 AA;
                                                                                      N-PSDB; AAQ87467
                                                                                                                                                      vector
                                                                                                                                                                                          Disclosure; Fig
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                                                                                                                                                      strains,
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inexpensive to purify in large amount. The pr
the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                          Disclosure; Page 139; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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                                                                                                   The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                              WKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                    Gaps
                                              Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                           Score 677; DB 2;
Pred. No. 4.4e-58;
2; Mismatches 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNPALVNOTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SK,
                                                                               Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collison
                                                                                                                                                                                                                                                           87.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                  Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA
            WPI; 1997-309886/28.
N-PSDB; AAT74142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA (sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERIY/TAF) mucleation depended assembly system of strains of Salmonella. Escherichia coli and Enchartaceae for the production of fimbriae comprising recombinant of AffA, CspA and AgfA-homologue fimbrin subunits, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are combinant or segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or comprising expertations and the host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to comprisity and adhesion properties relevant for an efficient live contraction the arrange of the properties relevant for an efficient live contraction the arrangement of the more contraction in the contraction that are presented in high numbers (up to continue the contract of the contraction protein protein protein live contraction the contraction the contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction and contraction contraction and contraction and contraction contraction and contraction contraction and contraction contraction con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
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81.9%; Pred. No. 4e-56;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA comparison that the modes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SEFIT/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and comparison of strains of finbriae comprising recombinant of Enterophysical and AgfA-homologue finbriae (SEFIT/TAP) nucleation depended composition of a recombination of a recombination of a recombinant gene into the chromosome of the homologue species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enteropacteriaceae host cell, from the host cell and introducing the contribution with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response imanungens, which may be important for directing an immune response in against the inserted epitope, and hybrid fimbriae are easy and inexted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                 Kay WW;
                                                                                                                                                                                                                                                                                                                              Disclosure; Page 137; 139pp; English.
                                                                                                 Collison SK,
                                             (UYVI-) UNIV VICTORIA
                                                                                                 Doran JL,
                                                                                                                                               WPI; 2000-672631/65.
N-PSDB; AAC64626.
05-APR-1999;
                                                                                                 White AP,
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Sequence 151 AA;

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61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA-------- 103
                                                                                                                  09
                                                                                                                                                                                              98
                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                             1 MKLLKVAAFRAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                        61 SDARK--------YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR
                                          Gaps
                                                                                                                                                                                                                                   104 ----DOWNAKUSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                        NNATIDOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                          44;
Score 619; DB 3; Length 151;
Pred. No. 2e-52;
); Mismatches 0; Indels '
                                        0;
  79.8%;
                                        Conservative
                    Local Similarity
                                        Matches 129;
                                                                                                                                                                                                                                                                          99
    Query Match
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Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                            AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                  (first entry)
                                    26-FEB-2001
            AAB36352;
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AAB36352 standard; protein; 151 AA.

RESULT 8 AAB36352 σ

RESULT

120

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbries (SEPI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enteropacteriacae for the production of fimbriae comprising recombinant of Enteropacteriacae for the production of fimbriae comprising recombinant of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinant gene comprising species; (3) directing recombination of a recombinant gene comprising separating an amino acid polywer comprising separating an amino acid polywer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino said sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polywer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which the theorem of system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial submit protein sare usually strong immunogens, which may be important for directing an immune response in anymonent. The present sequence is given in consideration of the present invention received in sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 609; DB 3; Length 151;
Pred. No. 1.9e-51;
0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGAD------
                                                                                                                                                                                                                                                                                                                     Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                   Collison SK,
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ilarity 73.6%;
Conservative (
                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                 99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 138; 139pp;
               Salmonella enteritidis.
Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                   Doran JL,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-672631/65.
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Matches 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC64628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
                                                                                                    WO200060102-A2
                                                                                                                                                                                                                                 05-APR-1999;
                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                   White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
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셤
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP1/7TAP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and CE DIRECTARCAGE of the Production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. COPY of that gene; and (4) eliciting an immune response in an animal comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, Coli or Enterobacteriaceae host cell, from the host cell and inroducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous artigens are presented in high numbers (up to System the heterologous artigens are presented in high numbers (munogenicity and adhesion properties relevant for an efficient live vector is munogens, which may be important for directing an immune response in an animal processes of communication in the processes of against the inserted epitope, and hybrid finabriae are usually strong immunogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                 agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                     AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                      vaccine; immune response; immunogen.
                     AAB36346 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-012788BP
                                                                                                             (first entry)
                                                                                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC64622.
                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                    WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1999;
                                                                                                           26-FEB-2001
                                                                                                                                                                                                 Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000
                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                 AAB36346;
AAB36346
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77.8%; Score 604; DB 3; Length 151; 80.8%; Pred. No. 5.9e-51; Live 6; Mismatches 23; Indels Query Match
Best Local Similarity 80.8
Matches 122; Conservative

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Gaps

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SERIT/TAFF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. Comprising separating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the coll sequence host cell, from the host cell and introducing the copy setul for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/Cell), the hybrid finbrian protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein possesses both the immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The presente sequence is given in SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNÅTIDQWNAKNSDITVGQYGG 120 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. 61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen. AgfA::PT3#2 amino acid sequence SEQ ID NO:14. NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 ||||||| | NNAALVNYDQLVTRVVTHEMAHANNATANQY 151 Kay WW; Disclosure; Page 136; 139pp; English. AA Collison SK, AAB36347 standard; protein; 151 05-APR-2000; 2000WO-CA000356. 99US-0127888P 26-FEB-2001 (first entry) Salmonella enteritidis. Escherichia coli. (UYVI-) UNIV VICTORIA. White AP, Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64623. WO200060102-A2. 05-APR-1999; 12-OCT-2000 Synthetic. AAB36347; 61 121 121 RESULT 10 g g ò

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Best Local S
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                                                                     Gaps
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                                               Length 151,
                                                                     Indels
                                             Score 602; DB 3;
Pred. No. 9.3e-51;
                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
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 of the present invention
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                                                                      5; Mismatches
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Synthetic.
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                         Sequence 151 AA;
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                                                                      Matches 123;
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                                                Query Match
Best Local
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine; the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.4%; Score 601; DB 3;
81.5%; Pred. No. 1.2e-50;
live 4; Mismatches 24;
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Matches 123; Conservative
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N-PSDB; AAC64624.

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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologue species, replacing the chromosome of the homologue species, replacing the native comprising separating an amino acid polymer comprising recombinant gale comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment of segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequence cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein mumbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the vaccine, the carrier fimbrial subunit protein possesses both the carrier fimbrial subunit protein are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and incompany contribution of the present invention
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Pred. No. 1.5e-50;
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81.5%;
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Best Local Similarity 81.5'
Matches 123, Conservative
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Synthetic.
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WPI; 2000-672631/65.

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a forzign DNA segment of the gene has been replaced by a segment of a forzign DNA sequence which encodes a forzign epitope or antigen. Also described are:

(I) use of thin aggregative finbriae (SEP1/7AF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Encoderationed for the production of fimbriae comprising recombinant of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of copy of that gene; and (4) eliciting an immune response in an animal. Copy of that gene; and (4) eliciting an immune response in an animal, or protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown and grown a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 567; DB 3; Length 15:
Pred. No. 2.4e-47;
5; Mismatches 24; Indels
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                                                                                                                                             Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36343 standard; protein; 151 AA
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Best Local Similarity 80.8%;
Matches 122; Conservative
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Best Local Similarity
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AAB36343
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Plasma protein; immune response; antibacterial; vaccine; gene therapy

Escherichia coli.

WO2003064446-A2

07-AUG-2003

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                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and Enterchacteriacae for the production of fimbriae comprising recombinant of Enterchacteriaes and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologue species; (3) directing recombination of a recombinant gene back into the chromosome of the homologue species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant for an efficient live vaccine, the carrier fimbrial subunit protein sare usually strong immunogens, which may be important for directing an immune response in against the innested epitope, and hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response in expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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; Pred. No. 7.5e-43;
17; Mismatches 29.
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                                                                                                Kay WW;
                                                                                                                                                                                                                                              Disclosure; Page 135; 139pp; English
                                                                                                Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.1%;
   05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105; Conservative
                                                               (UYVI-) UNIV VICTORIA
                                                                                                White AP, Doran JL,
                                                                                                                                 2000-672631/65.
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                                                                                                                                               N-PSDB; AAC64619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
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The invention relates to an isolated peptide capable of binding a mammal selected from sequences shown in ABRR2642. ABRR2648-49. The peptide or antibody is useful for treating a hedicamal infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigalla infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli

Sequence 151 AA;

15 kDa protein

New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.

Disclosure; Page 41-42; 42pp; English.

Herwald H;

Wikstroem M,

Olsen A,

Bjoerck L,

WPI; 2003-646136/61. N-PSDB; ACF36153.

30-JAN-2003; 2003WO-EP000943.

31-JAN-2002; 2002GB-00002275 (HANS-) HANSA MEDICAL RES AB

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61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                             1 MKLLKVEAIAAIVFSGSALAGVVPQYGGGGHGGGGNNSGPNSELNIYQYGGGNSALAD
                                       Gaps
                                       ..
   Length 151;
                                     Indels
; Score 516; DB 7; L;
; Pred. No. 2.3e-42;
17; Mismatches 30;
                                                                                                                                                                                                                  151
                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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   66.5%;
                                       Matches 104; Conservative
                                                                                                                                                                                                                                                                                                          Search completed: August
       Query Match
Best Local Similarity
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E. coli CsgA subunit 15 kDa protein

04-DEC-2003

ABR82651;

ABR82651 ID ABR XX AC ABR XX DT 04-XX XX

ABR82651 standard; protein; 151 AA

RESULT 15

(0108N) YUD18 8604 8141

Sequence

sequence 32, Appl sequence 8, Appli sequence 8, Appli sequence 8, Appli sequence 9, Appli sequence 10, Appli sequence 2, Appli sequence 2, Appli sequence 3, Appli sequence 3, Appli sequence 3, Appli sequence 26, Appli sequence 13, Appli sequence 13, Appli sequence 13, Appli sequence 13, Appli sequence 13, Appli sequence 14, Appli sequence 14, Appli sequence 14, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 13, Appli sequence 4, Appli sequence 4, Appli

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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 59, Application US/08233788A
| Sequence 59, Application US/08233788A
| Patent No. 5635617
| GENERAL INFORMATION:
| APPLICANT: Boran, James L. |
| APPLICANT: Asy, William W. |
| APPLICANT: Collinson, Karen S. |
| APPLICANT: Clouthier, Sharon C. |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61 |
| CORRESPONDENCE ADDRESS: 61 |
| CORRESPONDENCE ADDRESS: 62 |
| ADDRESSE: Seed and Berry |
| STREET: Seattle |
| STREET: Seattle |
| STREET: Washington |
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STATE: WASHINGTON

ZIP: 98104-7092

COMPUTER READABLE FORM:
MINDIUM TYPE: FIDEPPY disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

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COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC CAPP. 1994

CLASSIFTON NUMBER: 35,570

REGISTATION NUMBER: 35,570

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REGISTATION NUMBER: 35,570

TELEPHONE: (206) 682-4930

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TELEPHONE: (206) 682-6031

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US-09-540-236-3401
US-09-134-000C-5130
US-09-125-619-32
US-08-737-716-2
US-09-196-387-8
US-09-841-837-8
US-09-336-447A-9
US-09-336-447A-9
US-09-196-387-10
US-09-196-387-10
US-09-196-387-10
US-09-196-387-10
US-09-196-387-2
US-09-841-835-2
US-09-841-835-2
US-09-841-835-2
US-09-841-835-2
US-09-972-115A-8
US-09-352-6848-39
US-09-352-6914A-13
US-09-336-447A-13
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amino acid
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Best Local Similarity
Matches 136; Conservat
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US-08-233-788A-59
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Sequence 131,
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776
1 MKLLKVAAFAAIVVSGSALA........DSSVMVRQVGFGNNATANQY 151
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2: /cgm2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgm2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgm2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgm2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgm2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-844-57

US-08-864-038A-3

US-09-36-447A-5

US-09-495-880A-42

US-09-58-412C-337

US-09-56-412C-337

US-09-556-877-180

US-09-556-877-180

US-09-559-410-180

US-09-489-039A-7849

US-09-388-352-4764

US-09-252-991A-24717

US-09-252-991A-2658

US-09-252-991A-30710

US-09-252-991A-30710

US-09-252-991A-30710

US-09-252-991A-30710

US-09-252-991A-30710

US-09-252-991A-30710

US-09-252-991A-30710

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US-09-252-991A-30710

US-09-252-991A-30710

US-09-260-280

US-09-361-294

US-09-361-280

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US-09-361-387-312-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB seq
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Gaps

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ORGANISM:
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Matches
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                                         61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                            61 SDARKSETTITQSGYGNGADVQQADNSTIELTQNGFRNNATIDQWNARNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Ray, William W.
APPLICANT: Collinano, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                               121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                        121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
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STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                            Sequence 57, Application US/08233788A
Patent No. 5635617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/ACATION: 135.70

NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REPERRORY/DOCKET NUMBER: 92004
TELECOMPUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEX: 3723936 SEEDANBERX
INFORMATION FOR SEQ ID NO: 57:
SEQUIENCE CHARACTERISTICS:
LENGTH: 120 amino acids
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amino acid
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Best Local Similarity 87.5
Matches 98; Conservative
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Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:

RESULT 3 US-08-864-038A-3

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KUNIO NAKASHIMA et al. FENTIDE GENE CDNA, VECTOR FENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR FENTION: CONTÂLNING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID FENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING TENTION: SAID POLYPEPTIDE AND ANTIBODY TENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GGGAGALA---- 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible OPERATING SYSTEM: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 LLKSSASASASASASAG----GGGGGGNGGGNGGGG-
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IDENTIFICATION METHOD: E (by experiment)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-7uly-1996
ATTOMNY AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
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APPLICANT: HANSEN, ERIC J.
APPLICANT: ARBI, CRISTOPH
APPLICANT: COPE, LESTIE D.
APPLICANT: MACIVER, ISOBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NIMBER: F-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 738
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Isshinden
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COUNTR: JAPAN
ZIP: 514-01
MpHTM: -
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ADDRESSEE: 812-5 Hir
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                                                                   TITLE OF INVENTION: NO TITLE OF INVENTION: OF TITLE OF INVENTION: STITLE OF INVENTION: STITLE OF INVENTION: NOWHER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Isshind
CITY: Tsu-city
STATE: Mie-pref
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58 ALQSDARKSETTIT---QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LKVAAPPAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 LKAQASAG---NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 317, Application US/09598419

Patent No. 656886

GENERAL INPORMATION:
APPLICANT; Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46966
CURRENT APPLICATION NUMBER: US/09/598,415
CURRENT FILING DATE: 2000-06-20
NUMBER OF SIEGO ID NOS: 357
SOFTWARE: FFREESO ID NOS: 357
SOFTWARE: FREESO ID NOS: 357
                                                                                                                     US-09-620-412C-337

Sequence 337, Application US/09620412C

Sequence 337, Application US/09620412C

Sequence 337, Application US/09620412C

GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITION OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FRASESQ for Mindows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 585;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.1%; Score 86.5; DE ilarity 31.6%; Pred. No. 2.2; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.1%; Score 86.5; Di 31.6%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 VGQ-YGGNNAALVNQT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 GGGIYGEDNITLSNLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.6%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-620-412C-337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-598-419-337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-598-419-337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM:
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US-09-495-880A-42
US-09-495-880A-42

Sequence 42, Application US/09495880A

Parent No. 666150

APPLICANT: NUDERT, FRITZ

APPLICANT: RUDERT, FRITZ

APPLICANT: LIAG, VIC

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIUM

TITLE OF INVENTION: NUMBER: US/09/495,880A

CURRENT APPLICATION NUMBER: US/09/495,880A

CURRENT PILING DATE: 1998-004

PRIOR APPLICATION NUMBER: BP 97 11 3319.4

PRIOR PILING DATE: 1997-08-01

NUMBER OF SEQ ID NOS: 50

SOFTWARE: PARENTIN VOEL: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-peptide3-OTHER INFORMATION: gene IIIs encoded by phage vector fpep3_1B-IR3seq (circular)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDTN------DANGTYSTIGGGYYSRA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 -GNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG---GNNAALV---N 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 IGDSSTIGGG--YYNQATGEKSTVAGGRNNQATGNNSTVAGGSYNQATGNNSTVAGGSHN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 YQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VVPQWGGGGNH-NGGGNSSGPDSTLSI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KTAIAIAVALAGFATVAQADYKDVDCIVYHAHYLVAKCGGGGSEFNAGGGSGG----- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKNSDI-----TVGQYG-----GNNAALVNQTA-----SDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                           28 GGGNHN-----GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY---
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: 1959A1 AND USPA2 ANTIGENS OF MORAXELLA CATARHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 892;
                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 87; DB 4
26.8%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 OTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 OATGEGSF---AAGVENKANAN 218
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                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.8%
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Conservative
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Matches 43; Conserv
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US-09-495-880A-42
                                                                                                                                                                                                                                                                                  ; ORGANISM: MO.
US-09-336-447A-5
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58 ALOSDARKSETTIT---OSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114 258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQ 312 LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL 57 11. ALQSDAKGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDGDNS 167

В

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parent No. 6610836
GENRAL INFORMATION:
Patent No. 6610836
GENRAL INFORMATION:
Patent No. 6610836
GENRAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 100-01-27
PRIOR APPLICATION NUMBER: US 60/117,747.
PRIOR APPLICATION SEQ. 14342
SEQ. ID NO 7849
FERMANER OF SEQ. ID NOS: 14342
     440 GLYTDKNLSITNITGIIEIANNKATDVGGGA----YVKGTLTCENSHRLQFLKNSSDKQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ALQSDARKSETTIT---QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | | | : | | | | 440 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 GGLDRNGANANGOTDTFGIYAFDTLTLTERIEINGGLRLDNYHTKYDSATACGGSGRGAI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 VGQGADNYDQLVTRVVTHEMAHADQWNA-----KNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 IKAQASAG----NADAWASSSPQSGSGATIVSDSGDSSSGSDSDISEIVPVIAKGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Gaps
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                                                                                                                                                                                                                 US-09-598-419-180
; Sequence 180, Application US/09598419
; Patent No. 6562856
; Batent No. 6562866
; GENNEAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIACNOSIS OF CHLAMYDIAL INFECTION
; TITLE OF INVENTION: DIACNOSIS OF CHLAMYDIAL INFECTION
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FRSESQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%; Score 86.5; DB 4; Length 1752; 31.6%; Pred. No. 9; ive 12; Mismatches 58; Indels 23
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11.0%; Score 85.5; DB 4; Length 5.
Best Local Similarity 23.2%; Pred. No. 2.8;
Matches 32; Conservative 17; Mismatches 68; Indels
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7849
                                                        115 VGQ-YGGNNAALVNOT 129
                                                                                                                495 GGGIYGEDNITLSNLT 510
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Best Local Similarity 31.6%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Chlamydia
US-09-598-419-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-489-039A-7849
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LENGTH: 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 ALQSDARKSETTIT---QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    388 LKAQASAG---NADAWASSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG---- 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Bratia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Skeik, Yasi
APPLICANT: Skeik, Yasi
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TILLE OF INVENTION: DAGGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 180, Application US/09620412C

Sequence 180, Application US/09620412C

Patent No. 6448234

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

CURRENT APPLICATION UNBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 180

LENTH: 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%; Score 86.5; DB 4; Length 1752; 31.6%; Pred. No. 9; ive 12; Mismatches 58; Indels 23.
                                                                                                                                                                  Sequence 180, Application US/09556877
Patent No. 6432916
313 GGGIYGEDNITLSNLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 VGQ-YGGNNAALVNOT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.64
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 31.6
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-180
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; ORGANISM: Chlamydia
US-09-620-412C-180
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-09-556-877-180
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LENGTH: 1752
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RESULT 14

US-09-255-991A-30710

Sequence 30710, Application US/09252991A

RECURSAL INFORMATION:
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. Rubenfield et al.
APPLICANT MAIC J. RUBENGE LOS J. SELVEN APPLICANTON NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEC ID NOS: 33142

LENGTH: 812

LENGTH: 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26658, Application US/09252991A

Sequence 26658, Application US/09252991A

Sequence 26658, Application US/09252991A

Sequence 26658, Application US/09252991A

Patent No. 6551795

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: MUMBER: US/09/252,991A

CURRENT RILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR SEQ ID NOS: 33142

SEQ ID NO 26688

LENGTH: 1034
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                                    357 AARAPMPAITEPGRSGTGAPDPRRTAGTGEEGGELVVKDFAHPAYRLVTGQEIEGDSWNG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VSGSALAGVVPQWGGGGNHNG-----GGNSSGPDSTLSIYQYGS-ANAALALQSDAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 -QWNAKNSDITVGQYG--GN------NA-LVNQTASDSSVMVRQVGF 142
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                                                                                                                            -----AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.3%; Score 80; DB 4; Length 812;
Best Local Similarity 26.7%; Pred. No. 15;
Matches 31; Conservative 10; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30710
62 DARKSETTITOSG-YGNGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 47; Conserv
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US-09-252-991A-26658
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US-00-252-991A-24717

US-00-252-991A-24717

Sequence 24777, Application US/09252991A

Sequence 24777, Application US/09252991A

Sequence 24777, Application US/09252991A

Sequence 24777, Application US/09252991A

Sequence 24777, Application US/09252991A

TITLE OF INVENTION: APPLICATION: APPLICATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: APPLICATION: APPLICATION UMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQUENCE: APPLICATION UMBER: US 60/094,190

SEQUENCE: APPLICATION NUMBER: US 60/094,190

SEQUENCE: APPLICATION NUMBER: US 60/094,190
                                                                                                                                                                                                                                                    Sequence 4764, Application US/09328352
Sequence 4764, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BADMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 ALALQSDARKSETTI-----TQSGYG-----NGADVGQGADNYDQLVTRVVTHEM 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 AGNGIA-----SGNGEHNYGIGNGNGDDVDITAPITGVLNISGNSFTLIGNSSSSSVNT 353
     319 ACPPGQSTGSPVTTVDTAKSGNLVNWKAGALYRLJEQGNVYV-----NYALSQQPPGGS 372
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Best Local Similarity 25.6%; Pred. No. 7;
Matches 43; Conservative 20; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
10.6%; Score 82; DB 4; Length 975;
Best Local Similarity 24.1%; Pred. No. 12;
Matches 38; Conservative 15; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 --IGNGNGDDVDITSPITGIFNFSGNSFSLIGNSSSS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AHADQWNAKNSDIT----VGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDSTLSIYQYG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4764
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US-09-252-991A-24717
                                                                                                                                       373 SFALAASGSGNSANRTDF 390
                                                                                        134 SVMVRQVGFGNNATANQY 151
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Seguence 146, App	Sequence 147343,	Sequence 56041, A	Sequence 275468,	Sequence 57763, A	Seguence 1130, Ap	Seguence 1130, Ap	Seguence 445, App	Sequence 594, App	Sequence 45, Appl
ID	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369~493-20638	US-09-793-306-146	US-10-437-963-147343	US-10-425-114-56041	US-10-424-599-275468	US-10-425-114-57763	US-09-880-748-1130	US-10-293-418-1130	US-09-841-132-445	US-09-841-132-594	US-10-467-534-45
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% Query Match Length DB	151	151	131	131	445	597	271	369	486	507	251	251	1751	1751	1751
% Query Match	66.8	8.99	56.7	56.7	12.2	12.2	12.1	12.0	12.0	12.0	11.9	11.9	11.7	11.7	11.7
Score	518	518	440	440	95	9	94	93	93	93	92.5	92.5	91	91	16
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US-09-880-748-112	418-11	US-10-437-963-14	US-10-437-963-14	US-10-425-114-67	US-10-437-963-15	US-10-437-963-162	US-10-424-599-20	S US-10-369-493-20	6 US-10-437-963-18	0 US-09-952-267-5	6 US-10-437-963-10	2 US-10-634-862-42	US-09-841-132-337	US-09-841-132-18	6 US-10-437-963-1406	2 US-10-425-114-	2 US-10-282-122A-6779	6 US-10-437-963-1222	2 US-10-647-057-4	0 US-09-820-843A-2	6 US-10-437-963-18641	6 US-10-437-963-1707	6 US-10-437-963-16895	2 US-10-425-114-6152	0 US-09-880-748-209	2 US-10-293-418-209	0 US-09-880-748-115	-10-293-418-1	6 US-10-408-765A-99
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ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTURION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1991-11-06
PRIOR PELING DATE: 1991-11-06
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
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66.8%; Score 518; DB 12; Length 151;
Best Local Similarity 68.9%; Pred. No. 1.2e-44;
Matches 104; Conservative 18; Mismatches 29; Indels C
                     Sequence 4; Application US/09741873B; Publication No. US20020081722A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Escherichia coli
US-09-741-873B-4
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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3 10:54:39 2004

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DB 12; Length 131;
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1990-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
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Publication No. US20040096965A9
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.7%;
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Publication No. US20040096965A9

GENERAL INFORMATION: Staffan

APPLICANT: Obtan, Arne

APPLICANT: Obtan, Arne

APPLICANT: Olsen, Arne

TILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TILLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation

TILLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation

TILLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation

CURRENT APPLICATION NUMBER: US 09/741,873B

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR PILING DATE: 1997-11-26

PRIOR PILING DATE: 1997-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1994-01-28

PRIOR APPLICATION NUMBER: US 08/18,519

PRIOR PILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

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PRIOR FILING DATE: 1994-10-05
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Publication No. US20020081722A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Elbronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION UNMER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
                                                                                                                               61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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66.8%; Score 518; DB 12;
Best Local Similarity 68.9%; Pred. No. 1.2e-44;
Matches 104; Conservative 18; Mismatches 29;
                                                                                                                                                                                                             121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                     121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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PFPLICANT: Olsen, Arne
TILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPREBRED: 012899-064
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT PILING DATE: 2003-04-04
FRIOR APPLICATION NUMBER: US 8801723-1
FRIOR APPLICATION NUMBER: US 8801723-1
FRIOR APPLICATION NUMBER: US 08/978,878
FRIOR FILING DATE: 1998-05-04
FRIOR FILING DATE: 1998-05-04
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1994-01-28
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56.7%; Score 440; DB 12;
Best Local Similarity 65.6%; Pred. No. 8.3e-37;
Matches 86; Conservative 17; Mismatches 28;

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APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147343
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 FGNSGNNNIGFFNSG-NNNVGFFNSGNNN------FGFGNAGDINTGF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 GNAGDINIGFGNAGFFNMGIGNAGNEDMGYGNGGSFNYGYGN--AGNQS-----VGFGNA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA 85
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                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: mTTC#3-His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.1%; Score 94; DB 16; Length 271; 26.2%; Pred. No. 0.28;
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US-10-437-963-147343
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TITLE OF INVENTION: Of Tuberculosis FILE REFERENCE: 014058-008740US CURRENT APPLICATION NUMBER: US/09/793,306 CURRENT FILING DATE: 2001-02-25 PRIOR APPLICATION NUMBER: US 60/185,037 PRIOR FILING DATE: 2000-02-25 PRIOR FILING DATE: 2000-02-25 PRIOR FILING DATE: 2000-08-08 ON NUMBER OF SEQ ID NOS: 164 SOFTWARE: Percentin Ver. 2.1 SOFTWARE: Percentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 147343, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbaruk, Brad
APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 27,4% Matches 34; Conservative
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Best Local S:
Matches 37,
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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Sequence 20638, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Gac, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICANTION NUMBER: US/10/369,493

CURRENT APPLICANTION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20638
                                                                                                                                                                                                 81 VGGGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                              61 VGQGSDDSSIDLIQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 GKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTNDPGVFNKITQDSSSNGSKV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 TITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQW-NAKNSDITVGQ---YGGN-NA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 SVIQDGKNNVFSIKQGNTGNSTSVNQIGEWGMAYVRQGIGAAETDASTGNALPTGGNYNV 208
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APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Coitxa Oriporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
                                                                                                                             21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 GNHNGGGNSS-----LALQSDATLSIYQYGSANAA------LALQSDARKSET
                                          Gaps
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                                       28; Indels
              Pred. No. 8.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 ASITQNSAGLNYAVAVQGGGNS 230
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US-09-793-306-146
Sequence 146, Application US/09793306
Patent No. US20020098200A1
PATENT NO. USANATION:
APPLICANT: Campos-Neto, Antonio
           65.6%;
     Best Local Similarity 65.69 Matches 86; Conservative
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Best Local Similarity 24.6
Matches 35; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 57763
LENGTH: 507
    9
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                                                                                                                       180 GFGGGGNVSRSKSTQD-MYTR----AELEASAANKEDFFARKRAENESRPEGLPPSQG 232
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                                                                          14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                  74 GYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDS
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20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Gaps
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PPS23 Haribodies that Immunospecifically Bind BLyS FILE REFERENCE: PPS23 Haribodies (1809/880,748)
CURRENT APPLICATION NUMBER: 00/01-05-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.0%; Score 93; DB 12; Length 507; Best Local Similarity 26.3%; Pred. No. 0.76; Matches 36; Conservative 18; Mismatches 63; Indels 3
    Indels
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    63;
    Mismatches
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; Sequence 57763, Application US/10425114
; Publication No. US20040034888A1
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    18;
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        Conservative
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US-09-880-748-1130
36;
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    Matches
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: Encoa Thomas J
APPLICANT: Enco Yinua
APPLICANT: Cao Yongweil
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 39 21 (5323)B
CURRENT APPLICANTON NOWBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 275468
LENGTH: 486
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CURRENT APPLICATION NUMBER: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NOS: 73128
LENGTH: 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.0%; Score 93; DB 12; Length 369; larity 26.3%; Pred. No. 0.51; Conservative 18; Mismatches 63; Indels
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US-10-424-599-275468
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; OTHER INFORMATION: Clone ID: 701205720_FLI.pep
US-10-425-114-56041
                                                                                                                                                                                                                                                                                                     Sequence 56041, Application US/10425114
Publication No. US20040034888A1
BEDBEAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                              :: |: | : | :| :| 132
113 AARKVKYV-YANDLNPTAVEY 132
                                         SSVMVRQVGFGN--NATANQY
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26.3%;
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ORGANISM: Glycine max
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Best Local Similarity
Matches 36; Conserv
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Best Local Similarity
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US-10-424-599-275468
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                                     133
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129 T 129
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LENGTH: 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 ATTGALDMWGKGTLVTVSSGGGSGGGGGGGGGG------GSAQAVLTQPSSASGTPG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TITITQSGYGNGADVGQGADN-YDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Publication No. US2030323996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF533P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-02-15

PRIOR FILING DATE: 2001-03-24

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

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                                                                                                                                                                                                                                                                                                             Length 251;
                                                                                                                                                                                                                                                                                                                                                          51; Indels
                                                                                                                                                                                                                                                                                                       ; Score 92.5; DB 10;
; Pred. No. 0.36;
14; Mismatches 51;
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR PELING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
LENGTH: 251
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.7%;
Matches 33; Conservative 1.
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Best Local Similarity 27.78
Matches 33; Conservative
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ORGANISM: Homo sapiens
US-10-293-418-1130
                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-880-748-1130
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US-10-293-418-1130
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RESULT 13 US-09-841-132-445

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 NADAWASSSPOSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNIIG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
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APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: COMPOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: 110121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT APPLICATION NOWBER: US/09/841,132
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
                                                                          APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%; Score 91; DB 9; Length 1751; 33.1%; Pred. No. 5.7; tive 10; Mismatches 59; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 33.1%; Pred. No. 5.7;
Matches 40; Conservative 10; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Chlamydia trachomatis serovar D
Sequence 445, Application US/09841132 Patent No.: US20020061848A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 594, Application US/09841132; Patent No. US20220061848A1; GENERAL INFORMATION: APPLICANT: Bhatia, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: C. Trachomatis D serovar
US-09-841-132-594
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us-09-543-407-22.rapb

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RESULT 15

(Sequence 45, Application US/10467534)
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Search completed: August 2, 2004, 15:36:12 Job time : 37.8 secs

Sequence 30, 7 Sequence 20, 7 Sequence 24, 7 Sequence 57,

Sequence Sequence

Sequence Sequence

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Tue Aug
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Scoring table:

Minimum DB Maximum DB

Database :

Perfect score:

Sequence:

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OM protein

Run on:

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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASSESEQ for Windows Version 4.0
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:, OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
9 US-09-543-407-28

9 US-09-543-407-28

9 US-09-543-407-28

9 US-09-543-407-29

9 US-09-543-407-20

9 US-09-543-407-12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2309
2309
2309
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252
    US-09-543-407-22
                                                                                                                                                                                                                                                                                                                      2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                US-09-543-407-22
776
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                            6019581
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                            6019581 seqs, 976053577 residues
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                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Score

No. Result

Sequence 20216, A Sequence 24, Appl Sequence 20638, A Sequence 20638, A Sequence 146, App Sequence 146, App Sequence 147343,

Sequence 8854, Ap

Sequence 21, Appl Sequence 688, App Sequence 25488, A Sequence 25488, A Sequence 25607, A

Sequence 16, Appliance 16, Appliance 1, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appl

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Indels

Length 151;

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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                         87.9%; Score 682; DB 19;
90.7%; Pred. No. 1.5e-64;
live 2; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
                                                                                                                                                 ) ORGANISM: Salmonella enteritidis
US-09-543-407-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEBDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 amino acids
                                                                                                                                                                                                                                                   Best Local Similarity 90.7 Matches 137; Conservative
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US-08-233-642A-57
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                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQMNAKNSDITVGQYGG 120
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                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALO 60
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                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: CAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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Sequence 5, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: AAVINIAN W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REPERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407
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                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
91.8%; Score 712; DB 19; Length 151;
Best Local Similarity 91.1%; Pred. No. 9.1e-68;
Matches 144; Conservative 0; Mismatches 0; Indels 14
                                                                                                     Indels
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                                                   100.0%; Score 776; DB 19;
100.0%; Pred. No. 1.2e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-28
Sequence 28, Application US/09543407
; GENERAL INFORMATION:
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                                                                           Best Local Similarity 100. Matches 151; Conservative
     US-09-543-407-22
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LENGTH: 151
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                                                   Query Match
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Sequence 57, Application US/08233642A

GENERAL INFORMATION:

APPLICANT: Ray, William W.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Dann, James L.

TITLE OF INVENTION: BASED VACCINES

NUMBER OF SEQUENCES: S8

NUMBER OF SEQUENCES: -

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: Saedtle

STATE: Washington

COUNTRY: U.S.A.

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98104-7092

COMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: IBM PC compatible

OMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/233,642A
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Best Local Similarity 90.1%; Pred. No. 5.2e-64;
Matches 136; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPELICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATCOREY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UNMBER: 35,570
REPERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION: INFORMATION:
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-----YDQLVTRVVTHEMAHADQ 105
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9
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Sequence 30, Application US/09543407

SEQUENCE 30, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

FILE REFERENCE: 92043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                      1 MKLLKVAAFFAAIVVSGSALAGVVPQWGGGGHNGGGNSGPDSTLSIYQYGSANAALALQ
                                                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.405
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 20
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Pred. No. 7.4e-62;
0; Mismatches 0; Indels 30
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APPLICANT: White, Aaron P.
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Best Local Similarity 81.9%;
Matches 136; Conservative C
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ORGANISM: Artificial Sequence
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US-09-543-407-20
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US-09-543-407-30
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61 SDARKSETTITQSGYGNGADVGGGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDARK------YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR 98
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                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE SEQUENCES
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                                                                                                                                                                                                                                           44;
CRGALINE Artificial Sequence FEATURE:
CTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
THER INFORMATION: sequence containing the replacement fragment
CTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 ----DOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                         0; Indels
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78.5%; Score 609; DB 19;
Best Local Similarity 73.6%; Pred. No. 1.1e-56;
Matches 128; Conservative 0; Mismatches 0;
                                                                                                                                                                                        Ouery Match
Best Local Similarity 74.6%; Pred. No. 8.9e-58;
Matches 129; Conservative 0; Mismatches 0;
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APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT WILLIAM W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEN
TITLE OF INVENTION: PRESENTATION OF HETEROLG
FILE REPREMENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
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US-08-243-407-12
Sequence 12, Application US/09543407
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-543-407-24
; Sequence 24, Application US/09543407
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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DB 19; Length 151;

77.3%; Score 600;

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                APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTERO for Mindows Version 4.0
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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 14
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment , OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-12
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81.5%; Pred. No. 6e-56;
tive 5; Mismatches 23; Indels (
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Collinson, S. Karen
                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 123; Conserv
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US-09-543-407-14
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61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNARONSDITVGQYGG 120
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| APPLICANT: White, Aaron P. |
| APPLICANT: Doran, James L. |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Kay, William W. |
| TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR |
| TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| FILE REFERENCE: 920043.406 |
| CURRENT APPLICATION NUMBER: US/09/543,407 |
| CURRENT APPLICATION NUMBER: US/09/543,407 |
| NUMBER OF SEQ ID NOS: 59 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 26 |
| LENGTH: 151 |
| TYPE: PRT |
| TYPE: PRT |
| CRAMISM: Artificial Sequence |
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 9200433.40
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 151
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Best Local Similarity 81.5%; Pred. No. 7.7e-56;
Matches 123; Conservative 4; Mismatches 24;
                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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121 NNAALVNOTASDSSVMVRQVGFGNNATANQY
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-543-407-26
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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69.5%; Pred. No. 3e-47;
tive 17; Mismatches 29;
                                                                                                          Query Match
73.1%; Score 567; DB 19;
Best Local Similarity 80.8%; Pred. No. 3.4e-52;
Matches 122; Conservative 5; Mismatches 24;
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                                                             ; OTHER INFORM
US-09-543-407-16
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Matches 105;
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US-08-978-878-4
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US-09-543-407-7
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                      Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SSOTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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                    Indels
Pred. No. 9.8e-56;
5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 595; DB 19;
Pred. No. 2.8e-55;
2; Mismatches 12;
                                                                                                                                                                                                              NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
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US-09-43-407-16
US-09-43-40-16;
Sequence 16, Application US/09543407;
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
                                                                                                                                                                                                                                                                                                                             US-09-543-407-31; Sequence 31, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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Best Local Similarity 81.5%;
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 89.3%;
Matches 117; Conservative
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                                                                                                                                                                                                                                         61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION UNMER: SE 8801723-1
EARLIER APPLICATION UNMER: SE 8801723-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Doran James L.
APPLICANT:
APPLICANT:
Collinson, S. Karen
APPLICANT:
TITLE OF INVENTION: PRESENTAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASESQ for Mindows Version 4.0
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Length 151;
                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1981-10.05
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-10-05
EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER APPLICATION NUMBER: US 08/495,959
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EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER APPLICATION NUMBER: US 08/495,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; ORGANISM: Escherichia coli
US-08-978-878-4
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Search completed: August 2, 2004, 15:26:45 Job time : 168.9 secs

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Query Match
Best Local Simil
Matches 104;
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Sequence 2, Appli
Sequence 7906, Ap
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Sequence 445, App
Sequence 694, App
Sequence 670, App
Sequence 17306, App
Sequence 254240, Sequence 5, Appli
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                                                             2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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                                                                                                      US-09-543-407-22
776
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
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Sequence
Sequence
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| cgm2_6/ptodata/2/paa/VCT_NEW_COMB.pep:*
| cgm2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
| cgm2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
| cgm2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
| cgm2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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| cgm2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
| cgm2_6/ptodata/2/paa/US00_NEW_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-741-873C-2
US-00-741-873C-2
US-60-565-632-7906
US-60-565-632-7906
US-10-498-327-115
US-10-872-155-594
PCT-US-08-796-115-25420
US-09-248-796A-17306
US-10-872-155-594
PCT-US-08-155-115-33419
US-10-872-155-180
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US-10-425-115-343835
US-10-425-115-343835
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US-10-425-115-343835
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US-10-425-115-343835
US-00-565-632-7907
US-60-565-632-7907
US-60-561-351-11388
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                601315 seqs, 104695340 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Perfect score:
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                                          OM protein -
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Maximum DB
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                                                                                                                              Sequence:
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No.
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ALIGNMENTS

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RESULT 1
US-09-741-873C-4

i Sequence 4, Application US/09741873C

sequence 4, Application US/09741873C

sequence 4, Application US/09741873C

sequence 4, Application US/09741873C

APPLICANT: Olsem, Arie

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873C

CURRENT APPLICATION NUMBER: US 8801723-1

PRIOR APPLICATION NUMBER: US 08/378,878

PRIOR FILING DATE: 1997-11-26

PRIOR PLING DATE: 1998-05-04

PRIOR FILING DATE: 1998-05-04

PRIOR PLING DATE: 1991-11-06

PRIOR APPLICATION NUMBER: US 07/799,437

PRIOR APPLICATION NUMBER: US 07/799,437

PRIOR PLING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PARCETIN VERSION 3.0

SSTWARE: PARCETIN VERSION 3.0

SSTWARE: PARCETIN VERSION 3.0

SSTWARE: PARCETIN VERSION 3.0
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68.9%; Pred. No. 3.4e-37;
ive 18; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia coli
US-09-741-873C-4
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                          APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-084
CURRENT PFILIG DATE: 1920-012-22
CURRENT PFILIG DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SCOTUMARE PARCELLY VESION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VGQGSDDSSIDLIQRGFGNSATLDQWNGRONSEMTVKOFGGGNGAAVDOTASNSSVNVTOV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.7%; Score 440; DB 5; Length 131;
65.6%; Pred. No. 1.4e-30;
live 17; Mismatches 28; Indels
Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 65.64
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GFGNNATANOY 151
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Length 520;

DB 6;

12.6%; Score 97.5;

Query Match

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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
FILE REPERENCE: 38-21(53403) B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SEQ ID NO 7906
LENGTH: 941
                                                                                                                                                                         74 GYGNGADVG-----QGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                        ---AVNRVSSNIGAVAS 448
                                                                                                                      347 AGAGAAAAASAGAGAGGYGYGYGGGSS----ISYGATSSSATSSSTASSSRSGIVTSG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                         15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 GNHNGGG--NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG------YGNGADV
                          25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (810)..(810)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.9%; Score 92; DB 7; Length 841; Best Local Similarity 28.3%; Pred. No. 8.9; Matches 36; Conservative 16; Mismatches 59; Indels
                          62; Indels
Best Local Similarity 22.9%; Pred. No. 1.7; Matches 33; Conservative 24; Mismatches
                                                                                                                                                                                                                        403 GYGAGAAAGAGAAAAGAGSYSGSISKLSSAE--
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APPLICANT: Baum, James A
APPLICANT: Acvalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong;
APPLICANT: Nunyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
                                                                                                                                                                                                                                                                                                          449 GGASALPGVISNIFSGVSSSAGSY 472
                                                                                                                                                                                                                                                                          128 QTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                      US-60-565-632-7906

Sequence 7906, Application US/60565632
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Baum, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baum, James A
Kovalic, David K.
Larosa, Thomas J.
Lu, Maolong
Munyikwa, Tichifa R. I
Roberts, James K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Diabrotica virgifera
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APPLICANT:
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Matches
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394 NADAWASSSPOSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG 452
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                                                                     APPLICANT SKeiky, Yasir A.W.
APPLICANT SKeiky, Yasir A.W.
APPLICANT SKeiky, Yasir A.W.
APPLICANT SKeiky, Yasir A.W.
APPLICANT STORE PECED
TITLE OF INVENTION: CONFOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
CURRENT APPLICATION NUMBER: US/10/872,155
CURRENT FILING DATE: 2000-07-20
PRIOR PELING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 09/556,877
PRIOR APPLICATION NUMBER: 09/426,571
PRIOR PILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 09/426,571
PRIOR APPLICATION NUMBER: 09/426,571
PRIOR APPLICATION NUMBER: 09/426,571
PRIOR APPLICATION NUMBER: 09/426,571
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
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PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR PILING DATE: 1998-12-08
NUMBER OF SEQ ID NOS: 599
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APPLICANT Bhatia, Ajay
APPLICANT Bhatia, Ajay
APPLICANT Bhatia, Ajay
APPLICANT Bhatia, Ajay
APPLICANT Bhatia, Yasir A.W.
APPLICANT Bhatia, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLANYDIAL INFECTION
TITLE OF INVENTION: DIAGNOSIS OF CHLANYDIAL INFECTION
CURRENT APPLICATION NUMBER: US/10/872,155
PRIOR APPLICATION NUMBER: 09/620,412
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: 09/598,419
PRIOR APPLICATION NUMBER: 09/556,877
PRIOR APPLICATION NUMBER: 09/556,877
PRIOR APPLICATION NUMBER: 09/556,877
PRIOR APPLICATION NUMBER: 09/556,877
PRIOR PILING DATE: 2000-00-19
PRIOR PILING DATE: 1999-12-03
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llarity 33.1%; Pred. No. 25;
Conservative 10; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Chlamydia trachomatis serovar D
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GENERAL INFORMATION:
                       ; Sequence 445, Application US/10872155
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 40; Conserv
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US-10-872-155-594
JS-10-872-155-445
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LENGTH: 1751
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APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REPERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SEQ ID NO 7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 NADAWASSSPQSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 IIEIANNKATDVGGGA----YVKGTLTCENSHRLQFLKNSSDKQGGGIYGEDNITLSNL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       657 GNENGSAAENTGNADSQNDAGQ-GSANAA-----NADNNANTDAQNGADQGNENGSAAEI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 NGGADGQNE--NGAAASSGNADNQNNNNSNNDSGNNQNNGSNSVEENSKEDSGNESQEN 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 GQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 GNHNGGG--NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-----YGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

NAME/KEY: misc feature

LOCATION: (810)..(910)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-579-062-7906
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GENERAL INFORMATION:
APPLICANT: Grandi, Guido
APPLICANT: Ratti, Giuido
TITLE OF INVENTION: Immunisation Against Chlamydia Trachomatis
FILE REPERENCE: 002441.00085
CURRENT FILING DATE: 2004-06-10
PRIOR APPLICATION NUMBER: PCT/IB02/05761
PRIOR PILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 262
NUMBER OF SEQ ID NOS: 262
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.9%; Score 92; DB 7; Length 841; ilarity 28.3%; Pred. No. 8.9; Conservative 16; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 33.1<sup>3</sup>
Matches 40; Conservative
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Best Local Similarity
Matches 36; Conserv
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US-10-498-327-115
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LENGTH: 1751
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RESULT 10
10-09-248-96A-17306
Sequence 17306, Application US/09248796A
Sequence 17306, Application US/09248796A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR SEQ ID NOS: 28208
SEQ ID NO 17306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 254240, Application US/10425115
Sequence 254240, Application US/10425115
Sequence 254240, Application US/10425115
Sequence 254240, Application US/10425115
Sequence 254240, Application US/10425115
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Whuleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 254240
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                                                                                                                                                                                                                                                                                                    69 TITQSGYGNGA-----DVGQGADNYDQLVTRVVTHEMAHADQW---NAKNSD-- 112
                                                                                                                                                                                                                                                                                                                                                      368 SSGSTGGGNCAGVNVYPNWTARDWSGCAYNHANAGDQMVYQNSLYRANWYTNSVPGSDAS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 ELT-------NAGNIGLAKGTAPASISATYGESPSADYSKSGATGVVPATYLN 223
                                                                                                                                                                                             12 IVVSGSALAGVVPQWG---GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                            30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 89.5; DB 5; Length 388; 22.1%; Pred. No. 6;
                                                                                      Length 1010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 QLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTAS-----
                                                                                                                                           Indels
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           OTHER INFORMATION: Cellulose or protein binding domain
                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.5%; Score 89.5; DB 5; 1
Best Local Similarity 22.1%; Pred. No. 6;
Matches 33; Conservative 17; Mismatches 44;
                                                                                Query Match
11.6%; Score 90; DB 1;
Best Local Similarity 22.4%; Pred. No. 16;
Matches 32; Conservative 27; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 TSGAPTGSLNTAGVVGGAGFGDNSNTSSY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Candida albicans
US-09-248-796A-17306
                      PCT-US04-21492-402
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APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Hulliam, Derrick
TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN
TITLE OF INVENTION: THEM
TITLE OF INVENTION: E6462005540
CURRENT APPLICATION NUMBER: PCT/US04/21492
CURRENT FILING DATE: 2004-07-20
PRIOR FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 518
SOFTWARE: Patent In version 3.1
SEQ ID NO 402
LENGTH: 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 NADAWASSSPOSGSGATTVSNSGDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 --QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #53 IIEIANNKATDVGGGA----YVKGTLTCENSHRLQFLKNSSDKQGGGIYGEDNITLSNL 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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LOCATION: (39)...(300)
OTHER INFORMATION: Cellulase (glycosyl hydrolase
PRIOR APPLICATION NUMBER: 09/426,571
PRIOR FILING DATE: 1999-10-02
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR PLICATION NUMBER: 09/208,594
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR APPLICATION NUMBER: 09/208,277
PRIOR FILING DATE: 1998-12-08
NUMBER: OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 594
ILENGTH: 1751
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OTHER INFORMATION: Glycosyl hydrolases family 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: NAME/KEY: DOMAIN LOCATION: (393)...(428) OTHER INFORMATION: Carbohydrate binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 402, Application PC/TUS0421492 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: C. Trachomatis D serovar US-10-872-155-594
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.1%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (493)...(521)
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LOCATION: (1)...(30)
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FEATURE:
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NAME/KEY: DOMAIN
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PCT-US04-21492-402
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                     63 -- PYGAHASAGGGGAGGGASQN--GGSGYGSGSGSGSGSGSTYSQ------GGYYSGYG 110
                                                                                                                                                                                                                                                                                               47 IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQW 106
                                                                                                                                                                                                                                                     5 KLISLGLLVLIGIGLANAVRVARYSSADGTGTGEGQGGGYVNGGGSGSGSGGGGDSS-- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-09-952-267B-5
; Sequence 5, Application US/09952267B
; General INPORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABEL, CHRISTOPH
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: FISSE, MICHAEL J.
APPLICANT: FISSE, MICHAEL J.
APPLICANT: FISSE, MICHAEL J.
APPLICANT: FISSEN MICHAEL J.
TITLE OF INVENTION: USPAI AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPRESENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT FILING DATE: 1999-06-21
FRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOUTH NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 -GNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG---GNNAALV----N
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                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 193;
                                                                                                                                                                                                                                                                                                                                                                                107 NAKNSDITVGQYGGNNA-ALVNQTASDSSVMVRQVGFGNNAT-ANQY 151
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                                                                                                                                     Query Match 11.4%; Score 88.5; DB 6; Length 1
Best Local Similarity 26.3%; Pred. No. 3.3;
Matches 44; Conservative 22; Mismatches 62; Indels
                                                                          OTHER INFORMATION: Clone ID: MRT4577_163446C.1.pep
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GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABEL, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Moraxella catarrhalis
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Matches 38; Conservative
                                   ORGANISM: Zea mays
                                                                                    ; OTHER INFORMATION US-10-425-115-254240
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US-10-872-768-5
LENGTH: 193
TYPE: PRT
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Sequence 5) Application US/10872769

GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABEL GERIE D.
APPLICANT: FISCEL MICHAEL J.
APPLICANT: FISCE, MICHAEL J.
APPLICANT: FISCEL MICHAEL J.
APPLICANT: FREDRIBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF WORAXELLA CATARRHALIS
TITLE OF INVENTION NUMBER: US/10/872,769
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR PLING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 99

SOFTWARE: PATCHIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
APPLICANT: FISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/10/812,768
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN Ver. 2.1
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11.2%; Score 87; DB 6; Length 892;
Best Local Similarity 26.8%; Pred. No. 26;
Matches 38; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Length 892;
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26;
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Pred. No.
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US-10-872-768-5
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1 Similarity 26.8%;
38; Conservative 1
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RESULT 15

US-10-425-115-333419

i Sequence 333419, Application US/10425115

i Sequence 33419, Application US/10425115

i GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 333419

LENGTH: 125

TYPE: PRT

CRANISM: Zea mays

FEATURE:

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_67192C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | | | | | | | GYYGAHYGGG-----AAVAIQXHGYRKDVYGSETESEDDESDCEEAFSPRGGRMQGGVQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 TOSGYGNGADV - GOGADNYDQLVTRVVTHEM - AHADQWNAKNSDITVGQYGGNNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Gaps
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11.1%; Score 86.5; DB 6; Length 125;
Best Local Similarity 27.4%; Pred. No. 2.9;
Matches 32; Conservative 14; Mismatches 44; Indels 2'
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Search completed: August 2, 2004, 15:29:54 Job time : 18.8 secs

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August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Database :

SUMMARIES

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	Description	G	urlin	protei	curlin major subun	иď	cnjB protein - Tet	hypothetical glyci	hypothetical prote	probable PPE prote	probable PPE prote	hypothetical prote	14	hypothetical prote	probable PPE prote	ice nucleation pro	curlin nucleator p	minor curlin subun	curlin minor chain	ice nucleation act	ice nucleation pro	hypothetical prote	fimbrin protein ag	nucleation compone	probable PPE prote	ice nucleation pro	protein kinase sgg	hypothetical expor	hypothetical glyci	F3F19.21 protein -
	ID		AI0635	S70788		H85665	S42136	E95965	T26667	E70663	E70946	T21956	AD3143	H98144	F70825	S11672	S70787	C90806	G85665	JC2143	JQ0188	G71518	JC6040	AH0635	B70987	807053	835327	9601	940	C86266
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	Kesuit No.	 	7	m	4	ഗ	ω	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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A45621 B42049 844951	A11771 PL0221 S19916	S00275 C70830	A56038 S16356	F70675 D89723	T21998 A25547	B70663	AF2959	H98323
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45	n m		1341	101	23	hypothetical prote
					ALIGNMENTS	
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C,Date: 31-	Dèc-15	196 #sec	quence	re.	c-1996 #text_	change 08-Oct-1999
C, Accession	3000	39; PC	6015; } -bior	444	T Banger	3 3 3 4 4
J. Bacterio	1. 17E	3, 662-(667, 19	9 0	in encoding this	
A;Title: 5a A;Reference	numbe	r: JC6	039; MT	JID	MID:8550497	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
A; Molecule	: JC6(type:	DNA				
A, Cross-ref	erence	88: GB:1	043280	z	ID:g1184712; PIDN:AAC43599.	1; PID:g1184714
A;Accession A;Molecule	type:	protei	c			
A;Residues: A:Experimen	21-52 tal so	2 <c02></c02>	strain	27		
A, Note: the	autho	ors tra	nslate	ti i	for residue	44 as Ile xav ww
T. Bacterio	173	4773	7, D.; -4781,	19		
A, Title: Pu A, Reference	rifica	ation an	nd cha: 898; M	rac	of thin, aggreg PMID:1677357	ative fimbriae from Salmonell
A; Contents:	27655	10.0				
A; Accession A; Status: p	relimi	inary				
A, Molecule A, Residues:	type: 21-33	protein 3 <co3></co3>	ជ			
A; Note: seq C; Genetics:	sequence	extrac	ted fr	E O	NCBI backbone (NCBIP:45936)	
A;Gene: agfA C:Function:	A					
Not	oh: mabriae	ajor co bind t	component of this to fibronectin,	t o	n aggregative fimbria plasminogen, tissue	e plasminogen activator
C; Keywords: fimbr F;1-20/Domain: si F;21-151/Product:	rimo n: s duct	ria ignal sequence : fimbrin prot	equenca in prot	ր.#⊨ (0 Հ (0	<pre>! #status predicted <sig> :ein agfA #status experimental</sig></pre>	<mat></mat>
(t	6		,
Query Match Best Local S Matches 137	ch 11 Simi 137;	th Similarity 37; Conserv	87 90 ativ	u	Score 682; DB 2; Lenglin Pred. No. 1.2e-50; 2; Mismatches 12; Indel	T 25
δ		LLKVAAF	AAIWUS(GSA 	MKLIKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ	SIYQYGSANAALALQ 60
QD	1 M	LLKVAAF	AAIVVS	GSA	LAGVVPQWGGGGNHNGGGNSSGFUSTI	
yy ag	61 SDARI 61 SDARI	ARKSETT ARKSETT	ITQSGY, ITQSGY(ITQSGY)	GNG GNG	DARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQMNAKNSDITVGQYGG 	
	2	TOMY.144	מסמממת	2	151 YONATANNA	
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A; Description: major component of wild-type curli; interaction between CsgA and CsgB tri
A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         curlin major subunit CsgA [imported] - Escherichia coli (strain 0157:H7, substrain RIMD
A,Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A,Reference number: S31202, MUID:93211294, PMID:8459772
A,Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90806
A;Status: preliminary
A;Nolecule type: DNA
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A,Residues: 1-152 <HAY>
A,Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:913360880; GSPDB:GN00154
A,EXPERTIMENTAL SOURCE: strain O157:H7, substrain RIMD 0509952
C,Genetics:
A,Gene: ECs1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 QSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli
C;Daces : B-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D90806
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, F
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, F
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157
                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-13, 'RQRDSGMLM' <OLS3>
A;Cross-references: EMBL:L04979; NID:9280424; PIDN:AAA23616.1; PID:9280425
A;Experimental source: strain K-12, substrain W3110
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69.5%; Pred. No. 4.6e-37;
iive 17; Mismatches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                         A; Molecule type: protein
A;Residues: 21-42;44-50 < OLS2>
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library, October 1992
A;Reference number: 834559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                          A,Molecule type: DNA
A,Residues: 1-6,'V',8-151 <OLS1>
A,Cross-references: EMBL:L04979
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Matches 105; Conserv
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A,Map position: 23.15
C,Function:
                                                                                                                                                         A; Accession: S34560
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Cipecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: Lihis species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A10635
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P.; Davies, R.N.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'daora, P.
Nature 413. 484-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUDD:21534947; PMID:11677608
A;Accession: A10635
A;Status: prefilminary
A;Molecule type: DNA
A;Residues: 1-151 <PAR>
A;Conser-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
C;Genetics:
A;Gene: STY1181
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Pred. No. 1.2e-50;
2; Mismatches 12; Indels
  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 90.7%;
Matches 137; Conservative
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A,Cross-references: EMBL:X06462
C,Genetics:
A,Genetic cnjl:
A,Genetic cnjl:
A,Genetic cnje:
A,Genetic cnje:
A,Genetic cnje:
A,Genetic cnje:
A,Genetic cnje:
A,Genetic cnje:
A,Genetic cnje:
A,Introns:
B,3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
C,Reywords: £inc finger
C,Reywords: £inc finger
C,Ref motif
F)164-1450/Region: zinc finger CCHC motif
F)1501-1514/Region: zinc finger CCHC motif
F)1501-1543/Region: zinc finger CCHC motif
F)155-1568/Region: zinc finger CCHC motif
F)155-1568/Region: zinc finger CCHC motif
F)1602-1615/Region: zinc finger CCHC motif
F)1602-1615/Region: zinc finger CCHC motif
F)1602-1615/Region: zinc finger CCHC motif
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F)1602-1615/Region: zinc finger CCHC motif
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F)1602-1615/Region: zinc finger CCHC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 33.6%; Pred. No. 0.39;
Matches 37; Conservative 11; Mismatches 32; Indels 30
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                                                                                                                                                                                                                                                                                                                                               hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C; Species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (space: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: H35665
R; Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Reference number: AS5480; MUD:21074935; PMID:11206551
A; Accession: H35665
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-152 <870->
A; Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:216
A; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
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A; Residues: 1164-1174,1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-1
A; Residues: 1164-1174,1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-1
A; Martindale, D.W.; Taylor, F.M.
Nuclaic Acids Res. 16, 2189-2201, 1988
A; Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A; Reference number: $03650; MUID:88189811; PMID:3357771
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               QSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG 119
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C;Species: Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Bate: 19-Mar-1997 #sequence revision 18-Jul-1997 #text_change 07-Dec-1999
C;Accession: S42136; S42135; S0350
R;Taylor, F.M.; Martindale, D.W.
submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
A;Accession: S42136
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A; Residues: 1-1748 <TAY>
A; Cross-roces: EMBL:L03710; NID:g161751; PID:g161752
A; Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A; Title: Retroviral-type zinc fingers and glycine-rich reg
A; Reference number: S42135; MUID:94051569; PMID:8233798
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Pred. No. 3e-35;
3; Mismatches 30;
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A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
                                                                                                                        GNNAALVNQTASDSSVMVRQVGFGNNATANQY
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Best Local Similarity 67.8
Matches 103; Conservative
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Ryconsory, No. 18 Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Naturer, 333, 537-544, 1998
A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Rittle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A, Recession: E70946
A, Recession: E70946
A, Residues: preliminary, nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Residues: 1-590 <COL>
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A, Residues: 1-50
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Baccesion: T21956
C;Accession: T21956
R;Lennard, N.
Submitted to the EMBL Data Library, June 1996
A;Recence number: Z19493
A;Recencen unmber: Z19493
A;Recencen: T21956
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-407
A;Mcsesion: T21956
A;Residues: 1-407
A;Mcsesicus: 1-407
A;Residues: 1-407
A;Cross-references: EMBL:Z74033; PIDN:CAA98477.1; GSPDB:GN00023; CESP:F38B7.3
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                                                                                                                                                                                                                                                                      probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: E70946
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25.8%; Pred. No. 1.4;
live 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 FGNSGNNNIGFFNSG-NNNVGFFNSGNNN----
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A; Introns: 12/1; 57/3; 124/2; 163/1; 330/3
                                               459
Best Local Similarity 27.4% Matches 34; Conservative
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Best Local Similarity 25.81
Matches 34; Conservative
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A;Gene: CESP:F38B7.3
A;Map position: 5
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: E70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295997; PMID:9634230
A;Accession: E70663
A;Accession: E70663
A;Accession: E70663
A;Accession: E70663
A;Realusi preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-615 <COL>
A;Cross-references: GB:Z83860; GB:AL123456; NID:93261681; PIDN:CAB06165.1; PID:e290763;
A;Gene: PPE
A;Gene: PPE
                                                                                                                                                                  hypothetical protein Y38E10A.g - Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Accession: T26667
R;Wallis, J.
Submitted to the EMBL Data Library, September 1999
A;Reference number: Z20252
A;Accession: T26667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-586 < WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 NSASNGS-----YGSSANEVKSVGFGAQQYGGSVFAKPSGTGGGYVSAGSSARKSGE 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TG 401
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Best Local Similarity 28.8%; Pred. No. 0.44;
Matches 47; Conservative 14; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 SDITVGQYGGNNAALVNQTAS--DSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 SGAGGGGGAKASASYGSSANEVKSVGFG----AQQY
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                                                                                               RESULT 8
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ice nucleation protein - Xanthomonas campestris
C;Species: Xanthomonas campestris
C;Species: Xanthomonas campestris
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C;Accession: S11672
R;Zhao, J; Orser, C.S.
Mol. Gen. Genet. 223, 163-166, 1990
A;Fitle: Conserved repetition in the ice nucleation gene inaX from Xanthomonas campestr
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A;Experimental source: strain H37Rv
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C,Species: Mycobacterium tuberculosis
C,Species: Mycobacterium tuberculosis
C,Species: Mycobacterium tuberculosis
C,Space: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C,Accession: F70825
R,Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
R,Cole, S.T.; Brosch, R.; Parkhill, M.; Fellwell, T.; Genles, S.; Hamiln, N.; Holr,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A,Athurer 393, 537-544, 1998
A,Athurer S, Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Athurer Deciphering the biology of Mycobacterium tuberculosis from the complete shacesion: F7085
A,Accession: F7085
A,Accession: F7085
A,Accession: F7085
A,Athurer Drellminary: nucleic acid sequence not shown; translation not shown
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                                                                                            56 ALALQSDARKSETTITQSGYGNGADVGQ-GADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
1 MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYNR 60
                                                                                                                                                      -NGNRNVAG 95
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1567 <ZNA>
A;Residues: 1-1567 <ZNA>
C;Cross-references: EMBL:X52970; NID:g48531; PIDN:CAA37140.1; PID:g48532
C;Superfamily: ice nucleation protein
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                                                                                                                                                                                                                      VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                             ---HOYGRHNLSAVGÓEGHDNYGSTTQ-
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ilarity 28.2%; Pred. No. 6.9;
Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.0%; Score 93.5; DE
Best Local Similarity 24.5%; Pred. No. 2.6;
Matches 39; Conservative 17; Mismatches
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Best Local Similarity
Matches 42; Conserv
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I kriwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I kriwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell krimp, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A; Attherence number: AB2577; MUD:21608550; PMID:11743193
A; Accession: AD3143
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A; Residues: 1-145 < KURA
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C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Accession: H9844
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain CS
C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-145 < KURx
A, Cross-references: GB: AE007870; PIDN: AAK88682.1; PID: g15158413; GSPDB: GN00170
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A;Experimental source: strain C58 (Dupont)
C;Genetics:
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            SD---NDTTVTNNYYNYGDNDNNGGNNHSS-SSNAITDAPGNAGDQSQQQSD-----
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12.0%; Score 93.5; DB 2; Length 145;
Best Local Similarity 21.8%; Pred. No. 0.48;
Matches 34; Conservative 25; Mismatches 64; Indels 3:
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A;Map position: linear chromosome
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A;Map position: linear chromosome
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Total number of hits satisfying chosen parameters:

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1	Description	P55225 salmonella				P39828 escherichia	pantoea	P16239 erwinia her	chlamydi	Q8z7m3 salmonella				P23223 leishmania	P15706 leishmania	P08148 leishmania										_						P75411 mycoplasma	drosophi	P25074 oryza sativ
SOUTHWANTES				CSGA_ECO57	ICEN XANCT	CSGB_ECOLI	ICEN_PANAN	ICEN ERWHE	PMPB_CHLTR	SGB_SALTI	CSGB_SALTY	CEA_PANAN	YK98 MYCTU	P63_LEIDO	P63_LEICH	P63_LEIMA	P63_LEIME	338 BPT2	442_MYCTU	SAK_ECOLI	70 DROME	ICEN PSEFL	189_SCHPO	D33_MOUSE	YBIL_ECOLI	BUNZ DROME	PO33_RAT	۳,	PO33_HUMAN	YF48_MYCTU	HME1_HUMAN		\Box_{1}	GRP1_ORYSA
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PIR; JC6039; JC6039.
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WEDLINE-21218556; PubMed=11319125;
MILICH G.A., Keen J.E., Elder R.O.;
Mutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli O157:H7.";
Mutations Microbiol. 67:2367-2370(2001).

R. Appl. Environ. Microbiol. 67:2367-2370(2001).

R. Appl. Environ. Microbiol. 67:2367-2370(2001).

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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Major curlin subunit precursor.
CSGA OR 21676 OR ECS1420.
Escherichia coll 0157:HT.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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7 7 A -> E (IN REF. 1).
151 AA; 15049 MW; C003470D208D395F CRC64;
-!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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EMBL; X90754; CAA62282.1; --
EMBL; AB000205; AAC74126.1; --
EMBL; D90741; BAA5883.1; --
EMBL; S70748; SAA5840.1; --
PIR; S70788; S70788.
ECGGene; EG11489; csgA.
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SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-0157-017 N.T.
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MEDLINE-21156231; PubMed=11258796;
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Xanthomonadaceae, Xanthomonas
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"Conserved repetition in the ice nucleation gene inaX from axthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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us-09-543-407-22.rsp

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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                    -----DQLVTRVVTHEMAHAD------QWNAKNSDITVGQYG----GNNAALV 126
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                                                                                                                                                                                                                                                                                                                                     Gaps
-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLIDAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS OCTAPERTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERCOICITY IS SUPERIMPOSED.
-!- MISCELLANGOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                             12.0%; Score 93.5; DB 1; Length 1567; 28.2%; Pred. No. 4; ive 21; Mismatches 41; Indels 45;
                                                                                                                                                                                                                                                                              Ice nucleation, Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-07-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
More curlin subunit precursor.
CSGB OR B1041 OR 21675 OR ECS1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 AGYGSTQTAGSESSLT--AGYGSTQTAQQ 518
                                                                                                                                                                                                                                   InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleatio; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 83334;
                                                                                                                                                                                                            EMBL; X52970; CAA37140.1; -. HSSP; P06620; 11NA.
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Matches 42; Conserv
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                                                                                                       family
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Armqvist A., Olsen A., Normark S.;
Sigma S-dependent growth-phase induction of the csgBA promoter in
"Sigma S-dependent growth-phase induction of the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DESREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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STRAINE-157-117 / RIMD 0509952;
MEDLINE-2156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara M., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                     Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mortin H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0157:H7 (ED1933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Mayhew G. I. Burns P.S., Gregor J., Kirkpatrick H.A., Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Welch R.A., Blatther F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Amau B., Shoa Y., Shoa Y., "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y. Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
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MEDLINE=95157246; PubMed=7854117;
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EMBL; AE005315; AAG55787.1; -.
EMBL; AP002584; BAB34842.1; -.
PIR, C90806; C90806.
PIR, G85665;
PIR; S70787; S70787.
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                                                                                                                           38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVT 97
                                                                                                                                                   AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORTH BIOCHEM 1 BIOCHEM. S8:762-764(1994).

FUNCTION: I ce mucleation proteins enable bacteria to nucleate crystallization in supercooled water.

SUBCELLULAR LOCATION: Outer membrane.

DORAIN: CONTAINS: MPRREECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

MISCELLANGOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE MISCELLANGOUS: A STRUCTURAL MODEL IS SUGGESTED TO THAT OF ICE.

SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=KUIN-3;
MEDLINE=94264407; PubMed=7764866;
Michigami Y., Watabe S., Abe K., Obata H., Arai S.;
"Cloning and sequencing of an ice nucleation active gene of Erwinia
                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                             98 HEMAHADOWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANOY
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                                                                         11.9%; Score 92.5; DB 1; Length 151; 28.1%; Pred. No. 0.36; ive 15; Mismatches 62; Indels E
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                                      MINOR CURLIN SUBUNIT.
B18D266B964014B8 CRC64;
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                                                                                                                                                                                                                                                                                         (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                  PRT; 1034 AA
                          POTENTIAL.
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DOMAIN 162 993 OCTAPEPTII
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InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation, 51.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 34.
                                                                                                                                                                                                                                                                                                                                                        Pantoea ananas (Erwinia uredovora).
EG12621; csgB.
Signal; Complete proteome.
                                                  151 AA; 15882 MW;
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                                                                                                   Conservative
                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                   Best Local Similarity
Matches 32: Consert
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nes 46; Conserv
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01-NOV-1997
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             Fimbria;
SIGNAL
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                                                                                                                                                                                            -----GEESSQMAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSLIAGYGSTQTAGEDS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-:- SUBCELLULAR LOCATION: Outer membrane.
-:- DOMAIN: CONTAINS 126 IMPRERET REPEATS OF A CONSENSUS OCTABEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERINFOSED.
-:- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-:- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                         ALQSDARKSETTITQSGYGN-----GADVGQG-----ADNYDQLVTRVVTHEMAHAD-
--GPDSTLSIYQYGSANAAL
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                                                                                                                                                                                                                                                                                                     271 SLTAGYGSTQTAQKGSDLTAG-YGSTGTA----GADSSLI---AGYGSTQTAGE 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warren G.J., Corotto L.V., "The consensus sequence of ice nucleation proteins from Erwinia "The consensus sequence of ice nucleation proteins from Erwinia herbicola, Pseudomonas fluorescens and Pseudomonas syringae.", Gene 85:239-242(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1258 AA; 125084 MW; 590E8A130077FBD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 91.5; D 26.3%; Pred. No. 4.6; ative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS---
IVVSGSALAGVVPQW--GGGGNHNGGGNSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS, PROBER, ICE NUCLEATION, 65.
PRINTS, PROBERT, ICENUCLEATIN.
PROSITE, PS00314, ICE NUCLEATION, 45.
ICE NUCLEATION, 45.
DOMAIN 162 1217, OUTER MEMBYRHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000258; Ice_nucleatn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=M1;
MEDLINE=90152370; PubMed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M26382, AAA24823.1; -. PIR, JQ0188, JQ0188.
HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae; Pantoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ce nucleation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 -- OSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 IIEIANNKATDVGGGA-----YVKGTLTCENSHRLÖFLKNSSDKQGGGIYGEDNITLSNL 510
                       ------GEESSOMAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSLIAGYGSTQTAGEDS 270
---ADNYDQLVTRVVTHEMAHAD- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable outer membrane protein pmpB precursor (Polymorphic membrane
                                                             271 SLTAGYGSTQTAQKGSDLTAG-YGSTGTA----GADSSLI---AGYGSTQTAGE 316
                                                                                                                                                                                                                                                                                                  MEDLINE=99000899; PubMed=9784136; Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN PMPB.
                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
                                               ----OWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                        Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHCI-2DPAGE; O64418; --
InterPro; IPR03368; Chlamydia PMP.
InterPro; IPR03368; Chlamydia PMP.
TIGRPAMS; TIGRO1376; POMP. repeat; 18.
Outer membrane; Signal; Multigene family; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 91; DB 1; Length 1754; 33.1%; Pred. No. 7.3; ive 10; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
PROBABLE OUTER MEMBRANE PRO
W; 969CF8D85D36185D CRC64;
  --GADVGQG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE001314; AAC68010.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 1754 PROI
1754 AA; 183317 MW;
 ALQSDARKSETTITQSGYGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.1
Matches 40; Conservative
                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 T 129
                                                 105 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 T 511
                                                                                                                                                                                                        protein B).
PMPB OR CT413.
                                                                                                                                                                                                                                                                                                                                         Davis R.W.;
                                                                                                                                   CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                  PMPB CHI
084418;
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                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., anultiple drug resistant Salmonella enterica serovar Typhi CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMedt G. III, Mayhew G.F., Rose D.J.,
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 185:2330-2337 (2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNYDQL-----VTRVVTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Gaps
                                                                                                                                                                                                Bacteria, Prôteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 MINOR CURLIN SUBUNIT.
16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä.
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28.8%; Pred. No. 0.53
:ive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fimbria; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21534947; PubMed=11677608;
                                                                                                         Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AA069400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 1
151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                           Salmonella typhi
                                                                                                                                                                                                                                                                              NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSGB_SALTY
ID _CSGB_SALTY
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RESULT 9 CSGB_SALTI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90092494; PubMed=2599095;

MEDLINE=90092494; PubMed=2599095;

MEDLINE=90092494; PubMed=2599095;

The ice inucleation active gene of Erwinia ananas. Sequence similarity to those of Pseudomonas species and regions required for ice incleation activity.",

Thucleation activity.",

FEBS lett. 258:297-300(1989).

The PubCilon: Ice nucleation proteins enable bacteria to nucleate or ystallization in supercooled water.

The PubCilon: Ice nucleation proteins enable bacteria to nucleate or ystallization in supercooled water.

The DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-T-X-T, FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PRESIDUE THE PROTEIN ICE nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 OCTAPEPTIDE PERIODICITY.
131094 MW; 89B0EE24AA837039 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 GSTSTAGPDSSL-İAGYGSTQTA------GYNSİLTAGYG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 89.5; DE
26.8%; Pred. No. 7.1;
:ive 18; Mismatches
                                                                                                                                                                                                                                         1322 AA
                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 1281 OCTAPEPTID
SEQUENCE 1322 AA; 131094 MW; 89BOEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00818; Ice nucleation, 69.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                                                                         Pantoea ananas (Erwinia uredovora)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, S07053; S07053.
HSSP; P06620; IINA.
InterPro; IPR000258; Ice_nucleatn.
                                                                                                                                                                                                                                  ICEA PANAN STANDARD, B
P20469;
01-FEB-1991 (Rel. 17, Created)
    |:|| ||| |: | : | : | ISQSAYGNSAAIIQKGSGN-
                                                                                                                                                                                                                                                                                                                                                            Ice nucleation protein inaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X17316; CAA35194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 26.8
Matches 34; Conservative
                                                                        129 TASDSSVMVRQ 139
                                                                                                                       140 KOSHMAIRVTO 150
                                                                                                                                                                                                                                                                                                             (Rel. 17, (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                               01-FEB-1991
16-OCT-2001
                             104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --DAS 103
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                                                                                                                                                                                                                                                                                                             SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=S.typhimurium, STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryan E., Sun H., Florea L., Miller W., Stoneking T., Mhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 178:662-667(1996).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AL COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBROMECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
MINOR CURLIN SUBUNIT.
COFC5430E6DD361D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 ARVRQEGSKILSVISQ--EGGNNRAKVDQAGNYNFAYIEQTGNAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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ilarity 27.5%; Pred. No. 0.53;
Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ002301; CAA05316.1; -.
EMBL; AE008749; AAL20073.1; -.
PIRL; JC6040; AAC43598.1; -.
PIR; JC6040; JC6040.
StyGene; SG10609; csgB.
Fimbria; Signal; Complete protecome.
SIGNAL
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                                                                                                                                             Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 413:852-856(2001).
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                                                                                                                                                                                                                                              NCBI_TaxID=602, 592;
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151 A
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Matches
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us-09-543-407-22.rsp

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Leishmania donovani.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Eugle:
NCBI_TaxID=5661;
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P23223;
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CHAIN
PROPEP
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GP63_LEIDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRECISES M. The control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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MEDI.NE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J.A., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY.
-!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 59. Ref.1 sequence has been checked by authors in Ref.1 and they report that no errors have been found.
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SPECIES=M.Dovis; STRAIN=AF2122/97;
SPECIES=M.Dovis; STRAIN=AF2122/97;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating i., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. US. A. 100:7877-7882[2003].
-! SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                          01-00T-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypochetical glycine-rich protein Rv2098c/MT2159/Wb2125c.
RV2098C OR MT2159 OR MTCY49.38C OR MB2125C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                  491 AA
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                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis, and
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InterPro, IPR000084; PE_region.
Pfam, PF00934; PE, 1.
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                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laboratory strains."
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                                                                                            YK98 MYCTU
                                                                                                                                           010707
RESULT 12
YK98 MYCTU
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                                                                                                                                     264
                                                                                                            20 AGVVPQWGGGGN-----HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVATION PEPTIDE.
LEISHMANOLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                      Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                            75 YGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSD---ITVGQYGGN 121
                                                                                                                                                                                     YGNGGAAGSGGNGGD-AGTGVSSDGFAGLGGSGGRGGDAGLIGVGGGGGN 313
                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 491;
                                                                                      Indels
                                                                                                                                AGLIGHGGAGGNGCDGGHGGSGKAGGSGGSGGFGQFGGFGGFGLL----
ProDom; PD001223; PE_region; 1.
Hypothetical protein; Complete proteome.
CONFLICT 312 312 G -> GG (IN REF. 1).
SEQUENCE 491 AA, 41979 MW; 12C8630C59CA0C13 CRC64;
                                                                                      45;
                                                          Score 87; DB 1;
Pred. No. 3.8;
8; Mismatches
                                                                                                                                                                                                                                                 590 AA
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92107220; PubMed=1762629;
                                                             11.2%;
28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M60048; AAA29244.1; -.
HSSP; P08148; 1LML.
                                                         Query Match
Best Local Similarity 28.27
Matches 31, Conservative
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
87
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ACT_SITE
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EMBL; M28527; AAA29235.1;
           PIR; A44951; A44951.
HSSP; P08148; 1LML.
                                                                                                                            endopeptidase)
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J. Biol. Chem. 267:1888-1895(1992).

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- GATALYHIC ACTIVITY: Preference for hydrophobic residues at P1 and P1 and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyre'-Leu-Lys-Lys-.

-!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).

-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                              Gaps
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
Ramamoorthy R., Donelson J.E., Paetz E.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=44271;
                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
ZINC (CATALYTIC) (BY SIMILARITY).
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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LEMISHMANOLYSIN.
EMENSUED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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01-ANG-1986 (Rel. 08, Created)
01-ARP-1990 (Rel. 14, Lact aquence update)
10-CT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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MEDLINE-88154764; PubMed=3346625;
Button L.L., McMaster W.R.;
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
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InterPro, IPR001577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8; 1.
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J. Exp. Med. 171:589-589(1990)
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WEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Berges R., Metcalf P.;
Achlagenhauf E., Berges R., Metcalf P.;
The crystal structure of the Leishmania major surface proteinase
Teishmanolysin.";
Structure 6:1035-1046(1998).
C.!- CATALYTTA ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at Pl and Pl' and basic residues at Pl' and basic residues at Pl' and basic residues at Pl' and D' and basic residues at Pl' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' and D' 
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R InterPro; IPR00157; Peptidase_M8.
R Fine PR0157; Peptidase_M8.
R FRONTS; PR00182; LSHAMNOLVSIN.
R PROSITE; PR00142; ZINC_PROTEASE; 1.
R Hydrolase; Metalloprotease; Glycoprotein, Metal-binding; Zinc;
M Symogen; Signal; Cell adhesion; GPI-enchor; 3D-structure; Lipoprotein.
T SIGNAL 39 POTENTIAL.
T CHAIN 101 577 LEISHANOLVSIN.
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T ROPEP 578 602 REMOVED IN MATURE FORM.
T ACT 21E 264 ZINC (CATALYTIC).
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                                      X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDULNE-95406217; PubMed=7675788;
Schlagenhauf E., Etges R., Metcalf P.;
Chlagenhauf E., Etges R., Metcalf P.;
"Crystallization and preliminary X-ray diffraction studies of leishmanolysin, the major surface metalloproteinase from Leishmania
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N-LINKED (GLCNAC. ..) (POTENTIAL).
GPI-anchor amidated asparagine.
 the Leishmania major promastigote surface protease.";
J. Biol. Chem. 265:16955-16964(1990).
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PIR; PL0221, PL0221.
PDB; 1LML; 17-SEP-97.
MEROPS; M08.001; -.
                                                                                                                            major.";
Proteins 22:58-66(1995)
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Query Match
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Matches 17; Conservative 0; Mismatches 2; Indels

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MEDLINE=98053981; PubNed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.,
"Expression of thin, aggregative fimbriae promotes interaction of
Salmonella typhimurium SR-11 with mouse small intestinal epithelial Salmonella typhimurium. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella. NCBI_TaxID=602; . Query Match 86.7%; Score 673; DB 2; Length 152; Best Local Similarity 89.4%; Pred. No. 3.7e-47; Matches 135; Conservative 3; Mismatches 13; Indels 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64; Created) Last sequence update) Last annotation update) 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 Ā 152 PRT; cells."; Infect. Immun. 65:5320-5325(1997). EMBL; AJ000514; CAA04151.1; -NON TER 152 152 033802; 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19, PRELIMINARY; Agfa protein (Fragment) NON TER SEQUENCE 19 033802 RESULT 1 033802 d δ g δ ò

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MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Masko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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.Zogaj X., Bokranz W., Nimtz M., Romling U.;
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaces Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515700; CAD56672.1;
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 7:1151-4158 (2003).
EMBL; AJS15701; CADS66751; -.
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                  PRELIMINARY;
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01-OCT-2003 (TrEMBLre)
01-OCT-2003 (TrEMBLre)
Curlin-csgA protein,
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                                                                                                                                                                                                                                                                                                        Curlin-csgA protein.
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Q7X240; Q7X240

RESULT 3 Q7X240

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SEQUENCE FROM N.A.

TRANSPOSON=Insertion sequence 181;

MEDLINE=99314153; PubMed=1036375;

La Ragione R.M., Collighan N.J., Woodward M.J.;

La Ragione R.M., Collighan coli O78:K80 isolates associated with

"Non-curliation of Escherichia coli O78:K80 isolates associated with

"ISI inserti on in csgB and reduced persistence in poultry infection.";

FEMS Microbiol. Lett. 175:247-253(1999).

EMBL; AJ131756; CAB45380.1; -.
                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                    Score 122; DB 2; Length 29;
Pred. No. 0.0025;
1; Mismatches 2; Indels
                                                                                                                                                                                              E290DFC07ABBB243 CRC64;
                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                   curlin subunit CsgB, putative
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MEDLINE=22297686; PubMed=12368813;
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                                                                                                                                                                                                                       15.7%;
llarity 89.7%;
Conservative 1
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Best Local Similarity 28.3
Matches 30; Conservative
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                Escherichia coli
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01-MAR-2003
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                                                                                                                                                                                   61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SB30;
Cox J.M., Eglezos S., Woolcock J.B.;
"Virulence of Salmonella enteritidis in chickens correlates with
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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"Production of Cellulose and Curli Fimbriae by Members of the Enterobacteriaceae Isolated from the Human Gastrointestinal Tr. Infect. Immun. 72:4151-4158 (2003).
BEMBL, AJ515702; CAD55678.1; - SEQUENCE 150 AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
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                                                                               Length
                                                                                                        Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Last annotation update)
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                                                                              Score 421.5; DB 2
Pred. No. 9.2e-27;
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                                                                                                        Mismatches
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                                                                                                        25;
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58.9%;
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54.5%;
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                                                                                                        89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
                                                                               Query Match
Best Local Similarity
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Q983J5;
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Q54069;
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Q54069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Read T.D. Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanam M., Brinkac L., Daugherty S., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Melbiyum T.V., Smith H.O., Vanter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.8%; Score 115; DB 16; Length 13
28.3%; Pred. No. 0.061;
.ive 19; Mismatches 33; Indels
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                                                                                                 Last sequence update)
Last annotation update)
139
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1686 QTGGGWGSNDNQQQ-----QNENTGGGGWGSSNSNQTNNESSWGSNNQA 1729
             Hypothetical protein, Complete proteome.
SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                          50;
                                                                   14.1%; Score 109.5; DE 23.8%; Pred. No. 0.79; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR001878; Znf CCHC.
Pfam; PF00098; zf-CCHC; 7.
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                                                                                                                                                29 GGNHNGGGNSSGPDSTLSIYQYGSANAA-
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SMART; SM00343; ZnF CZHC; 7.
PROSITE; PS50158; ZF CCHC; 7.
CONFLICT 251 251 M ::
CONFLICT 256 256 I :>
SEQUENCE 1748 AA; 199624 MW;
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                                                                     Query Match
Best Local Similarity 23.8%
Matches 39; Conservative
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TIGR; S00865;
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Nat. Biotechnol. 20:1118 1123 (2002).
                                                                                                                                                                                                                                                       STRAIN-USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium addythiozobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005954; BAC50564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 130; Score 110; DB 16; Length 130; Local Similarity 25.8%; Pred. No. 0.14; les 39; Conservative 28; Mismatches 56; Indels 29
                                                                                                                                                                Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
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                                                                       Last sequence update)
Last annotation update)
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                                                     Created)
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                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                              Bradyrhizobium japonicum.
                 PRELIMINARY;
                                                               01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Bl15299 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 AA;
                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome
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                                                                                                                                                                                                    NCBI_TaxID=375;
                                 Q89JI4;
01-JUN-2003 (
01-JUN-2003 (
                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Best Loca Matches

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RESULT 10 Q8EIH4

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                                                                                                                                                                                                                         ---N 107
                                                                                                                                                                                                                                                                               406 ADVTALQHRGDLNLIDLIIEGDENAAEIT-----QAGSGNWVGGDSSSSFAASSFGVS 458
                                                                                                            78
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                                                                                                               ---LALQSDARKSETTITQSGYGNG
                                                                                                                                                    Tetrahymena thermophila.
Bukaryota, Alveolata, Ciliophora, Oligohymenophorea, Hymenostomatida,
Tetrahymenina, Tetrahymena.
NCBI_TaxID=5911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1640 QFGGGGNSNGGQSWGTSSGSDWN------COSNVQESTTTSSGGWGSSGSGN
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94051569; PubMed=8233798;
Taylor F.M., Martindale D.W.;
"Retroviral type Zinc fingers and glycine-rich repeats in a protein encoded by cnjB, a Terrahymena gene active during meiosis.";
Nucleic Acids Res. 21:4610-4614(1993).
EMBL; X06462; CAB37323.1; ---
EMBL; X06462; CAB37323.1; ---
EMBL; K06403; R0637171.1; ---
EMBL; S42136, S42136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
"Multiple introns in a conjugation-specific gene from Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q94821; P92146; P92145; P92144; P92143; P92142; P92141; Q94820; O1-FBB-1997 (TYEMBLrel. 02, Created)
01.FBB-1997 (TYEMBLrel. 02, Last sequence update)
01.OCT-2003 (TYEMBLrel. 25, Last sequence update)
                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 GADVGOGA-DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ--YGGNNAA 124
DB 16; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109; DB 5; Length 1748;
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                            108 AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32; Indels
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I -> N (IN REF. 1).
WW; OB03F210104008A3 CRC64;
                                                                                                                                                                                                                            79 ADVG-------QGADNYDQLVTRVVTHEMAHADQW--
                                                                                                                                                                                                                                                                                                                                                                             GDNNSLMITQTGNDNLVLGSQAGNNNSISVTQSGDMNVATVVQY
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MEDLINE 21681879; PubMed = 11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693 AIATAGAGAVGILAQSIGGGGGN---GGNATGGDAGFGSFOIGGGGGGGGYANTANVGFK 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                750 GLTLTTQGSHAAGIVAQS-VGGGGGTGGTASSYSAGI-------GFTASVAV 793
                                                                                                                                                                                                                                                                                                                                                STRUCTURE 21396508; PubMed=11481431;

WEDLINE=21396508; PubMed=11481431;

Rinan T.M., Weidner S., Wong K., Becker J., Chain P.,

Pinan T.M., Weidner S., Wong K., Becker A., Cowie A., Gouzy J.,

A Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,

A Golding B., Puehler A.;

The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-

fixing endosymbiont Sinorhizobium meliloti.";

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

PREBL, ALGOS465, CAC49389.1; -.

PIR; B95965; E59966.

A GO: GO:0004601; F: Percoxidase activity; IEA.

GO; GO:0004601; F: Percoxidase activity; IEA.

GO; GO:0004601; F: Percoxidase activity; IEA.

RO; GO:0004601; F: Percoxidase activity; IEA.

RO; GO:0004601; Percoxidase activity; IEA.

RO; GO:0004601; Percoxidase activity; IEA.

RO; GO:0004601; Percoxidase.

InterPro; IPR002016; Percoxidase.

InterPro; IPR002016; Percoxidase.

InterPro; IPR002016; Percoxidase.

InterPro; IPR002016; Percoxidase.

InterPro; IPR002016; Percoxidase.

R PROSITE; PS00435; PERCXINASE.1; 1.

PROSITE; PS00435; PERCXINASE.1; 1.

PROSITE; PS00633; PERCXINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.

PROSITE; PS006481; PROMENINASE.1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 27.0%; Pred. No. 5.1;
Matches 40; Conservative 20; Mismatches 52; Indels 36;
                                                                                                                                                                                                                                                        Rhizobiales;
                                                                                                                                                                                                                                      Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiale
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutinin-related protein.
RSC0887 OR RSO6116.
                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SWb21548.
RB0989 OR SMB21548.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 3501 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                794 GGTGGNGGAGGEVSVSLTDSAIRTGQGG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burkholderiaceae; Ralstonia.
NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                 NCBI_TaxID=382;
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                                             RESULT 12
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Azianoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S., Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Squier P., Thebault P., Malen M., Wincker P., Levy M., Weisenbach J., Boucher C.A.;

Resembach J., Boucher C.A.;

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Resembach J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Boucher J., Bouch
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Weissenbach J., Boucher C.A.;
Weissenbach J., Boucher C.A.;
Warure 415:497-502(2002)

BMBL; ALG46079; GAD17691.1;
BMBL; ALG46079; GAD17691.1;
GG; GG: 00046811; C: extrachromosomal DNA; IEA.
GG; GG: 00046812; F: endomulease activity; IEA.
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Burkholderiaceae; Ralstonia.
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1.MAR-2002 (TrEMBLrel. 20, Last sequence update)
01.OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutinin-related protein.
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Ralstonia solanacearum (Pseudomonas solanacearum).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDITVGQYGGNNAALVNQTASDSSVM 136
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InterPro: IPR008619; Fil haemagg.
InterPro: IPR008638; Haemagg.act.
Pfam: PP05594; Fil haemagg; 20.
Pfam; PP05860; Haemagg_act; 1.
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MEDLINE=21681879; PubMed=11823852;
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MEDLINE=98083981; PubMed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes interaction of
Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhimurium.
Bacteria, proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriacee, Salmonella.
NCBL_TaxID=602;
                                                                                                                                                                                                                                             39;
                                                                                                                                                       Query Match
13.7%; Score 106.5; DB 16; Length 3552;
Best Local Similarity 29.5%; Pred. No. 15;
Matches 43; Conservative 19; Mismatches 45; Indels 39;
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13.7%; Score 106; DB 2; Length 179;
Best Local Similarity 32.3%; Pred. No. 0.44;
Matches 41; Conservative 17; Mismatches 55; Indels
PROSITE; PS01070; NUCLEASE NON_SPEC; 1.
Plasmid; Complete proteome.
SEQUENCE 3552 AA; 352934 MW; C5432AABE2CCF59C CRC64;
                                                                                                                                                                                                                                                                                                                       15 SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA---
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Infect. Immun. 65:5320-5325(1997).
EMBL; AJ000514; CAA04150.1; -.
SEQUENCE 179 AA; 19318 MW; A2BCCB648B3C0B0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-0EC-2001 (TrEMBLrel. 19, Last annotation update)
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6: geneseqp2031s:*

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ALIGNMENTS

RESULT 1

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copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or the containing a replacement segment or actid sequence or sequences grown on a Salmonella, E. coli or the contained in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and incorpusation of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SDARKSETTITQSGYGNGADVQQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                     Score 775; DB 3;
Pred. No. 1.6e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36347 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 151; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAC64623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36347;
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of thin aggregative finbriae (SEP17/7AR) mucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and attered for the production of fimbriae comprising recombinant Garacembination of a recombinant gene are directing recombination of a recombinant gene are into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer response in an animal, comprising separating an amino acid polymer comprising a recombinant and protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, B. coli or acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for a useful in emunogens, which may be important for directing an immune response in manimal in response in manimal are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN-----YDQ 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 714; DB 3; Length 15:
Pred. No. 1.8e-62;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 LVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.1%;
ilarity 91.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 144; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 151 AA;
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(UYVI-) UNIV VICTORIA

White AP,

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Salmonella; AgfA; vaccine.
                                                                                                                               Query Match
Best Local Similarity 89.9
Matches 143; Conservative
                                                                                                                         Sequence 151 AA;
           N-PSDB; AAC64631
                                                                                                                                                                                                                  AgfA sequence.
                                                                                                                                                                                                        25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                              Salmonella
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 690; DB 2; Length 151;
Pred. No. 4.1e-60;
                                                                                                                                                                                                                                                                                                                                                                         Doran JL;
                                                                                                                                                                                                                                                                      VICTORIA INNOVATION & DEV CORP
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                                                                                                                                                                                                                                                                                                                                                                     Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 7B; 95pp; English.
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                                                                                                                                 94WO-IB000207.
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Best Local Similarity 91.4
Matches 138; Conservative
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                                                                                                                                 26-APR-1994;
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                                                              10-NOV-1994.
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(KING/)
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                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA control of the encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbried (SEPIJ/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and control of the production of finbria copi and control of the production of finbria comprising recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a manino acid polymer comprising a recombinant part of protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or comprising separating an amino acid polymer comprising the mina in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response consideration of the present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 700; DB 3; Length 151;
Pred. No. 4.2e-61;
0; Mismatches 0; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 HEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                        Kay WW;
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR74625 standard; protein; 151 AA
                                        Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.3%;
89.9%;
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                                            Doran JL,
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Kay WW;

Collison SK,

Doran JL,

White AP,

WPI; 2000-672631/65

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epicope or antigen. Also described are:

(1) use of thin aggregative finbriae (SEPI7/TAP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacterriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacterriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluter. (I) is useful for the expression of recombinant AgfA protein into the animal in conjunction with a carrier of diluter. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the the response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 coppies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response in mannagens, which may be important for directing an immune response in mannagens, which may be important for directing an immune response in mannagens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 89.0%; Score 690; DB 3; Best Local Similarity 91.4%; Pred. No. 4.1e-60; Matches 138; Conservative 2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 HEMAHANQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                              Disclosure; Page 135; 139pp; English
  N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 151 AA;
g
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                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                              9
                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
   Gaps
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Enteropathogenic bacteria, enterobacteria, S.enteritidis, antibody.
                                                                         Salmonella enteritidis 27655-3b agfA.
                                                                                                                                 Location/Qualifiers
         AAW23570 standard; protein; 151 AA
                                              (revised)
(first entry)
                                                                                                              Salmonella enteritidis
                                                                                                                                         Misc-difference 123
                                             25-MAR-2003
29-SEP-1997
AAW23570
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gene replacement; fimbrin; epitope;

AgfA::PT3#1 amino acid sequence SEQ ID NO:12.

(first entry)

26-FEB-2001

AAB36346;

AAB36346 standard; protein; 151 AA

RESULT 7 AAB36346 vaccine; immune response; immunogen.

Salmonella enteritidis

Sscherichia coli

Synthetic.

WO200060102-A2.

12-OCT-2000

05-APR-2000; 2000WO-CA000356.

/note= "Encoded by GCC"

Salmonella; agfA; chromosomal

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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQMGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
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llarity 91.4%; Pred. No. 5.2e-60;
Conservative 2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 7; 85pp; English.
                                                                                                                                                                         94US-00233788
                                                                                                                                                                                                                                                          93US-00054452
                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1997-309886/28.
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es 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-309886/
N-PSDB; AAT74142
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                                                                                                                                                                                                                                                                                                                                                                                                                          Collinson SK,
                                                                                                                                                                         26-APR-1994;
                                                                                                                                                                                                                                                          26-APR-1993;
US5635617-A.
                                                                                    03-JUN-1997
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    NAME OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA concewhich encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SPEPA)/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and concern the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologue fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologue species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene comprising separating an amino acid polymer comprising a recombinant of cortaining a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino cortaining a natural no acid polymer comprising a replacement segment or segments of foreign amino cortaining an amino acid polymer comprising a replacement segment or segments of foreign amino cortaining a natural in conjunction with a carrier or diluent. (I) is acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which as useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response consecution, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbriae are easy and given in the exemplification of the present invention
                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                Collison SK, Kay WW;
                                                                                                                                                                                                                                                                                                                 Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
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79.8%;
99US-0127888P
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                                                (UYVI-) UNIV VICTORIA.
                                                                                                White AP, Doran JL,
                                                                                                                                              WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                     N-PSDB; AAC64622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Kay ww;

Collison SK,

(UYVI-) UNIV VICTORIA White AP, Doran JL,

WPI; 2000-672631/65. N-PSDB; AAC64629

05-APR-2000; 2000WO-CA000356.

Salmonella enteritidis. Escherichia coli.

WO200060102-A2 12-OCT-2000

Synthetic.

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SETI/TAF) mucleation depended assembly system of strains of Salmonella, Escherichia coli and casembly system of strains of Salmonella, Escherichia coli and content of gene of strains of salmonella, Escherichia coli and complete in a precupinant gene into the chromosome of the homologous species, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing in conjunction with a carrier or diluent. (1) is polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to colicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live the expensive to purify in large amount. The present sequence is given in examination of the present invention
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Pred. No. 1.2e-56;
Transparence 0; Indels 34;
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Gaps

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vaccine; immune response; immunogen.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA or sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finhuriae (SFF)/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and context accase for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of foreign and an amino acid polymer comprising a recombination of a recombination of foreign amino acid sequence or sequences grown on a Salmonella. E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in confunction with a carrier or diluter. (1) is cuseful for the expression of recombinant AgfA protein which is useful for electing an immune response in an animal. In a fimbrial presentation of system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrial subunit protein possesses both the immuned in mind an immune response of intervent for an efficient live immunorance which an immune an immune are immuned an immune in immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an immune an Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; Length 151; AgfA::PT3#6 amino acid sequence SEQ ID NO:22. Kay WW; Disclosure; Page 137; 139pp; English. vaccine; immune response; immunogen. AAB36351 standard; protein; 151 AA Collison SK, 05-APR-2000; 2000WO-CA000356 99US-0127888P 26-FEB-2001 (first entry) Salmonella enteritidis. (UYVI-) UNIV VICTORIA. Doran JL, 2000-672631/65. Escherichia coli. Synthetic. N-PSDB; AAC64627 Sequence 151 AA; WO200060102-A2. 05-APR-1999; 12-OCT-2000 White AP, AAB36351; AAB36351

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 MKLLKVAAPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 Gaps Score 609; DB 3; Length 151 Pred. No. 4.2e-52; 0; Mismatches 0; Indels Query Match 78.6%; Best Local Similarity 73.6%; Matches 128; Conservative

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98 HEMAHADOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVROVGFGNNATANOY 151 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen. AgfA::PT3#4 amino acid sequence SEQ ID NO:18. 3 Kay Disclosure; Page 136; 139pp; English AAB36349 standard; protein; 151 AA Collison SK, 05-APR-2000; 2000WO-CA000356. 99US-0127888P (first entry) Salmonella enteritidis. Escherichia coli. (UYVI-) UNIV VICTORIA, Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64625. 121 HEMAHA-WO200060102-A2. 05-APR-1999; 26-FEB-2001 12-OCT-2000 White AP, Synthetic. AAB36349; g ð g

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEPI)/TAFD nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacceriaceae for the production of finbriae comprising recombinant AgfA, CSA, and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologue species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for every the homologue fin an animal. In a fimbrial presentation every manner than the homologue for an animal. In a fimbrial presentation Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120 61 SDARKSETTITQSGYGNGADVGQGAD--------NYDQLVTRVVT 97 system the heterologous antigens are presented in high numbers (up to 550,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in

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WPI; 2000-672631;
N-PSDB; AAC64630
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                                                              Length 151;
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                                                                Score 608; DB 3; L
Pred. No. 5.2e-52;
5; Mismatches 22;
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 of the present invention
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vaccine, immune response, immunogen.
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                                                                78.5%;
Local Similarity 82.1%;
les 124; Conservative
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Escherichia coli.
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the exemplification
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N-PSDB; AAC64626.
                                  Sequence 151 AA;
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                                                                  Query Match
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. [1] is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response againer the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Pred. No. 8.2e-52;
5; Mismatches 22
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nes 124; Conserv
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cc assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and strains of Salmonella, Escherichia coli and strains of Salmonella, Escherichia coli and strains of Salmonella, Escherichia comprising recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising are main acid polymer comprising are combinant gene comprising a replacement segment or segments of foreign amino acid polymer comprising are combinant part protein containing a replacement segment or segments of foreign amino acid polymer into the animal in conjunction with a carrier or diluter. (I) is notymer into the animal in conjunction with a carrier or diluter. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the the networlogous are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sequence is given in immunogens, which may be important for directing an immune response in mount in the present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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Pred. No. 3.2e-51;
3; Mismatches 25; Indels
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81.58;
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151 AA;
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AAB36348
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA control of the encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SPETA/TAP) mucleation depended assembly system of strains of Salmonella. Escherichia coli and control of the adgraderized and AgfA-homologue fimbriae (SPETA/TAP) mucleation depended assembly system of a recombination of a recombinant gene into the chromosome of the homologue fimbriae species; (3) directing recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologue species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences in an animal in a contrier or diluent. (I) is useful for the expression of recombinant AgfA protein which and adhesion properties relevant for an efficient live and manned the inspection of the present invention immune response in an animal in control publify in large amount. The present sequence is given in the exemplification of the present invention
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                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.2%; Score 575; DB 3;
llarity 81.5%; Pred. No. 9.5e-49;
Conservative 5; Mismatches 23.
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                                                                                                                                        Page 136; 139pp; English.
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N-PSDB; AAC64624.
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                                                                                                                                           Disclosure;
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hes 123;
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Plasma protein; immune response; antibacterial; vaccine; gene therapy
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                                                                                                                                                                                                                                     Disclosure; Page 135; 139pp; English.
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                                                                                                Collison SK,
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         05-APR-2000; 2000WO-CA000356.
                                      99US-0127888P
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Best Local Similarity 70.2
Matches 106; Conservative
                                                                    (UYVI-) UNIV VICTORIA
                                                                                                Doran JL,
                                                                                                                              WPI; 2000-672631/65.
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                                                                                                                                             N-PSDB; AAC64619.
                                      05-APR-1999;
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia oli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
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                                                                                                                                                                                                                                                                                                                                                              Herwald H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                 Wikstroem M,
                                                                                                                                                                               30-JAN-2003; 2003WO-EP000943.
                                                                                                                                                                                                                                            31-JAN-2002; 2002GB-00002275.
                                                                                                                                                                                                                                                                                                       (HANS-) HANSA MEDICAL RES AB
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N-PSDB; ACF36153.
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Escherichia coli
                                                          WO2003064446-A2.
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-941-835-10

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US-09-972-115A-8

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US-09-352-991A-32096

US-09-138-452A-171

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US-09-252-991A-30227

US-09-489-095A-12003

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Gapop 10.0 , Gapext 0.5
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APPLICANT: Kay, William W.
APPLICANT: Callinson, Karen S.
APPLICANT: Callinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONBELA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: U.S.A.
ZIP: 99104-7092
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88.9%; Score 689; DB 1; Length 151;

Best Local Similarity 91.4%; Pred. No. 1.8e-60;

Matches 138; Conservative 2; Mismatches 11; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NORMER: US/08/23,788A
FILING DATE: 26-APR-1994
CLASSIFICATION NORMER: US/08/23,788A
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: 35.570
REGISTRATION NUMBER: 35.570
REFERENCE/DOCKET NUMBER: 32.0043.403C2
TELEPHAN: (206) 622-4900
TELEPHAN: (206) 622-490
TELEPHAN: (206) 622-6031
TELEPHAN: (206) 622-6031
TELERA: 1373836 SEEDANBERY
INFORMATION FOR SEO ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: amino acids
US-09-328-352-7735
US-09-489-803A-7973
US-09-496-803A-7973
US-09-919-172-41
US-09-919-172-41
US-09-073-898-6
US-09-085-351A-6
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         TOPOLÓGY: linea.
TOPOLÓGY: linea.
TECULÉ TYPE: protein
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                                                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/08233788A
Patent No. 5635617
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
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APPLICANT: Collinson, Karen S
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Pred. No. 1.7e-42;
2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCES:
CORRESPONDENCES:
CORRESPONDENCES:
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: CS-APR-1994
CLASSIFICATION: 435
ATTOAREY/AGBNT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (206) 622-4900
TELEFRAX: (206) 622-4900
                                                                                                                                                                                                                                    121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                              TELEFAX: (206) 622-4900
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
TYDE
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Patent No. 6277613
GENERAL INFORMATION:
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amino acid
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Best Local Similarity 88.4°
....nes 99, Conservative
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US-08-233-788A-57
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US-08-233-788A-57
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US-09-196-387-8
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65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSBLAESPEAA
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                                      A PROTEIN THAT BINDS TO TRF1 AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THAT BINDS TO TRF1 AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PetentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.4%; Pred. No. 1.1;
Matches 42; Conservative 16; Mismatches 61;
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Sequence 8, Application US/09841835

Patent No. 6506587

CENERAL INFORMATION:

APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan

TITLE OF INVENTION: A PROTEIN THAT BINDS TO

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Kauber & Jackson

STREET: Hackensack

CITY: Hackensack

COUNTRY: USA
                                                                                                                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600-1-230 CIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAVE: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600-1 TELECHONN: 201-487-5800 TELEFAN: 201-343-1684
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEII
TITLE OF INVENTION: OF USE TI
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jacksc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-09-196-387-8
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MEDIUM TYPE: Floppy
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAXNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DVSRVKRLVDA--- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 90.5; DB 3; Length 949; 28.4%; Pred. No. 1.8; Live 16; Mismatches 61; Indels 29
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG---
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| Patent No. 6506587
| GENERAL INFORMATION: Titia APPLICANT: General Susan; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TITLE OF SEQUENCES: 12
| NUMBER OF SEQUENCES: 12
| CORRESPONDENCE ADDRESS: ADDRESSE: Klauber & Jackson STREET: 411 Hackensack Avenue, 4th Floor
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-487-5800
TELEFAX: 201-31-1684
INFORMATION FOR ESQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600-1-230 CIP1
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION
PRICE APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
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ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 28.47
Matches 42, Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear; MOLECULE TYPE: protein US-09-196-387-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                 amino acid
3Y: linear
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US-09-841-835-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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US-09-196-387-10
Sequence 10, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 90.5; DB 4; Length 673; 28.4%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Indels
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                               NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKTA NUMBER: 600-1-230 CIP1
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 ----ANVNAKDMAGRKSSPLHFAAGFG 227
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APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 28.4;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 673 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hackensack
New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Ne COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
                                                             99 VAAAPVVPAVSTSSAAGVAFNPAGSGSNNSPSSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                              65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                        ---- DVSRVKRLVDA--- 204
                                      6 VAAFAAI-VVSGSALAGVVFQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSBPTSS-SSSSPGSPGSSLAESPEAA
                                                                                                                                                                                                                                                                                                  APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 411
CITY: Hackensack
STATE: New Technique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.7%; Score 90.5; DB 4; Length 1327; ilarity 28.4%; Pred. No. 2.8; Conservative 16; Mismatches 61; Indels 29
Indels
61;
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                        158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
MAME: Jackson Beg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECHONE: 201-487-5800
TELEPRAN: 201-343-1684
                                                                                                                                                                                                121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                    ----ANVNAKDMAGRKSSPLHFAAGFG 227
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                       US-09-841-835-2

Sequence 2. Application US/09841835

Patent No. 6506587

GENERAL INFORMATION:
  16;
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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    42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Drote
HYPOTHETICAL: NO
9-841-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentI
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Best Local Similarity
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Matches
    Matches
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                                                                                                                                                                                                                                                     99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                      65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                      158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-----DVSRVKRLVDA--- 204
                                                                                                                                                                                                                          6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
GENERAL SMITH, SUSAN
TITLE OF INVENTION:
APPLICANT:
OF INVENTION:
OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 1327;
                                                                                                                                           11.7%; Score 90.5; DB 4; Length 949; 28.4%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/196,387 FILING DATE: CLASSIFICATION: PRIOR APPLICATION: APPLICATION NUMBER: 09/095,225 FILING DATE: June 10, 1998 ATTORNEY/AGRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 90.5; D
Pred. No. 2.8;
                                                                                                                                                                                    16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                  205 ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                      121 HEMAHANOTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1327 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%;
28.4%;
                                                                                                                                                                                      42; Conservative
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NO
      SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
ZIP: O7601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201-343-1684
                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                             Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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HYPOTHETICAL:
                                                                                                         US-09-841-835-10
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Sequence 171, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev.
TITLE OP INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF, SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 LLKSSASASASASASASASAG-----GGGGGGNGGGNGGGG------GGGAGALA----460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        859 TVSPEDYAAVQAALA--AYVRKHESLIV-STYGLGAQEGQTSSKVTTLMRDLHAVEELVE 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ELTO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 89.5; DB 3; Length 738; llarity 35.4%; Pred. No. 1.6; Conservative 4; Mismatches 26; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%; Score 87; DB 4; Length 1156; 32.0%; Pred. No. 5.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          916 MG-----VETYRLNRSDQILHRV--HSVLHSHLRDSDSS 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 NGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E (by experiment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 26, 1997
PRIOR APPLICATION DATE:
APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. BRUCE Hamburg
REGISTRATION NUMBER: 22,389
REGISTRATION NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)956-2340
TELEPHONE: (212)953-7733
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AALAAAGAGGGLGGGGG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 ARKSETTITQSGYGNGADVGQG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 32; Conserva
                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Matches 29; Conserv
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Patent No. 6001592

GENERAL INFORMATION:
APPLICANT: Kunio NAKASHIMA et al.
APPLICANT: Kunio NAVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: 812-5 Hirano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 1327;
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: Microsoft Windows 95 SOFTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                               Sequence 8, Application US/09972115A
Patent No. 6599726
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: General Mories B.
APPLICANT: Greeg, Morin B.
APPLICANT: Maler, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US 69/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2001-0-05
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
NUMBER OF SEC DI NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 90.5; DB; Pred. No. 2.8; 16; Mismatches
                                     121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                    ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%;
28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.4%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1327
TYPE: PRT
CRGANISM: Homo sapiens
US-09-972-115A-8
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CITY: TE
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58 HIYGVDAPSAFYGYGWAQARSQGDNILRLYGEAR------GKGAEYWGPDYEQTT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 IELTQNGFRNNATIDQWNAK-----NYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATURE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PERENTIA RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: PC-DOS/MS-DOS
APPLICATION NUMBER: US/07/731,157A
FILING DATE: 19910509
CLASSIFICATION: 435
PRICE APPLICATION DATA:
APPLICATION NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER PH.D. BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-027/00US
TELEPHONE: 415-494-7663
TELEPHONE: 415-494-7663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                       APPLICANT: Misset, Onno
APPLICANT: Misset, Onno
APPLICANT: Misset, Onno
APPLICANT: Wan der Laam, Jan M.
APPLICANT: Uan der Laam, Jan M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: ADDRESS: COOLES GONNARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 81.5; DB 1;
ilarity 25.8%; Pred. No. 9.5;
Conservative 17; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   Sequence 2, Application US/07731157A
Patent No. 5457032
GENERAL INFORMATION:
126 ANOTASDSSVMVROVGFGNN 145
                                            180 ANOATGESSTV---AGGSNN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-541-780-2; Sequence 2, Application US/08541780; Patent No. 5935831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 720 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: FIVE PALO CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                 US-07-731-157A-2
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          Sequence 20096, Application US/09252991A

Sequence 20096, Application US/09252991A

Sequence 20096, Application US/09252991A

Sequence 20096, Application US/09252991A

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32096

LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQ---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 -----TSVLQSGYGNTLNNYSNPNTASLSNSANNVSGNLGVNV-AAGNFNQQKND 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KVAAFFAAIVVSGSALAGVVPQWGG-----GGNHNGGGNSSGPDSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-336-447A-15
US-09-336-447A-15
Sequence 15, Application US/09336447A
Fatent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEB1, CHRISTOPH
APPLICANT: REDEBNORM, ESOBEL
APPLICANT: FREEDENBURG, ESOSEA
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT FALLION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.9%; Score 84.5; DB 4; Length 339;
Best Local Similarity 21.5%; Pred. No. 1.8;
Matches 34; Conservative 32; Mismatches 67; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 83; DB 4; Length 889; llarity 27.9%; Pred. No. 8.9; Conservative 16; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 LVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 LAAAVSNGOYSTAGSAASOTSTGNTTVNSANYAYGGTY 201
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moraxella catarrhalis
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SEQ ID NO 15
LENGTH: 889
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Best Local Similarity
Matches 39; Conserv
       US-09-252-991A-32096
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US-09-336-447A-15
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us-09-543-407-24.rai

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58 HIYGVDAPSAFYGYGWAQARSQGDNILRLYGBAR-------GKGABYWGPDYEQTT 106
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Best Local Similarity 25.8%; Pred. No. 9.5;
Matches 46; Conservative 17; Mismatches 56; Indels 59; Gaps
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Misset, Onno
APPLICANT: Waset, Onno
APPLICANT: Van der Laan, Jan M.
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES:
SOCRESPONDENES:
ADDRESSEE: COCLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FATVE PALO ALTO SQUARE, 4TH FLOOR
CITY: PALO ALTO
CITY: PALO ALTO
COUNTY: DALO ALTO
COUNTY: DALO ALTO
COUNTY: USA
ZIF: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPY MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,780
FILING DATE: 18-AR-1990
ATTORNEY AGENT INFORMATION:
FILING DATE: 18-AR-1990
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 23,750
REFERENCE/DOCKET NUMBER: 23,750
REFERENCE/DOCKET NUMBER: 23,750
REFERENCE/DOCKET NUMBER: 23,750
REFERENCE/DOCKET NUMBER: 23,750
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REFERENCE/DOCKET NUMBER: 23,750
RELECOMMUNICATION NUMBER: 23,750
RELECOMMUNICATION NUMBER: 23,750
RELECOMMUNICATION POR SEQ ID NO: 2:
SEQUENCE TELECOMMUNICATION: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 720 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-541-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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Search completed: August 2, 2004, 14:58:35 Job time: 12 secs

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                                                                                August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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775
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                     1291235
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                  Title:
Perfect score:
Sequence:
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                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	206	Sequence 7876, Ap	Sequence 49960, A	Sequence 8, Appli	Sequence 10, Appl	Seguence 2, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 56041, A	Sequence 275468,	Sequence 57763, A
	ID	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-032-585-7876	US-10-425-114-49960	US-09-841-835-8	US-09-841-835-10	US-09-841-835-2	US-09-972-115A-8	US-10-199-937-4	US-10-425-114-56041	US-10-424-599-275468	US-10-425-114-57763
		12	12	12	12	15	14	12	0	9	0	10	14	12	12	12
	Query Match Length DB	151	151	131	131	445	688	263	673	949	1327	1327	1327	369	486	507
%	Query Match	68.4	68.4	58.3	58.3	14.3	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.5	11.5	11.5
	Score	530	530	452	452	111	91	90.5	90.5	90.5	90.5	90.5	90.5	60	в 6	в 0
	Result No.		01	m	4	S	9	7	ω	6	10	11	12	13	14	15

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	RESULT 1  US-09-741-873B-4  Sequence 4, Application US/097; PUDLICATION NO. US20020081722A  GENERAL INFORMATION: APPLICANT: OLSON, Staffan APPLICANT: OLSON, ARM TILLE OF INVENTION: Fibronect FILE REFRENCE: 01289-084 CURRENT APLICATION NUMBER: US PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-10 PRIOR FILING DATE: 1991-11-06 PRIOR FILING DATE: 1991-11-06 PRIOR FILING DATE: 1994-01-28 PRIOR FILING DATE: 1994-01-28 PRIOR FILING DATE: 1994-01-28 PRIOR FILING DATE: 1994-10-05 NUMBER OF SEQ ID NOS: 10 NUMBER OF SEQ ID NOS: 10 NUMBER OF SEQ ID NOS: 10 NUMBER OF SEQ ID NOS: 10 TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT TYPE: PRT T

1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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Query Match 68.4%; Score 530; DB 12; Length 151; Best Local Similarity 69.5%; Pred. No. 7.2e-46; Matches 105; Conservative 19; Mismatches 27; Indels

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Gaps

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US-09-741-873B-4

Publication No. US20040096965A9

Publication No. US20040096965A9

GENERAL INFORMATION:
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 08/09/74,873B

CURRENT APPLICATION NUMBER: US 08/978,878

PRIOR PILING DATE: 1989-05-06

PRIOR FILING DATE: 1989-05-06

PRIOR FILING DATE: 1989-05-07

PRIOR PELING DATE: 1991-11-06

PRIOR PLING DATE: 1991-11-06

PRIOR PLING DATE: 1991-11-06

PRIOR PLING DATE: 1994-01-28

PRIOR PLING DATE: 1994-01-28

PRIOR PLING DATE: 1994-01-05

PRIOR PLING DATE: 1994-10-05

PRIOR PLING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 151
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                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGPRNNATIDQWNAKNYDQLVTRVVT 120
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Publication No. US20020081722A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
1 MKLIKVAAIAAIVFSGSAVAGVVPQYGGGNHGGGGNNSGPNSELNIYQYGGGGNSALALQ 60
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                                                                                                                                                        121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                     121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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US-09-741-873B-4
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US-09-741-873B-2
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US-09-741-873B.

US-09-741-873B.

Sequence 2, Application US/09741873B

Publication No. US2004009665A9

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Normark, Staffan

TITIE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 01289-084

CURRENT FILING DATE: 2003-04-04

PRIOR PLLING DATE: 1998-05-06

PRIOR PELING DATE: 1998-05-06

PRIOR PELING DATE: 1997-11-26

PRIOR PELING DATE: 1997-11-26

PRIOR PELING DATE: 1997-11-06

PRIOR PELING DATE: 1997-11-06

PRIOR PELING DATE: 1997-11-06

PRIOR PELING DATE: 1997-11-06

PRIOR PELING DATE: 1994-01-08

PRIOR PELING DATE: 1994-01-08

PRIOR PELING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NOS: 10

SOFTWARE: Patentin Version 3:0

LENGTH: 131

TYPE: PRI

US-09-741-873B-2
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Best Local Similarity 66.4%; Pred. No. 5e-38;
Matches 87; Conservative 18; Mismatches 26;
         PRIOR FILING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-26
PRIOR APPLICATION WUMBER: US 07/347,189
PRIOR APPLICATION WUMBER: US 07/347,189
PRIOR APPLICATION WUMBER: US 07/789,437
PRIOR FILING DATE: 1998-05-04
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION WUMBER: US 08/187,865
PRIOR APPLICATION WUMBER: US 08/187,865
PRIOR APPLICATION WUMBER: US 08/187,865
PRIOR APPLICATION WUMBER: US 08/187,865
PRIOR APPLICATION WUMBER: US 08/187,865
PRIOR PRIOR DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
SOFTWARE: PATENTING DATE: 1994-10-05
SOFTWARE: PATENTING DATE: 1994-10-05
SEQ ID NOS: 10
SEQ ID NOS: 10
SEQ ID NOS: 10
FILING DATE: 1998-05-06
APPLICATION NUMBER: US 08/978,878
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CRGANISM: Escherichia coli
US-09-741-873B-2
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DB 12; Length 131;

58.3%; Score 452;

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Length 688;

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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545 KSKKKSNFDNNSNS---ALNNLDKSKLKINTWEITNISETTSNSSSPVINLNHGGRSS 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 IELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                               488 GNNNGSGNSSGTTNNSNNYNNKSISKKNEIDDGDDLNPISITNN---TGLINNNNSKSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: 12
CORRESPONDENCE ADDRESS:
ADDRESSED: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 GGMGGGANGAYGSGAGGGGVGKGEGVSGVALAPSSNGYYNGGAAD 182
                                                                                                                                                                                                                                                                                                59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 -----YGNGA--DVGQGADNSTIEL--TQNGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 90.5; DB 12;
27.9%; Pred. No. 0.62;
iive 15; Mismatches 39;
                                                                                                                                                                                                                                          Query Match
11.7%; Score 91, DB 14;
Best Local Similarity 23.7%; Pred. No. 1.9;
Matches 28; Conservative 25; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; CTHER INFORMATION: Clone ID: 700071884_FLI.pep
US-10-425-114-49960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 49960, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
     CURRENT FILING DATE: 2001-12-2
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Detentin version 3.1
SEQ ID NO 7876
LENGTH: 688
                                                                                                                                        ) TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-114-49960
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US-09-841-835-8
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Fublication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Geo, Yongwei
APPLICANT: Glodan, Barry S.
APPLICANT: Glodan, Barry S.
APPLICANT: Glodan, Barry S.
APPLICANT: Glodan, Barry S.
APPLICANT: Glodan, Barry S.
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APPLICANT: Glodan, Barry S.
APPLICANT: Glodan, Barry S.
APPLICANT: Glodan, Barry S.
APPLICANT: Barry S.
APPLICANT: Slade, Sarry S.
APPLICANT: Salo(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
FRIOR FILING DATE: 2003-02-21
                                                                                                                                                                                           140
                                                                                                                                                                                                                      RESULT 6

US-10-032-585-7876

Sequence 7876, Application US/10032585

Publication No. US20030180953A1

GENERAL INFORMATION:

APPLICANT: Perry, Roemer D.

APPLICANT: To, Jiang

APPLICANT: Howard, Bussey

TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery

FILE REFERENCE: 10182-005-999

CURRENT APPLICATION NUMBER: US/10/032,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 GNSNSV-----GRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110
                                                                                                                                        09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 AAFAADSNIVYINQIGNDQQANIIQSGNGNSVGAFNGNSGFIQENGTLSGA-NLLIVKQS 77
                                                                                                                     1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                                       21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                           81 VGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQV
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Indels 30; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 YDQLVTRVVTHEMAHAN----QTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 DPGVFNKITQDSSSNGSKVSVIQDGKNNVFSIKQGNTGNSTSVNQ 174
LOCATION: (1)..(445)
CTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20638
          ; Pred. No. 5e-38
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Rhodopseudomonas palustris
          66.4%;
        Best Local Similarity 66.49
Matches 87; Conservative
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Best Local Similarity
Matches 42; Conserv
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US-10-369-493-20638
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7,4

Gaps

21;

Indels

Length 263;

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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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US-00-841.835-2
US-00-841.835-2
Patent No. US20020076795A1
Patent No. US20020076795A1
GENERAL INPORMATION:
APPLICANT: de Lange, Titia
APPLICANT: SMith, Submortain THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%; Score 90.5; DB 9; Length 949; 28.4%; Pred. No. 3.1; ive 16; Mismatches 61; Indels 2
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CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
CONPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATCHIN Release #1.0, Version #1.30
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411 Hackensack Avenue, 4th Floor
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Best Local Similarity 28.48
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-09-841-835-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.7%; Score 90.5; DB 9; I
Best Local Similarity 28.4%; Pred. No. 2;
Matches 42; Conservative 16; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-487-5800
TELEPAX: 201-33-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
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CITY: Hackensack
STATE: New Jersey
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                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
Hackensack
: New Jersey
<Y: USA
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                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-841-835-8
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US-10-199-937-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                        99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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| Publication No. US20030032769A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Geron Corporation
| APPLICANT: Geron Corporation
| APPLICANT: Malter, Funk D.
| APPLICANT: Malter, Funk D.
| TITLE OF INVENTION: A Second Mammalian Telomerase
| FILE REFERENCE: 080/033C
| CURRENT APPLICATION NUMBER: US 60/128,577
| PRIOR APPLICATION NUMBER: US 60/128,577
| PRIOR PELING DATE: 2000-04.10
| PRIOR FILING DATE: 2000-04.10
| PRIOR FILING DATE: 1999-04.13
| NUMBER OF SEQ ID NOS: 64
| SEQ ID NOS: 64
| SEQ ID NOS: 64-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                ; Score 90.5; DB 9;
; Pred. No. 4.8;
16; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                     121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 ----ANVNAKDMAGRKSSPLHFAAGFG 227
11.7%;
Local Similarity 28.4%;
les 42; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.4%
Matches 42; Conservative
                                                                                              TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-8
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US-09-841-835-2
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RESULT 12 US-10-199-937-4

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Sequence 5641, Application US/10425114
; Sequence 5641, Application No. US2004003488BA1
; Sequence 5641, Application No. US2004003488BA1
; Publication No. US2004003488BA1
; APPLICANT; Liu, Jingdong
; APPLICANT; Zhou, Yihua
; APPLICANT; Cao, Yongwei
; APPLICANT; Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION UNMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALOSDAR
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11.5%; Score 89; DB 12; Length 369;
Best Local Similarity 26.3%; Pred. No. 1.4;
Matches 36; Conservative 20; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                               APPLICANT DeMaggio, Anthony J.
APPLICANT Goldman, Phyllis S.
APPLICANT Goldman, Phyllis S.
APPLICANT Goldman, Phyllis S.
TITLE REPERENCE: 27866/36559
CURRENT APPLICATION TANKTRASE2 MATERIALS AND METHODS
FILE REPERENCE: 2066/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 90.5; DB 14;
llarity 28.4%; Pred. No. 4.8;
Conservative 16; Mismatches 61;
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US-10-425-114-56041
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Sequence 4, Application US/10199937
Publication No. US20030190739A1
GENERAL INFORMATION:
APPLICANT Christenson, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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Best Local Similarity
Matches 42; Conserv
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US-10-425-114-56041
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Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA Rosa Thomas J
APPLICANT: Expos Thomas J
APPLICANT: Cao Younge
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Asonomic Role of the Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SIG ID NOS: 73128
SEQ ID NO 57763
LENGTH 507
                        180 GFGGGGNV----SRSKSTQDMY-TRAELEASAANKEDFFARKRAENESRPEGLPPSQG 232
74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVVTHEMAHANQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 89; DB 12; Length 486; 26.3%; Pred. No. 1.9;
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US-10-425-114-57763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CTHER INFORMATION: Clone ID: PAT_MRT3847_90769C.1.pep
US-10-424-599-275468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57763, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                              116 G---KYVGFGSGPAPNQ 129
                                                                                 134 SVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 SVMVRQVGFGNNATANQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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ORGANISM: Glycine max
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Matches 36, Conserv
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US-10-424-599-275468
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US-10-425-114-57763
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LENGTH: 486
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Sequence 30,
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Sequence
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: White, Aaron P.
APPLICANT: White, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REPERBUCK: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF.SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
                                                                                                                                                                                                                                                                                                   US 09-252 691-5834

US 09-252 6910-5834

US 09-252-6910-5834

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US-09-543-407-24

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   US-09-543-407-24
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     2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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                                                                                                                                                                         UŠ-09-543-407-24
775
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                             version 5.1.6
- 2004 Compugen Ltd.
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SUMMARIES

ij

Query Match Length DB

Score

Result

hits satisfying chosen parameters: 6019581 segs, 976053577 residues

Total number of

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Perfect score:

Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

seq length: 0 seq length: 2000000000

Minimum DB s Maximum DB s

7

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APPLICANT: Kay, William W.
                                                                                                                                                                                                            ; OTHER INFORM?
US-09-543-407-30
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                                                                             LENGTH: 151
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                                                                                                   TYPE: PRT
                                                                                                                                           FEATURE:
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                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Col, Innon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 92043.407
CURRENT APPLICATION NUMBER: US/09/543,407
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                                       Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.1%; Score 714; DB 19; Length 151; Best Local Similarity 91.1%; Pred. No. 9.2e-68; Matches 144; Conservative 0; Mismatches 0; Indels 1.
                                                                               Indels
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                                   100.0%; Score 775; DB 19;
100.0%; Pred. No. 2.7e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                             121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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GENERAL INFORMATION:
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                                                                               Conservative
                                     Query Match
Best Local Similarity
Matches 151; Conserv
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US-09-543-407-30
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US-09-543-407-24
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LENGTH: 151
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                        OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                 Length 151;
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APPLICANT: White, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                           90.3%; Score 700; DB 19;
89.9%; Pred. No. 2.9e-66;
iive 0; Mismatches 0;
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ilarity 91.4%; Pred. No. 3.4e-65;
Conservative 2; Mismatches 11;
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
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US-08-233-642A-57
Gequence 57, Application US/08233642A
, GENERAL INFORMATION:
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                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.9
Matches 143; Conservative
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Best Local Similarity
Matches 138; Conserv
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121 NNAALVNYDQLVTRVVTHEMAHA-----
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
                                                    ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-543-407-26
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APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
STREF: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTY: U.S.A.
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88.9%; Score 689; DB 6; Length 151;
Best Local Similarity 91.4%; Pred. No. 4.4e-65;
Matches 138; Conservative 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

CIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BATCH COMPATION
SOFTWARE: PATCHNES: PC-DCS/NS-DOS
SOFTWARE: PATCHNIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 26-APR-1994
ATTCRNEY/AGENT INFORMATION:
NAME: King Joshus
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
TELEPRATION NUMBER: 35,570
TELEPRATION NUMBER: 35,570
TELEPRATION INFORMATION:
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TELEX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 151 amino acids
amino acid
3Y: linear
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US-09-543-407-12
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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Sequence 22, Application US/09543407

SEQUENCE 22, Application US/09543407

SEQUENCE 22, Application US/09543407

SEQUENCE 22, Application US/09543407

APPLICANT White, Aaron P.

APPLICANT Collinson, S. Karen

APPLICANT Kay, William W.

TITLE OF INVENTION BEATERIAL FINBRIAL SYSTEM FOR

TITLE OF INVENTION BEATERIAL FINBRIAL SYSTEM FOR

TITLE OF INVENTION BRESSHYATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT FAPLICATION UNBER: US/09/543,407

CURRENT FILING DAME: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE FASTSEQ for Windows Version 4.0

LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEMAHADOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
78.6%; Score 609; DB 19; Length 151;
Best Local Similarity 73.6%; Pred. No. 1.6e-56;
Matches 128; Conservative 0; Mismatches 0; Indels 46;
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 -----NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                   Length 151;
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                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                   Query Match

84.5%; Score 655; DB 19;
Best Local Similarity 79.8%; Pred. No. 1.9e-61;
Matches 134; Conservative 0; Mismatches 0;
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TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 118; Conserva
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT: White, Aeron P.

APPLICANT: Doran, James L.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

FILE REFERENCE: 92004,9407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENGHH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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APPLICANT: Collinson, S. Karen
APPLICANT: Ray, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FINESCOURDED
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 609; DB 19;
Pred. No. 1.6e-56;
4; Mismatches 23;
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US-09-543-407-18
; Sequence 18, Application US/09543407
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.6%;
Best Local Similarity 82.1%;
Matches 124; Conservative
                                                                                                                                                                                                                                          TYPE: PRT
ORGANT
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                                                                                                                                                                                                                      SEQ ID NO 26
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                 APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICANTON NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 92043.4466
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILE SECOND NOS: 59
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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ilarity 90.1%; Pred. No. 5.9e-56;
Conservative 2; Mismatches 11;
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82.1%; Pred. No. 3.4e-56;
tive 5; Mismatches 22;
                                       121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                 61 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQV 120
                                                                  81 VGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
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MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
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APPLICANT: White, haron P.
APPLICANT: Woran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, william W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NOMBER: US/09/543,407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for windows Version 4.0
SEQ ID NO 16
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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77.4%; Score 600; DB 19;
Best Local Similarity 81.5%; Pred. No. 1.5e-55;
Matches 123; Conservative 3; Mismatches 25;
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                                                                                                                                                                                                                                                                                       US-09-543-407-28; Sequence 28, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-543-407-16; Sequence 16, Application US/09543407; GENERAL INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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US-09-543-407-28
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NORMARK.
TITLE OF INVENTION FIBROHECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
FABLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1998-05-06
                                                                                                                                                                                                                                    MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
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APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543, 407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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Recombinant Salmonella enteritidis 3b afgh sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                                                                            Length 151;
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                                                                                                                          Score 575; DB 19; Length 1 Pred. No. 7.2e-53; 5; Mismatches 23; Indels
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Best Local Similarity 81.5%;
Matches 123; Conservative
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Best Local Similarity 70.2<sup>3</sup>
Matches 106; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
                                                   ; OTHER INFORMATION:
US-09-543-407-16
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US-09-543-407-7
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US-08-978-878-4
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Sequence 602, App Sequence 603, App Sequence 607, App Sequence 110, App Sequence 577, App Sequence 609, App Sequence 377, App Sequence 31875, Sequence 351875,

ALIGNMENTS

4, Appli 51, Appli 51, Appl 654, App 554, App 570, App 570, App 571, App 602, App 602, App 603, App 603, App 603, App 603, App

Sequence Sequence

PCT-USO4-09385-4 US-10-809-790-4 US-10-809-790-4 US-10-724-972A-4638 US-60-566-425-574 US-60-566-425-574 US-60-566-425-571 US-60-566-425-571 US-60-566-425-571 US-60-566-425-571 US-60-566-425-573 US-60-566-425-573 US-60-576-812-602 US-60-576-812-602 US-60-576-812-603 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610 US-60-576-812-610

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Sequence 4, Application US/09741873C

Sequence 4, Application US/09741873C

Sequence 4, Application US/09741873C

APPLICANT: Normark, Staffan

APPLICANT: Normark, Staffan

APPLICANT: Oleen, Arne

FILE FOR INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE FERRENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873C

FRIOR APPLICATION NUMBER: SE 8801723-1

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1994-11-03

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 11

PROMPTER OF SEQ ID NOS: 11

PROMPTER PRIOR PRIOR PRIOR PARENTION NUMBER: US 08/187,865

PRIOR FILING DATE: 1994-10-05

PRIOR PRIOR FILING DATE: 1994-10-05

PRIOR PRIOR PRIOR PARENTON NUMBER: US 08/187,865

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ORGANISM: Escherichia coli
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Query Match
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Matches 105; (
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Sequence 49, Appl
Sequence 30134,
Sequence 17304,
Sequence 2, Appl
Sequence 2, Appl
Sequence 7907, Ap
Sequence 7907, Ap
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 285216,
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Sequence 21109, A
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Sequence 2, Appli
Sequence 17559, A
Sequence 300390,
Sequence 312468,
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Sequence 21, Appl
                                                                                           2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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Sequence
Sequence
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1: /cgn2_6/ptcdata/2/paa/USO5_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/USO5_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO7 NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

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5: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*
              version 5.1.6
- 2004 Compugen Ltd.
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US-09-741-873C-4
US-09-748-73C-2
US-09-248-796A-17559
US-10-425-115-312468
US-10-170-205E-35751
US-10-170-205E-3751
US-10-170-205E-741
PCT-US04-02338-49
US-10-170-205E-741
PCT-US04-02338-49
US-10-425-115-3136
PCT-US04-1492-88
US-10-425-115-346132
US-10-425-115-368-15
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Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
              GenCore
Copyright (c) 1993
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68.4%; Score 530; DB 5; Length 151; 69.5%; Pred. No. 1.8e-39; Live 19; Mismatches 27; Indels

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APPLICANT: In CONTROL of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society of Society 
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APPLICANT: Es Rosa, Thomas J.
APPLICANT: Es Rosa, Thomas J.
APPLICANT: Covo, Yihus
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE BEFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 312468
LENGTH: 295
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30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                                                                             90 IELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                        576 KSKKKSNFDNNSNS---ALNNLDKSKLKINTNEITHISETTSNSSSPVINLNHGGRSS 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 SALAGVVPQWGGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 90.5; DB 6; Length 258; ilarity 27.9%; Pred. No. 2.1; Conservative 15; Mismatches 39; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 -----YGNGA--DVGQGADNSTIEL--TONGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_37025C.1.pep
US-10-425-115-300390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
US-10-425-115-312468
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Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: unsure at all Xaa locations FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 300390, Application US/10425115 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-425-115-312468
; Sequence 312468, Application US/10425115
; GENERAL INFORMATION:
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33.3%;
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Best Local Similarity
Matches 29; Conserv
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Best Local Similarity
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                         US-10-425-115-300390
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GENERAL INFORMATION:
APPLICANT: Keith Weinsteck et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: 1899-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                 APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERENCE: 01289-084
FILE REPERENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
FRICE APPLICATION NUMBER: US 8801723-1
FRICE APPLICATION NUMBER: US 80978,878
FRICE APPLICATION NUMBER: US 08/978,878
FRICE APPLICATION NUMBER: US 07/347,189
FRICE APPLICATION NUMBER: US 07/347,189
FRICE APPLICATION NUMBER: US 07/39,437
FRICE APPLICATION NUMBER: US 07/789,437
FRICE APPLICATION NUMBER: US 07/789,437
FRICE FILING DATE: 1991-11-03
FRICE FILING DATE: 1992-11-03
FRICE FILING DATE: 1994-10-28
FRICE FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SEQ ID NO S: 11
FRICE PRODE THE TRANSION NUMBER: US 08/318,519
FRICE FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.7%; Score 91; DB 5; Length 719;
Best Local Similarity 23.7%; Pred. No. 6.2;
Matches 28; Conservative 25; Mismatches 59; Indels
                                       Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                                      APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans
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US-09-248-796A-17559
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; ORGANISM: Candid
US-09-248-796A-17559
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LENGTH: 719
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APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF TITLE OF INVENTION: USE
FILE REPERENCE: EXO4-003C-PC
CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT APPLICATION NUMBER: US60/443,484
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR PILING DATE: 2003-01-29
PRIOR PELING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR PILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US60/461,789
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR PILING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR SPLING DATE: 2003-05-14
PRIOR SPLING DATE: 2003-05-14
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR PILING DATE: 2003-05-14
PRIOR PILING DATE: 2003-05-14
PRIOR SPLING DATE: 2003-05-14
PRIOR SPLING DATE: 2003-05-19
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VEISION 3.2
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION WINDER: US/10/170,205E
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 741
LENGTH: 1203
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                                                                                                                                                                                         403 GYGAGAAAAGAGAAAAGAGSYSG----SISRLSSA---EAVNRVSSNIGAVASGGASAL 454
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                                                                       347 AGAGAAAASAGAGAGGYGGGYGVAGGSS----ISYGATSSSATSSSTASSSRSGIVTSG 402
                                                                                                                                               GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
15 SGSALAGVVPQWGGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
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11.7%; Score 90.5; Di
Best Local Similarity 28.4%; Pred. No. 13;
Matches 42; Conservative 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 741, Application US/10170205E; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                455 PGVISNIFSGVSSSAGSY 472
                                                                                                                                                                                                                                                                                               134 SVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens US-10-170-205E-741
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US-10-170-205E-741
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PCT-US04-02338-49
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GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
FILE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 35551
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GENERAL INFORMATION:
APPLICANT: Bond A. Roth
APPLICANT: Randolph V. Lewis
APPLICANT: Randolph V. Lewis
APPLICANT: The University of Wyoming
TITLE OF INVENTION EXPRESSION of Spider Silk Proteins in Higher Plants
FILE REFERENCE: WYO. 02-0004US
CURRENT APPLICATION NUMBER: US/10/479,638
CURRENT FILING DATE: 2003-12-03
FRIOR APPLICATION NUMBER: FCT/US02/18256
FRIOR APPLICATION NUMBER: 60/296,184
FRIOR FILING DATE: 2001-06-06
FRIOR FILING DATE: 2001-06-06
FRIOR FILING DATE: 2001-06-06
FRIOR FILING DATE: 2001-06-06
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FRIOR FILING DATE: 2001-06-06
FRIOR FILING DATE: Z001-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-------DVSRVKRLVDA--- 204
                                                                                                                                                           138 YGGGGYSSGGGYSSG-GYAANGYGVGSGSGNYSNASGGGYSGS----DGYGNGAASGGYA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                      26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Indels 29; Gaps
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; Pred. No. 2.5;
16; Mismatches 61; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 11.7%; Score 90.5; DB 6; Length 520; I Similarity 24.6%; Pred. No. 4.8; 34; Conservative 27; Mismatches 64; Indels 1
                  44; Indels
                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                      193 NNLSSGYNSNGRYNTIGSSDGNTGGYN 219
                                                                                                                                                                                                                                      86 DNSTIELTQNGFRNNATIDQWNAKNYD 112
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Best Local Similarity 28.4%;
Matches 42; Conservative 1.
                      29; Conservative
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-170-205E-35751
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US-10-479-638-21
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LENGTH: 520
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RESULT 12
PCT-USO4-21492-88
; Sequence 88, Application PC/TUS0421492
; Sequence 88, Application PC/TUS0421492
; GENERAL INFORMATION:
; APPLICANT: Diversa Corporation
; APPLICANT: Callen, Walter
; APPLICANT: Pulliam, Derrick
; APPLICANT: Pulliam, Derrick
; TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN; TITLE OF INVENTION: THEM
; TITLE OF INVENTION: THEM
; FILE REPRENCE: S6462003540
; CURRENT APPLICATION NUMBER: PCT/US04/21492
; CURRENT APPLICATION NUMBER: 604484,725
; PRIOR APPLICATION NUMBER: 604484,725
; NUMBER OF SEQ ID NOS: 518
; NUMBER OF SEQ ID NOS: 518
; SOFTWARE: Patent In version 3.1
                                                                                                                      9
                                                                                                                                                                                                                                                                                              177 PELTNAGNIGLAKGTAPASISAIYGESPSADYSKSGAIGVVPATYLNISGAPIGSLNIAG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 NAALALQSDARKSETTITQ-----SGYGNGADVGQGADNSTIELT-QNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 IVVNGQTRQAENQSVNTGVWANNQCGGSGNSEWLHCNGYISFGNVSGSSSSSSSSSSSSSSS 420
                                                                                                                                                                    30 GNHNGGGNSSGFDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                                                                                                                                                                                               90 IELTQNG------FRNNATIDQWNAKNYDQL-VTRVV--THEMAHANQTAS-DSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 IVVSG-----SALAGVVP--QWGGGGN----HNGG----GNSSGPDSTLSIYQYGSA
                                                                                                                      29;
                                                                                                                                                                                                11.0%; Score 85; DB 1; Length 535; 25.0%; Pred. No. 15; ive 19; Mismatches 62; Indels
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Obtained from an environmental sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TVNGSGTAVTTIG 506
                                                                 ; Score 85.5; DB 5;
; Pred. No. 9.4;
16; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 WNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-491-733-2; Sequence 2, Application US/10491733; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           :| |||:|: |
237 VVGGAGFGDNSNTSSY 252
                                                                 Query Match'
Best Local Similarity 27.9%;
Matches 38; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 WGVSNFTGRTISV-----
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Best Local Similarity 25.0%
Matches 39; Conservative
; ORGANISM: Candida albicans
US-09-248-796A-17306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
PCT-US04-21492-88
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Sequence 17306, Application US/09248796A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: EOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
TYPE: PRI
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FILE REFERENCE: 38-2153223 B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 301334
LENGTH: 256
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                                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                          158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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                                                                                                                      29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
                                                                      Length 1327;
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Best Local Similarity 27.9%; Pred. No. 2.6;
Matches 29; Conservative 14; Mismatches 40; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 SGYGNGAD------VGQGADNSTIEL--TQNGFRNNATID 104
                                                                                                                    Indels
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                                                                                                                    61;
                                                                 Query Match 11.7%; Score 90.5; DB 1; Best Local Similarity 28.4%; Pred. No. 14; Matches 42; Conservative 16; Mismatches 61;
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US-10-425-115-301334
                                                                                                                                                                                                                                                                                                                                                                                                ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 301334, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
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US-10-425-115-301334
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US-09-248-796A-17306
     ; OKGANISH: xxcm.
PCT-US04-02338-49
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                            St
APPLICANT: Weislo, Laura J.

TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic STITLE OF INVENTION: Resistance, Yield, Disease Resistance and Nutritional Quality & FILE REPERENCE: 60127WOPT.

CURRENT APPLICATION NUMBER: US/10/491,733

CURRENT PILING DATE: 2004-04-05

PRIOR APPLICATION NUMBER: 60/334,501

PRIOR PILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NS-10-425-115-346132

| Sequence 346132, Application US/10425115
| Sequence 346132, Application US/10425115
| GENERAL INFORMATION: Thomas J.
| APPLICANT: Evalic, David K.
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
| FILE REFERENCE: 38-21(53222)B
| CURRENT EPPLICANTION NUMBER: US/10/425,115
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 LAGVVPQWGGGG-----NHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSBTTI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 SALAG-----GGGG--GGGGGGGGCKD-----FGSMAMDELLRSIWTAEESQAMASASG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQS--DARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 SAAGVGVAVGAPPISLQ-RQGSLTLPRTL---SAKTVDEVWRNLVRDE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 YGNGADVGOGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.8%; Score 83.5; DB 6; Length 179; ilarity 30.4%; Pred. No. 5.8; Conservative 8; Mismatches 33; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 31.5%; Pred. No. 12;
Matches 34; Conservative 15; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: MRT4577_78839C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 EESGNNQNAGAGAGA-----ENGAANNGT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 TOSGYGNGADVGQGADNSTIELTQNGFRNNAT 102
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; Sequence 7907, Application US/60565632
; General INFORMATION: Technology, LLC
APPLICANT: Monsanto Technology, LLC
APPLICANT: Baum, James A
, APPLICANT: Kovalic, David K.
, APPLICANT: Lu, Maolong
                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Oryza sativa
US-10-491-733-2
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Matches 28; Conserv
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ORGANISM: Zea mays
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LENGTH: 179
                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 376
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APPLICANT Munyikwa, Tichifa R. I.
APPLICANT Roberts, James K.
APPLICANT W., Wei Bei
APPLICANT W., Wei Bei
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
FILE REPERDICE: 38-21 (53403) B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 AAADNNGSADAA-----QGNDNRAAAENNANADAQTDAAQ-GSANEANAENNANADAQND 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ARKSETTITQSGYGNGADVGQGADN-STIELTQN----GFRNNATID------QMNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AAQANDNGAAAENNGNADAAQGTDNEAAAENSGNENGTGAENNANADAQTDVAQGSTNEA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA-----LQSD 62
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10.8%; Score 83.5; D
Best Local Similarity 27.8%; Pred. No. 22;
Matches 45; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2, 2004, 15:29:54
Munyikwa, Tichifa R.
Roberts, James K.
Wu, Wei
                                                                                                                                                                                                                                                                                                                      LENGTH: 573
TYPE: PRT
ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August
Job time : 17.8 secs
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(0108N) YUD/8 @60d S/4/

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-543-407-24 775 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

<b>5</b> 3	Description	fimbrin protein ag	major curlin chain	curlin protein csg	curlin major subun	hypothetical prote	hypothetical prote	cnjB protein - Tet	fimbrin protein ag	nucleation compone	curlín nucleator p	minor curlin subun	curlin minor chain	probable PPE prote	probable sugar ABC	DNA-binding protei	ovo protein - frui	conserved hypothet	hypothetical prote	merozoite 45K surf	glycine-rich prote	tail fiber protein	F3F19.21 protein -	hypothetical glyci	RNA-binding protei	leishmanolysin (EC		leishmanolysin (EC	leishmanolysin (EC	leishmanolysin (EC
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	CT147 hypothetical	conserved hypothet	probable disease r	probable PPE prote	probable secreted	protein C05B5.3 [i	protein kinase sgg	hypothetical prote	hypothetical prote	probable sugar ABC	hypothetical prote	hypothetical prote	hemolysin [importe	leishmanolysin (EC	hypothetical prote	probable outer mem
	F86509	C81558	G84687	F70675	T35789	C88571	835327	866852	A83401	AC1182	H71607	T19581	AI0452	C42049	T05221	F90892
	7	~	7	7	7	N	~	(1	7	(7	7	~	N	N	N	(7
	1537	1537	447	585	438	401	575	296	340	439	764	423	1635	639	343	382
	11.2	11.2	11.1	11.1	11.0	11.0	11.0	11.0	10.9	10.8	10.8	10.8	10.8	10.7	10.6	10.6
is	87	87	86	.86	85.5	85	8 2	85	84.5	84	84	83.5	83.5	83	82.5	82
	30	31	32	33	34	35	36	37	33	М	40	41	4.2	43	44	45

## ALIGNMENTS

RESULT 1 JC6039 fimbrin protein agfA precursor - Salmonella enteritidis	C;Species: Salmonella enteritidis C;Date: 31.Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C:broesion: IT6619: PC6015: A44898	R. Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.	J. Baccellol. 176, 802-807, 1379 A,Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A,Reference number: JC6039; MUID:96146512; PMID:8550497	A, Modecule type. DNA A:Residues: 1-151 < COL>		A; Molecule type: protein A; Residues: 21-52 <co2></co2>	A,Experimental source: strain 27655-3b A,Note: the authors translated the codon ACG for residue 44 as Ile	R;Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. J. Barreriol, 173, 4773-4781, 1991	A,Title: Purification and characterization of thin, aggregative fimbriae from Salmonell A,Reference number: A44898; MUID:91310586; PMID:1677357	A; Contents: 27655	A) factors preliminary  M. Martin preliminary	A, Mossiques: 21-33 < COS *** * Wateridues: 21-33 < COS *** * Wateridues: 21-33 < COS *** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** * Wateridues: 21-33 ** *		n: major component of thin aggregative fimbriae	A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C:Kevwords: fimbria	$F_1 = 20/Domain:$ signal sequence #status predicted <sig> $F_2 = 21-151/Product:$ fimbrin protein agfA #status experimental <mat></mat></sig>	Query Match Best Local Similarity 91.4%; Pred. No. 4.7e-51; Matches 138; Conservative 2; Mismatches 11; Indels 0; Gaps 0;	Qy 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIXQYGSANAALALQ 60	Db 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	Qy 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120	Db 61 SDARKSETTITQSGYGNGADVGQADNSTIELTQNGFRNNATIDQWNARNSDITVGQYGG 120	Qy 121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151	
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Gaps

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A)Description: major component of wild-type curli, interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers Fi-20/Domain: signal sequence #status predicted <SiG>F:21-151/Product: curlin #status experimental <MAT>
A,Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A,Reference number: S31202, MUID:93211294, PMID:8459772
A,Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain R C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: D90806 R; Advanti, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Tile: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and (A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAXNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Residues: 1-152 <HAY>
A,Cross-references: GB:BA000007, PIDN:BAB34843.1, PID:g13360880, GSPDB:GN00154
A,Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-133,'RQRDSGWLW' <0LS3>
A;Cross-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.8%; Score 533; DB 2; 70.2%; Pred. No. 7.1e-38; iive 18; Mismatches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                        A; Molecule type: DNA
A; Residues: 1-6, VV, 8-151 <01.51>
A; Cross-references: BMBL:L04979
A; Accession: 834560
A; Molecule type: protein
A; Residues: 21-42;44-50
R; Olsen, A.N.; Arnqvist, A.M.
B; Reference number: 834559
A; Accession: 834559
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C; Function:
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hes 106;
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NyAlternate names: csgA protein, major curlin protein
Cippedies: Escherichia coli
Cippedies: Escherichia coli
Cipate: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
Cipate: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
Cipate: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
Cipate: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
Cipate: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
Rimmarx, M.; Arngwist, A.; Bain, 2.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A; Title: Expression of two csg operons is required for production of fibronectin- and Cc A; Reture: nucleic acid sequence not shown; translation not shown
A; Molecule Pype: DM
A; Residues: 1-151 cHAM>
A; Reserve represented sequence was submitted to the EMBL Data Library, August 1995
A; Roses Du; Mau, B; Shao, Y.
Conserveference: Ad4720; MulD:97426617; PMID:9778503
A; Reture: number: A64720; MulD:97426617; PMID:9778503
A; Reture: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Reserved Biands
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                                                                                                                                                                              major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Typhi (5)Species: Salmonella enterica subsp. enterica serovar Typhi A,Note: Salmonella enterica subsp. enterica serovar Typhi G,Date: Obvor-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C,Accession: A10635 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C,Accession: A10635 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C,Accession: A10635 P; Cromer, C.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cromin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A,Athcher Complete genome sequence of a multiple drug resistant Salmonella enterica serova A,Reference number: AB0502; MUID:21534947; PMID:11677608
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R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S.
Mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
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Pred. No. 4.7e-51;
2; Mismatches 11
   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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91.4%;
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Matches 138; Conserv
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Approcession; 3242.03

A; Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
A; Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
A; Cross-references: EMBL: 10.87.10
B; Martindale; D.W.; Taylor, F.W.
Nucleic Acids Res. 16, 2189-2201, 1988
A; Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A; Reference humber: 803650; MUID:88189811; PMID:3357771
A; Recession: 803650
A; Molecule type: DNA
A; Residues: 236-250, 'I', 252-255, 'N', 257-773 < MAR>
A; Residues: 236-250, 'I', 252-255, 'N', 257-773 < MAR>
A; Residues: 236-250, 'I', 252-255, 'N', 257-773 < MAR>
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A; Residues: 236-250, 'N', 257-773 < MAR>
A; Residues: 236-250, 'N', 257-773 < MAR>
A; Residues: 236-250, 
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Cipecies: Tetrahymena thermophila
Cipecies: S42136; S42136; S30509
Right of the EMBL Data Library, October 1992
A;Reference number: S42136
A;Rolecule type: DNA
A;Residues: 1-1748 <TAX>
A;Cross-references: EMBL: L03710; NID:g161751; PID:g161752
R;Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats in a protein enco A;Reference number: S42135; MUID:94051569; PMID:8233798
A;Accession: S42135; MUID:94051569; PMID:8233798
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---SNQTNNESS--- 1722
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                             ATIDOWNAK 109
                                                                                             192 YONNOGRHOGOGGGHSSSSNSVMSNNGYSSNSGYGNNNGPTPSFLNNVSSSAAODYYNIV 251
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Best Local Similarity 28.0%; Pred. No. 3.1;
Matches 37; Conservative 16; Mismatches 31; Indels 4
                                                                                                                                                                                                                 | | | | : : | | : | | : | | : | | | NKSLTTNQINEQ---ASNWASANSVQAQYIQYETNRSA 287
                                                                                                                                                                    NYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATA
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                                 YGN - - GADVGQGADNSTIE - - - LTQNGFRNN
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                                                                                                                                                                                                                                                                                                                              hypotherical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: L6.Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: H85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew liler', L., Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H8565
A;Status: preliminary
A;Residues: DNA
A;Residues: L-152 csTO>
A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:216
A;Gene: csgA
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60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVV 119
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A;Experimental source: clone F13E9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F13E9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
C;Accession: T20847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGGNSALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%; Score 511.5; DB 2; Length 152; 68.4%; Pred. No. 4.6e-36; ive 19; Mismatches 28; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 2; Length 409; 0.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
                                                                                                                                                  121 GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 THEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                     120 THEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%; Score 101; 23.3%; Pred. No. 0
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Best Local Similarity 68.4
Matches 104; Conservative
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Matches 37; Conservative
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A,Map position: 4
A;Introns: 32/1, 275/3; 337/3
C;Superfamily: loricrin
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A; Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CG
A,; Rose, D.G.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albescription: minor component of wild-type curli; interaction between CsgA and CsgB tri
A:Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F:1-21/Domain: signal sequence #status predicted <51G>
F:22-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-151 <BLAT>
A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278;
A;Experimental source: strain K-12, substrain MG1655
NyAlternate names: csgB protein; curlin nucleation component; minor curlin protein C;Species: Escherichia coli C;Species: L2-Reb-1998 #text_change 01-Mar-2002 C;Accession: 370787; F64846 F;Hammar, M.; Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Micobiol. 18, 661-670, 1995 Mol. Micobiol. 18, 661-670, 1995 A;Fithe: Expression of two csg operons is required for production of fibronectin- and A;Reference number: S70783; MUID:96414468; PMID:8817489 A;Accession: S70787 A;Accession: S7087 A;Accession: S7087 A;Accession: S7087 A;Accession: S7087 A;Accession: S7087 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession: S7088 A;Accession:
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-151 <HAM>
A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.5%; Score 96.5; DB
.larity 25.6%; Pred. No. 0.31;
Conservative 24; Mismatches
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Best Local Similarity
Matches 30, Conserv
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A;Molecule type: DNA
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L.; White, N.; Farrar,
                                                                                                                                       Cydecession: JCG040

R;Collinson, S.K.; Clouthler, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 179, 662-667, 1996

A;Title: Salmonella entertitidis agfBAC operon encoding thin, aggregative fimbriae.
A;Reference number: JC6039; MUID:96146512; PMID:8550497

A;Residues: 1-151 cC01>
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A;Residues: 1-151 cC01>
A
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A;Note: this species has also been called Salmonella typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0635
R;Parkhill, J: Dougan, G:; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Chur th, T.; Connerton, P.; Crohin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fa Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens A;Reference number: Apostore sequence of a multiple drug resistant Salmonella enterica A;Reference number: AB0502; MUD:21534947; PMID:11677608
A;Accession: AH0635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <PAR>A;Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
C;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGFRNNATIDOWNAKNYD-OLVTRVVTHEMAHANOTASDSSVMVRQVGFGNNATANOY 151
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                    fimbrin protein agfB precursor - Salmonella enteritidis
C,Species: Salmonella enteritidis
C,Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
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870787
curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 98.5; DB 2; Length 151; 28.8%; Pred. No. 0.21; cive 17; Mismatches 48; Indels 1
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12.7%; Score 98.5; DB 2;
Best Local Similarity 28.8%; Pred. No. 0.21;
Matches 34; Conservative 17; Mismatches 48;
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Matches 34; Conserv
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Qy 51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105	QY 64 RKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
Qy 106 WNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151 	Qy 121 HEMAHANQTASDSSVMVRQVGFGNNAT 147  Db 463DSGLTNSGFGNTGT 476
RESULT 12 G8565 curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain O157:H7 c)Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequencerevision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: G8565 R;Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Status: preliminary A;Residues: 1-151 c5TO> A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z16 A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Gene: csgB	RESULT 14 AD1539 probable sugar ABC transporter, periplasmic sugar-binding protein homolog lin0852 [impo C;5pecies: Listeria innocua C;5pecies: Listeria innocua C;5pecies: Listeria innocua C;5pecies: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AD1539 #text_change 27-Nov-2001 C;Accession: AD1539 #text_changeu. L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.D.; Jones, L.M.; Karst, U.Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M A;Attle: Comparative genomics of Listeria species. A;Attle: Comparative genomics of Listeria species. A;Accession: AD1539 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule t
Gaps 4; NATIDQ 105	Appertuents source: strain criptizes A;Genetics: A;Gene: lino852 Query Match Best Local Similarity 23.8%; Pred. No. 2.3; Matches 39; Conservative 23; Mismatches 59; Indels 43; Gaps 5;
106 WNAKNYDQLVTRVVTHEMAHANQTASDSSVWVRQVGFGNNATANQY 151 74 EGSSNRAK-IDQTGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129	1 MKLLKVA-AFAAIVVSGSALAGVVPQWGGGCNHNGGGN
don, s yd, s.	Jakkal - v
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Recession: D70604 A; Accession: D70604 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1.552 cCOL> A; Cross-references: GB: 292774; GB: ALL23456; NID: g3261729; PIDN: CAB07133.1; PID: g1877289 A; Experimental source: strain H37Rv C; Gpenetics: C; Genetics: PPE C; Superfamily: Phaseolus glycine-rich cell wall protein 1.8	C;Species: Drosophila melanogaster C;Date: 01-Dec-1995 #text_change 21-Jul-2000 C;Accession: A56038 R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P. Mol. Cell. Biol. 14, 6809-6818, 1994 A;Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogast A;Reference number: A56038, MuID:95021209; PMID:7935398 A;Accession: A56038 A;Catus: preliminary A;Molecule type: mRNA A;Residues: 1-1028 <agr.> A;Residues: 1-1028 <agr.> A;Residues: 1-1028 <agr.> A;Cross_references: GB:U11383; NID:9520526; PIDN:AAB60216.1; PID:9520527</agr.></agr.></agr.>
7;	C.Genetics: A;Gene: ovo A;Cross-references: FlyBase:FBgn0003028  Query Match Best Local Similarity 26.7%; Pred, No. 5.9; Asset Local Similarity 26.7%; Pred, No. 5.9;
Db 353 SGSGNIGVFNTGANTLVPGDLNNLGVGNSCNANIGFGNAGVLNTGFGNASILNTGLG 409	%0; CONSELVACIVE 1%; EXEMINACIONES 51; INCES 55; CAPE 3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62

: :	63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNYDQLVTRVVTHE 122	105GGNGYINCGGVG-GPNNSDGNNLLNFASVSNYNESNSKFHNHH 147	123 MAHANQTASDSSVWVRQVGFGNNATA 148	148 HHHQHNNNNNGGQTSMMGHPFYGGNPSA 177	Search completed: August 2, 2004, 14:56:24 Job time : 9.4 secs
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	Description	5225 salmonell	P28307 escherichia	Q93u24 escherichia	Q8z7m3 salmonella	P55226 salmonella	P39828 escherichia	P51521 drosophila	095271 homo sapien	Q03646 plasmodium	P07875 bacteriopha	P23223 leishmania	P15706 leishmania	P08148 leishmania	P43150 leishmania	006653 r outer mem	P34291 caenorhabdi	Q10778 mycobacteri	Q03297 drosophila	chlamydom		bsend	Q05925 homo sapien	oryza		Q915d6 brevundimon						pantoea	erwini	P20469 pantoea ana
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J. Bacteriol. 173:4773-4781(1991)
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
'Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-S.enteritidis, STRAIN-27655-3B;
MEDLINE-SHIOS66; PubMed-1677557;
COllinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ
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SPECIES-S. enteritidis; STRAIN-27655-3B;
SPECIES-S. pubmed-8550497;
Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                      SPECIESES.enteritidis; STRAIN=27655-3B; MEDLINE=94013373; PubMed=8104955; Doran J.L., Collinson S.K., Burian S., Sarlos G., Todd E.C.D., Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; "DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae."; J. Clin. Microbiol. 31:2263-2273(1993).
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SVMVRQVGFGNNATANQY -> DSYTQVAS
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B7DAC0D16B621359 CRC64;
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                                                                 Bacteriol. 185:2330-2337(2003)
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Best Local Similarity
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Collinson S.K., Emcedy L., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLIED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96414468; PubMed=8817489; Hammark S.; Ariqvist A., Bian Z., Olsen A., Normark S.; Ariqvist A., Bian Z., Clsen A., Broduction of Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Naimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano A., 118-kb DNA sequence of the Escherichia coli K.12 genome corresponding to the 12-28.0 min region on the linkage map.",
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SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
MEDLINE=92211284; PubMed=8459772;
Olsen A., Arnqvist A.;
"The Rpos sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding curli in
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STRAIN-KI2 / MG1655;
MEDLINE-S7426617; PubMed=9278503;
MEDLINE-S7426617; PubMed 11, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
Mau B., Shao Y.;
                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MEDLINE-93023873; PubMed=1357528;
Arndvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.;
"The Crl protein activates cryptic genes for curli formation and fibronectin binding in Bscherichia coli HBIO1.";
MOI. Microbiol. 6:2443-2452(1992).
                                                     01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                   151 AA
                   PRT;
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SEQUENCE OF 21-31.
MEDLINE=91310586; PubMed=1677357;
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                                                                                                                                                                                                                                                                                                                                               Escherichia coli.";
Mol. Microbiol. 7:523-536(1993)
                                                                                                       Major curlin subunit precursor.
CSGA OR B1042.
                   STANDARD;
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SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
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                                                                                                                                               Escherichia coli.
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                                                     01-DEC-1992
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CSGA ECOLI
ID CSGA ECOLI
AC P28307;
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NCBI_TaxID=601;
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in curli
expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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Enterobacteriaceae, Escherichia.
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7 7 A -> E (IN REF. 1).
AA; 15049 MW; C003470D208D395F CRC64;
  SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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28-FEB-2003 (Rel. 41, Last sequence update)
A9-FEB-2003 (Rel. 41, Last annotation update)
A9-FC curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
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EMBL; X90754; CAA62282.1; -.
EMBL; AB000205; AAC7426.1; -.
EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
PTR; S70788; S70788.
EcoGene; EG11489; csgA.
Finbria; Signal; Complete proteome.
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SEQUENCE FROM N.A.
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Matches 106;
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Q93U24;
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SEQUENCE
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STAINSOLD FROM N.A.

SEQUENCE FROM N.A.

STAINSOLS7:H7 / RIND 0509952;

XX MEDLINE=21156231; PubMed=11258796;

XA Hayashi T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli

RT "Complete genome sequence of enterohemorrhagic Escherichia coli

RT "Complete genome cequence of enterohemorrhagic scherichia coli

C157:H7 and genomic comparison with a laboratory strain K-12.";

BNA Res. 8:11-22(2001).

C157:H7 and genomic comparison with a laboratory strain K-12.";

RL "COLIED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH

CC TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the burspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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MAJOR CURLIN SUBUNIT.
EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            FIBRONECTIN. SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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68.4%; Pred. No. 1.5e-36;
iive 19; Mismatches 28
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
Salmonella typhi.
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MEDLINE=21534947; PubMed=11677608;
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EMBL, AE005315, AAG55788.1, -.
EMBL, AP002054, BAB34843.1; -.
PIR, D90806, D90806.
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Best Local Similarity 68.49
Marches 104; Conservative
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CSGB ECOLI
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CSGB_ECOLI
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                                                                                                                 SEQUENCE FROM N.A.
STRAILE-TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                            J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBROMECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.typhimurium, STRAIN=SR-11,
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGÖVGTDNSARVROEGSKLLSVISÖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Feltwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitchhead S., Barrell B.G.; Whitchhead S., Barrell B.G.; enterice genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
MCBI_TaxID=602, 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%; Score 98.5; DB 1; Length 151; 28.8%; Pred. No. 0.099;
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit)
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURLIN SUBUNIT
                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL627269; CAD08267.1; -.
EMBL; AE016840; AAO69400.1; -.
Fimbria; Signal; Complete proteome.
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Best Local Similarity
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                                                         McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., McComplete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 178:662-667(1996).

FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

NCBL TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES Senteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=855049; Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W salmonalla enteritidis agfakC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 151;
STRAIN=LT2 / SGSC1412 / ATCC 700720;
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MINOR CURLIN SUBUNIT.
, COFC5430E6DD361D CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor.
CSGB OR BI041 OR Z1675 OR ECS1419.
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
FIR, JC6040; JC6040.
StyGene; SG10609; csgB.
Fimbria; Signal; Complete proteome.
Fimbria; Signal; Complete Proteome.
          SPECIES=S.typhimurium; STRAIN=LT2 /
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16182 MW;
                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=0157.H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi W., Murata T., Tanaka M., Tobe T.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Kida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterchemorrhagic Escherichia coli
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arnqvist A., Olsen A., Normark S.,
"Sigma S-dependent growth-phase induction of the csgBA promoter in
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSGIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
SEQUENCE FROM N.A.
STRAIN=K1Z / MC4100,
MEDLINE=56414468; PubMed=8817489;
MEDLINE=56414468; PubMed=8817489;
MEDLINE=56414468; PubMed=8817489;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97061202; PubMed=8905232;
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ishama T., Alba H., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                  STRAIN=K12 / MGJ655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21074935, PubMed=11206551,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rosefai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N. W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                        Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95157246; PubMed=7854117;
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DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 EGSSNRAK-IDQIGDYNLAYIDQAGSANDASISQGAYGNIAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mevel-Ninio M.T.M., Terracol R., Kafatos F.C.;

"The ovo gene of Drosophila encodes a zinc finger protein required for ovo gene of Drosophila encodes a zinc finger protein required EMBO of emale germ line development.";

-I. FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE CELLS. PLAYS A ROLE IN GERM LINE SEX BETERMINATION.

-I. SUBCELLULAR LOCATION: NUCLEAR (POCENTIAL).

-I. DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN UNRASE CELLS DURING OCCENESIS. STORED IN THE EGG, BUT, IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.

-I. SIMILARITY: Contains 4 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 WNAKNYDQLVTRVVTHEMAHANQ--TASDSSV------MVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=95021209; PubMed=79353388;
MEDLINE=95021209; PubMed=79353388;
MAICHINES M.D., Wang J., Liang Y., Mahowald A.P.;
"Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
as its content
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B18D266B964014B8 CRC64;
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PS1521; Q9XZU4;
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                       EMBL, D90741; BAA35631.1; --
EMBL, AE002315; AAG55787.1; --
EMBL, AP00254; BAB34842.1; --
PIR, C90806; C90806.
PIR, C90806; C90806.
PIR, S40787; S70787.
EcoGene, EG12621; csgB.
Finbria; Signal; Complete proteome.
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OVO OR SVB.
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MEDLINE=91293102; PubMed=1712294;
                                                                                                                                  EMBL, X90754; CAA62281.1; -.
EMBL, AE000205; AAC74125.1; -.
EMBL, D90741; BAA35831.1; -.
EMBL; AE005315; AAG55787.1; -.
EMBL, AP002554; BAB34842.1; -.
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InterPro; IPR007087; Znf C2H2.
InterPro; IPR007087; Znf C2H2.
SMaRT; SM0035; ZnF C2H2; 4.
PROSITE; PS00628; ZINC_FINGER_C2H2_1; 3.
Zinc_finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | : | : HHHQHNNNNNNNGGQTSMMGHPFYGGNPSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                      EMBL; X59772; CAB36921.1; ALT_SEQ.
PIR; A56038; A5638.
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CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insoid=095271-2; Sequence=VSP 004518, VSP 004539; Note=No experimental confirmation available; Insue SPECIFICITY: Ubiquitous; highest levels in testis. PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases.
                                                                                                                                                                                                                                                     nuclear pore complexes and centrosomes."; Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21602874; PubMed=11739745;
Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and
                                                                                                                                                                                                                                                                                                                           FUNCTION, AND PHOSPHORYLATION.
MEDLINE=20556282; PubMed=10988299;
Thin N.-W., Lodish H.P.;
"Tankyrase is a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
                                                            Euteleostomi;
                                                                                                                                                             Smith S., Giriat I., Schmitt A., de Lange T.; "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres."; Science 282:1484-1487(1998).
Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1) (TRF1-interacting ankyrin-related ADP-ribose polymerase).

TNKS OR TNKS1 OR TIN1 OR TINF1 OR PARPL.

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by MAPK kinases.
--- PTM: ADP-ribosylated (-auto).
---- SIMILARITY: Belongs to the PARP family.
---- SIMILARITY: Contains 15 ANK repeats.
---- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                             Eukaryoča, Metazoa, Chordata, Craniata; Vertebrata, Butele
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=095271-1; Sequence=Displayed;
                                                                                                                                                                                                                                                     Smith S., de Lange T., "Cell cycle dependent localization of
                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUB=Testis;
MEDLINE=99040105; PubMed=9822378;
                                                                                                                                                                                                                         SUBCELLULAR LOCATION.
MEDLINE=99454782; PubMed=10523501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF082556; AAC79841.1; -
                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 AGNGACNGAGNGAGNGAGNGAVASAGNGAGNGAVASAGNGAVAERSSSTPATTTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETTITQSGYGNGA--DVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQ-----LVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 AGNGAVASAGNGAGNGAGNGAGNGAGNGAG-----NGAGNGA---GNGAGNG
                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-91156885; Pubmed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
-!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATURATION
                                                                                                                                                                                                                                                                                                                                                       erythrocyte.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                 Plasmodium falciparum (isolate Nig32 / Nigeria).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                               antigen 2.";
Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: May play a role in the merozoite attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 90; DB 1; Length 347; 24.3%; Pred. No. 1.3; ive 16; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR01136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat; GPI-anchor; Merozoite.
SIGNAL
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MERGAGOTE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING I (BY SIMILARITY).
POLYMORPHIC REGION.
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                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Merozoite surface antigen 2 precursor (MSA-2)
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       347 AA.
         PRT;
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       STANDARD;
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347
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36
224
2296
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321
347 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FIId=VSP 004539.
H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.
E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
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                                                                                                                                                                             R InterPro; 1PR002110; ANK.
R InterPro; 1PR002110; ANK.
R Pfam; PF00236; SAM.
Pfam; PF00236; SAM; 19.
R PRINTS; PR01415; ANKYRIN.
R SWART; SW00248; ANK; 17.
R SWART; SW00448; SAM; 11.
R PROSITE; PS50088; ANK REPEAT; 15.
R PROSITE; PS50105; ANM CAPEAT; 15.
R PROSITE; PS50105; SAM DOWAIN; 1.
Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere; W Nuclear protein; Repeat; ANK repeat; ADP-ribosylation; Phosphorylation; ANK repeat; ANK repeat; ADP-ribosylation; ANK PREPAT
                                                                                                MIM; 603303; -. Golfnomosome, telomeric region; IDA. GO; GO:0000781; F:NAD ADP-ribosyltransferase activity; IDA. GO; GO:0005515; F:protein binding; IPI. GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.
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/FTId=VSP 004538.
Missing (in isoform 2).
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EMBL, AF082558; AAC79843.1; -.
EMBL, AF082559; AAC79844.1; -.
HSSP, Q00420; 1AWC.
Genew; HGNC:11941; TNKS.
MIM; 603303; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1327 AA; 142010 MW;
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Ą. 262 PRT; STANDARD; RESULT 10 VG38_BPT2 ID VG38_BPT2 AC P07875;

RESULT 9 MSA2_PLAF2

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117

Gaps

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Query Match
Best Local Similarity
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FUNCTION: Has an integral role during the infection of macrophages
in the mammalian host.
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87283911; PubWed=3302276; MEDLINE=87283911; PubWed=3302276; MEDLINE=87283911; PubWed=3302276; MEIGHT C., Drexler K., Eschbach M.L., Henning U.; Eschbach M.L., Henning U.; Eschbach M.L., Henning U.; As sequence of genes 38 encoding a receptor-recognizing protein of bacteriophages T2, K3 and of K3 host range mutants."; J. Mol. Biol. 194:31-39(1987).
J. Mol. Biol. 194:31-39(1987).
Lie phage recognition site to the cellular receptor.
Lie phage recognition site for the cellular receptor.
LIE PROTEILANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS CMPF AND TTR
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MEDLINE=22107220; PubMed=1762629;
MEDLINE=22107220; McMaster R.W.;
Mebb J.R., Button L.L., McMaster R.W.;
"Heterogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.";
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PO CT-2003 (Rel. 20, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Viruses, dsDNA viruses, no RNA stage, Caudovirales, Myoviridae,
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25801 MW; 0567366918F6C745 CRC64;
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                                          01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
Receptor recognizing protein (Protein Gp38).
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InterPro; IPR007932; Tail_fibre_GP38.
Pfam; PF05208, GP38.
Piber proctein; Phage recognition.
SEQUENCE 262 AA; 25801 MW; 0567366
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Best Local Similarity 34.4'
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        01-AUG-1988 (Rel.
01-AUG-1988 (Rel.
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NCBI_TaxID=10664;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=44271;
                                   p1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr--Leu-Lys-Lys-. CORACTOR: Binds 1 zinc ion per subunit (By similarity). -: CORACTOR: Binds 1 zinc ion ber subunit (By similarity). -: SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. -: SIMILARITY: Belongs to peptidase family M8.
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01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (BC 3. 4. 24. 36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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CATALYTIC ACTIVITY: Preference for hydrophobic residues at
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HSSP; P08148; 11ML.
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Leishmania major.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCEL TaxID=5664;
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                                                 P08148; P15906; 01.AUG-1988 (Rel. 08, Created) 01.APR-1990 (Rel. 14, Last sequence update) 10.OCT-2003 (Rel. 42, Last annotation update) Leishmanolysin precursor (RC 3.4.24.36) (Cell surface protease) (Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDLINE=88154764; PubMed=3346625;
Button I.L., Andmatter W.R.;
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91009116; PubMed=2145267; Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Schneider P., Bordier C.; Schneider C.; Structure of the glycosyl-phosphatidylinositol membrane and the Leishmania major promastigote surface protease."; J. Biol. Chem. 265:16955-16964 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                           K-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                  Button L.L., McMaster W.R.;
J. Exp. Med. 171:589-589(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins 22:58-66(1995).
                                                                                                                                endopeptidase)
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           "Three distinct RNAs for the surface protease gp63 are differentially
                                                              SEQUENCE FROM N.A.
MEDLINE=92112918; PubMed=1370484;
Kamamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
Wilson M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE.
LEDISHANDLYSIN.
LEMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks
Arg-Gly-Asp sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

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N-LINKED (GLCNAC. . .) (POTENTIAL)
GPI-anchor amidated asparagine (By
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HISSP, P08148; 11ML.

MEROPS, M08.0010.25; Pept M Zn BS.

InterPro; IPR00107; Peptidase_M8.

Ffam; PF01457; Peptidase_M8.

PROSITE; PS00142; ZINC_PROTEASE; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogan; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
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Pred. No. 4.4;
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746730AE8E2A2E7C CRC64;
                          Arg-Gly-Asp sequence.";
Wol. Biochem. Parasitol. 39:267-274(1990).
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89.5%;
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                                                                                                                                                                                                                                                             -!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl', and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
-!- CORACTOR: Binds 1 zinc ion per subunit.
-!- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- PTM; THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, L16:0, AND C18:0).
                                       MEDLINE=98416698; PubMed=9739094; Schlagenhauf E., Etges R., Metcalf P., He crystal structure of the Leishmania major surface proteinase leishmanolysin."; Structure 6:1035-1046(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to peptidase family M8.
X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
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Mismatches

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108 AKNYDQLVTRVVTHEMAHA 126 ASRYDQLVTRVVTHEMAHA 266

Pred.

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74.100-1995 (Rel. 32, Created)
71.100V-1995 (Rel. 32, Last sequence update)
71.100V-1995 (Rel. 32, Last sequence update)
71.10-0CT-2093 (Rel. 42, Last annocution update)
71.10-0CT-2093 (Rel. 42, Last annocution update)
72.10-0CT-2093 (Rel. 42, Last annocution update)
73.10-0CT-2093 (Rel. 42, Last annocution update)
74.10-0CT-2093 (Rel. 42, Rel. 43, Relation (Promastigote surface of the standard in the surface of the surface of the surface of the surface is the surface of the surface of the surface of the surface of Leishmania.
73.10-0CT-2003 (Rel. 42, Rel. 2003)
74.11-10-10CT-2003 (Rel. 2003)
75.11-10CT-2003 (Rel. 2003)
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Best Local Similarity
Matches 17; Conserv
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GP63_LEIME
AC P43150;
DT 01-NOV-1995
DT 10-OCT-2003
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R InterPro; IPR006025; Pept M Zn BS.
R InterPro; IPR001577; Peptidase_M8: 1.
R PRIM: PR0457; Peptidase_M8: 1.
R PRIMIS: PR00782; LSHWANGLYSIN.
R PROSITE; PR00142; ZINC_PROTEASE; 1.
R Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Mydrolase; Metalloprotease; Glycoprotein; 3D-structure; Lipoprotein.
T SIGNAL 39 POTENTIAL.
T CHAIN 101 S77 LEISHMANOLYSIN.
T PROPEP 40 100 ACTIVATION PEPTIDE.
T CHAIN 101 S77 LEISHMANOLYSIN.
T PROPEP 578 602 REMOVED IN MATURE FORM.
T ACT SITE 264 ZINC (CATALYTIC).
T METAL 268 ZINC (CATALYTIC).
T METAL 334 334 ZINC (CATALYTIC).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-anchor amidated asparagine.
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Best Local Similarity
Matches 45; Conserv
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                                                                                                                                 NCBI_TaxID=35790;
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                                                                                                                                                                                                    Uchiyama T.;
                                                                                                                                                                                                                                      japonica.";
                                                                                                                                                                                    STRAIN=YH;
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstains the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Blochem. Parasitol. 57:31-46(1993).
FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
                                            CATALYTICAL ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-
COFACTOR: Binds 1 zinc ion per subunit (By similarity).

DEVELOPMENTAL STAGE: Expressed in both the promastigote and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PROOTOS; LEHRANDOZYSIN
PROSITE; PS00142; ZINC PROTEASE; 1.
Hydrolase; Metalloprotesse; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; Multigene family.
PROPEP 139 POTENTIAL.
PROPEP 40 102 ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 87; DB 1; Length 646; Pred. No. 4.8;
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                                                                                                                                 amastigote forms.
-!- SIMILARITY: Belongs to peptidase family M8.
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Last sequence update)
Last annotation update)
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InterPro; IPR0066025; Pept M Zn BS.
InterPro; IPR001577; PeptIdase_M8.
Pfan; PF01457; Peptidase_M8, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.2%;
llarity 89.5%;
Conservative
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DT 16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: THE 32 KDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 VLAAGAITLDGSATI-----TGDIGNGGG-------GAALQSITLANDATK
Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Scas) (TompB) (romp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptidel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequencing of the gene encoding the protein romp B of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                               oner
Rickettšia japonica.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 kDa SURFACE-EXPOSED PROTEIN. 32 kDa BETA PEPTIDE. POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   layer with hexagonal symmetry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2%; Score 87; DB 1; Length 1656; 6%; Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168097 MW; 3132A69C9DD5999F CRC64;
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InterPro; IPR065546; Autotransporter.
Pfam; PF03797; Autotransporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB003681; BAA20138.1; -.
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CHAIN 1 1338
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29.6%;
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(Oldsu) Anola elph simi

Q9n8n5 trypanosoma Q7nc21 shigella fl Q81ru7 shigella fl Q89ji5 bradyrhizob Q88hgo pesudomonas Q2x44 citrobacter Q8cw64 escherichia Q8nty neurospora Q8nty campylobact Q9nGm8 drosophila Q9ngf7 drosophila Q9ngf7 drosophila Q9ngf7 drosophila Q9ngf7 drosophila Q8nty mycobacteri Q7tw76 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycobacteri Q8viy0 mycoballa Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 shewanila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophila Q8viy0 mycophil

score:

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Scoring table:

Minimum DB Maximum DB

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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98053981; PubMed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
Normark S.J., Rhen M.;
Expression of thin, aggregative fimbriae promotes interaction of
Salmonella typhimurium SR-11 with mouse small intestinal epithelial
cells.";
EMBL, AJO0514; CAA04151.1, -.
NON TER: 152
NON TER: 152
NON TER: 152
                                                                                                                                                                                                                                                                                                                                                       Salmoneila typhimurium.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
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Pred. No. 2e-46;
3; Mismatches 12; Indels
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Last annotation update)
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                      Q89JI5
Q88HG0
Q7X244
Q8CW64
Q8NIV1
                                                               0841Y5
09NGM8
09NGF7
09NGF7
09NGF7
09NGF7
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90.1%;
033802;
01-JAN-1998 (TrEMBLrel. 0:
01-JAN-1998 (TrEMBLrel. 0:
01-DEC-2001 (TrEMBLrel. 1:
AgfA, protein (Fragment).
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Best Local Similarity 90.1
Matches 136; Conservative
440
1222
13222
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1615
191
152
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Q8x237 enterobacte
Q9s35 escherichia
Q9s35 escherichia
Qeeih4 shewanella
Qeeih3 shewanella
Q10414 caenothabdi
Q7x238 enterobacte
Q89v84 mycoplasma
Q89ji3 bradythizob
Q89v84 mycoplasma
Q89ji3 bradythizob
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Q7x243 citrobacter
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                                                               (without alignments)
1604.150 Million cell updates/sec
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                                                                                                      1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY
                                                        2, 2004, 14:39:17 ; Search time 29.7 Seconds
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                              hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                       protein search, using sw model
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07X238
08EV84
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07X243
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sp bacteria:*
sp bucteria:*
sp human:*
sp invertebrate:*
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sp phage:*
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seq length: 200000000
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121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151

27X243;

Q7X243 RESULT 2 Q7X243

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                                   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAXNYDQLVTRVVT 120
                                                                     SDARKSDVTITOHGRGNGAVVGQGADDSTISLKQTGFQNSATIDQWNAKNADISVTQFGG 118
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1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=06:11 / CFT073 / ATCC 700928;
MEDLINE=2138624; PubMed=12471157;
MEDLINE=2238624; PubMed=12471157;
MWelch R.A., Butland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhaw G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U. S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia.
(VEI_TaxID=217992;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Enterobacter.
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                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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                                                                                                                             119 RNGALVNOTASDSNVLIQQVGFGNNATANQH 149
                                                                                                        121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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STRAIN=Fec39;
Zogaj X., Bokranz W., Nimtz M., Romling
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Curlin-csgA protein.
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Escherichia coli O6
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).

EMBL, AJ515701; CAD566751; -
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
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Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJS15700; CAD566721; -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cirrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                  Citrobacter sp. Fec2.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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78.8%; Pred. No. 2.3e-39;
                        151
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Matches 119; Conservative
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
EMBL; AJSIS702; CADS66781; -. SEQUENCE 150 AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
                                                                                        Gaps
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Enterobacteriaceae, Salmonella.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Pred. No. 2.1e-23;
                                                        55.7%; Score 431.5; DB 2; Leny...
59.6%; Pred. No. 1e-26;
Mismatches 33; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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MEDLINE-22297686; PubMed=12368813; Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T.; Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Neidman J., Impraim M., Lee K., Berry K., Lee C., Weller: J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome: sequence of the dissimilatory metal ion-reducing bacterium Shewanlla oneidensis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 QGDDNDITIKÓKGDSNGAEFQVWGDSNDVDLKORGDANFATFGAYGTDNDFDLSSKGDNN
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SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
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                                                                                                                                                                                                                                                                                                                            15.7%; Score 122; DB 2;
89.7%; Pred. No. 0.0042;
iive 1; Mismatches 2
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Best Local Similarity
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3 10:54:41 2004

Tue Aug

Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanam M., Brinkac L., Daugherty S., Madupu R., Dodson R.J., Umayam L.A., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Wanelhevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J. Utterback T.R., McDonald L.A., Reldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium STRAIN=MR-1; MEDLINE=22297686; PubMed=12368813; Shewanella oneidensis. 

Complete proteome. SEQUENCE 139 AA; 14811 MW; 41ECICFA76957920 CRC64; Nat. Biotechnol. 20:1118-1123(2002). EMBL; AE015532; AAN53942.1; -. SO0866; -.

Query Match
Best Local Similarity 30.1%; Pred. No. 0.28;
Matches 34; Conservative 19; Mismatches 46; Indels 14

SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFR 39

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NNATIDOWNAKNYDOLVTRVVTHEMAHANGTASDSSVMVROVGFGNNATANOY 151 NKASITQIGNDNLVQL------NQLGS-GNFSIQQIADGAAISITQY

PRELIMINARY; 07UWZ8; RESULT 10 SON KRA RAP REPUBLICAN RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA RAPARA

PRT; 7716 AA

Last sequence update) Last annotation update) Created) 25, 25, 25, 01-OCT-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel. Hypothetical protein.

Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales, Planctomycetaceae, Pirellula. Rhodopirellula baltica.

STRAIN=1; MEDLINE=22735913; PubMed=12835416; SEQUENCE FROM N.A. NCBI_TaxID=117;

Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1.",

Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
EMBL, BX294135, CAD72214.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 7716 AA, 797868 WW, D391A25BD96405C0 CRC64;

13.4%; Score 104; DB 16; Length 7716;

9 4048 GDGNHGTLGGGVASQEPTRSSYSVGEDGTLSV---SVGNGLLANDIEMDGDSLTITEIN- 4103 GNGADVGQG----ADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASD 132 28 GGGNHN--GGGNSS------GPDSTLSIYQYGSANAALALQSDARKSETTITQSGY 57; 29.1%; Pred. No. 81; ative 18; Mismatches TSVAITIIG-GNDA 4176 SSVMVRQVGFGNNA 146 39; Conservative Best Local Similarity Matches 39; Conserv 76 133 g 염 à à

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium. Last sequence update)
Last annotation update) Hypothetical exported glutamine-rich protein. (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last seq
(TrEMBLrel. 24, Last ann PRT; STRAIN=USDA 110; MEDLINE=22484998; PubMed=12597275; Bradyrhizobium japonicum. PRELIMINARY; FROM N.A. NCBI_TaxID=375; 01-JUN-2003 ( 01-JUN-2003 ( 01-JUN-2003 ( SEQUENCE Q89D03 Q89D03; 

RESULT 11

Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T., Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K., Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada I Tabata S.;

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14; Gaps

"Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; APO05962; BAC52907.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 362 AA; 39058 MW; D447EE0D4E8433EC CRC64;

13.3%; Score 103; DB 16; Length 362; 31.6%; Pred. No. 2.6; Indels 80; 14; Mismatches 50; Conservative Query Match Best Local Similarity Matches

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113 59 2 KILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDST----LSIYQYGSANAAL 58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATI----DQWNAKNYDQ g δ ð

60 STNSAQTQSPSSTGQSAAGQTTNSGTGT-NTTQAPTSNNSTNQAQTSQPSNQTNAPS-DQ 114 LVTRVVTHEMAH-ANQTASDSSVMVRQVGFGNNATANQ 150

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118 TOTNPPTDNRAQSANPPASGASQAQSPTGSNSTNTAQO 155

Created) 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24, PRELIMINARY; 019414 RESULT 12 OCCUPATOR

PRT;

Last sequence update) Last annotation update) F13E9.4 protein. F13E9.4.

Caenorhabditis elegans. Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.

Query Match

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TPTIKKEVSLSGALSKIYDANKSTSDLIAEDIKANPTNYFDNGEALKDLIKDATVSVNGG 120
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsurucka H., Wada T., Yamada M.,
Tabata S.;
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DNA Res: 9:189-197(2002).
EMBL; AP005954; BAC50565.1; -.
                                                                                                                                  Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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                                                                                                                                                                                                                                             Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Yoshimo C., Horino A., Shiba T., Sasaki T., Hattori M.; Yoshimo C., Horino A., Shiba T., Sasaki T., Hattori M.; The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans."; Muclatic Acids Res. 30:5293-5300(2002).

EMBL; Ap004172; BAC4476.1; --
InterPro; IPR000437; Prok lipoprot S.
Lipoprotchi; Complete procesome.

Elipoprotchi; Complete procesome.

Elipoprotchi; Complete procesome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17448 MW; 995DB08C01498381 CRC64;
                                                  Created)
Last sequence update)
Last annotation update)
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Last annotation update)
                    362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99.5;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                12.9%; Score 100; 23.9%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                  STRAIN=HF-2;
MEDLINE=22354719; PubMed=12466555;
                                                (TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%;
25.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                  lipoprotein homolog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                              NCBI_TaxID=28227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
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CSGA OR BLL5300.
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                                                01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q89JI3 ;
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Best Local
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Q89JI3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 YQNNQGRHQGGGGGGGSSSSNSVMSNNGNNGSVGNNNGPTPSFLNNVSSSAAQDYYNIV 251
                                                                                                                                                                                                                                                                                                                                                                                                           134 SGOQASGSMNSFGGQGGYGQNQNGFGGQSGFSGQSGWGSNSLSSANSNGNNNQG--SSSG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQİRQEGSKLLSVVSQ-----DGAGNRARVD-----QSGTYNLAWIDQS-GNGNDAG 103
                                                                                                                                                                                                                                                                                                                                                                                 74
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                                                                                                                                                                                                                                                                                                                                                                              SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG
                                                                                                                                                                                                                                                                                                                                                  Gaps
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Enterobacteriaceae, Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%; Score 101; DB 5; Length 409; 23.3%; Pred. No. 4.3; ive 26; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 100; DB 2; Length 151; 31.8%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Indels
                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                platform
                                                                                                                                                                                                                                                                    48; 1.
43231 MW; BO7DF0E4175C5739 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYDOLVTRVVTHEMAHANOTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNKSLTINQINEQ---ASNWASANSVQAQYIQYETNRSA 287
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Last annotation update)
                                                                                                                                              Genome sequence of the nematode C.elegans: A
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01-OCT-2003 (TrEMBLrel. 25, Last sequenc)
01-OCT-2003 (TrEMBLrel. 25, Last annotation component of curlin monomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                               Onchocerca_Ag.
                                                                                                             MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z69383; CAA93412.1; -.
PIK; T20847; T20847.
                                                                                                                                                                                                                            WormPep; F13E9.4; CE05606.
InterPro; IPR003677; Oncho
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                             Pfam; PF02520; DUF148;
SEQUENCE 409 AA; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacter sakazakii
                                              McMurray A.A.;
Submitted (FEB-1996)
                                                                                                                                                                                                                                                                                                                            Local Similarity
les 37; Conserv
                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                             SEQUENCE FROM N.A
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NCBI_TaxID=6239;
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Best Local S:
Matches 35
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Q7X238; 07X238

RESULT 13 Q7X238

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Best Loca Matches

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Local Similarity

RESULT 14

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92

38;

T., Furuya K.,

4 ;	09	8
Gaps	AALALQ 6	GSSVTQ 78
31;	OYGSAN	QVGLVN
Indels	PDSTLSIY	VITSTN
63;	GNSSG	
21; Mismatches 63; Indels 31; Gaps	VPQWGGGGNHNGC	
21;	ALAGV	AQAA-
40; Conservative	LLKVAAFAAIVVSGS	KLFFASVAVLALSSA
40;	ц Ж	40 MR
Matches	ò	QQ

10	~
61 SDARKSETTITIQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVT 116	 79 NGLINDSSSTTÖLGILNGASTMÖGTSSPSLNNVSTVNQAGVQNSATTGQVAFGNNGSAIT 138
SDA	 NGL
61	79

Op

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Search completed: August 2, 2004, 14:54:40 Job time: 29.7 secs

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August 2, 2004, 14:35:42 ; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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782
1 MKLIKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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A Geneseq 29Jan04:*

1: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2003as:*

7: geneseqp2003as:*

8: geneseqp2003as:*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ripti	Aab36353 AqfA::PT3			534.	357	534	535	534(	534,	5353	535.	335	348	Aab36343 Escherich	Abr82651 E. coli C	276.	Aaw23569 Salmonell	2664 Fibr	2663 FN	Aab36316 Salmonell	5318 8	Aab36321 Salmonell	5326	Aab36338 Salmonell	Abr82644 E. coli c
SUMMARIES		ID	AAB36353	AAB36350	AAR74625	34	57	AAB36349	AAB36354	34	AAB36347	35	AAB36351	AAB36355	34	4,	ABR82651	Ø	AAW23569	AAR52664	99	AAB36316	31	AAB36321	32	AAB36338	ABR82644
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Aab36344 Escherich	Aab36322 Salmonell	Aab36327 Salmonell		Aab36342 Salmonell	Aau08231 Polypepti	Abr82649 E. coli V	Aaw64378 Mycobacte	Aaw81745 M. tuberc	Aay39032 M. tuberc		Abu36445 Protein e	Aaw56163 New DNA s	Abb65764 Drosophil	Abb62708 Drosophil	Aag29728 Arabidops	Aag29727 Arabidops	m	Aab36336 Salmonell	Aab36328 Salmonell
AAB36344	AAB36322	AAB36327	AAB36337	AAB36342	AAU08231	ABR82649	AAW64378	AAW81745	AAY39032	AAY39175	ABU36445	AAW56163	ABB65764	ABB62708	AAG29728	AAG29727	AAB36323	AAB36336	AAB36328
151 3	22 3	22 3	22 3	151 3	597 4	26 7	943 2	943 2	943 2	943 2	300 6	738 2	850 4	1028 4	447 3	468 3	19 3	19 3	19 3
14.3	14.2	14.2	14.2			13.0				12.8						12.3	12.3	12.3	12.3
112	111	111	111	107	105	102	100	100	100	100	100	98.5	97.5	97.5	96.5	96.5	96	96	
36		28	29	30	31	32	33	34	32	36	37	38	8	40	41	42	43	44	<b>4</b> 5

## ALIGNMENTS

XX	
DT	AAB36353;
۸۸	26-FEB-2001 (first entry)
(日)	AgfA::PI3#8 amino acid sequence SEQ ID NO:26.
(25)	Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine; immune response; immunogen.
8000 8000	Salmonella enteritidis. Escherichia coli. Synthetic.
X Z	WO200060102-A2.
X & ;	12-OCT-2000.
Y Y	05-APR-2000; 2000WO-CA000356.
X K	05-APR-1999; 99US-0127888F.
X E	(UYVI-), UNIV VICTORIA.
X II I	White AP, Doran JL, Collison SK, Kay WW;
\$ # # # # # # # # # # # # # # # # # # #	WPI, 2000-672631/65. N-PSDB; AAC64629.
ST TA	Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
X & ;	Disclosure, Page 138; 139pp; English.
<b>\$</b> 8	inant agfA gene
88	segment, of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
ខ្លួ	(1) userot thin aggregative imbrise (SEF17/TAF) nucleation depended assembly evetem of strains of Salmonella Racherichia coli and
38	
88	homologue fimbrin subunits, respectively; (2)
S 5	directing recombination of a recombinant gene into the chromosome of the
38	nomorogous species; (3) directing recommunation of a recomminate yene back into the chromosome of the homologous species, replacing the native

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copy of that gene; and (4) eliciting an immune response in an animal, compurising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriacese host cell, from the host cell and introducing the Colymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                            is
for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 782; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.3e-67;
Matches 151; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; immune response; immunogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36350 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
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                                                                                                                                                                                                                                                                                                             151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                               Sequence
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of the nacdative and replaced segment of assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and directing recombinate compirating recombinant conditions and AgfA. CsgA and AgfA-homologue imborins ubunits, respectively; (2) directing recombinates of the chromosome of the homologous species; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of corigination of solymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finitrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens, and hybrid finbriad and in the properties are say and incoming the inserted espector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKYDQLVTRVVTHEMAHA-----GQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 709; DB 3; L. Pred. No. 2.5e-60; O; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UXVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.9
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA sequence.
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26-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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cc (1) use of thin aggregative fimbriae (SEF17/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriacae for the production of fimbriae comprising recombinant GafA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologue species, respectively; (2) directing recombinant gene into the chromosome of the homologue species, replacing the native comprising separating an amino acid polymer comprising the native comprising separating an amino acid polymer comprising a recombinant AgfA cromption containing a replacement sequent or sequents of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the confirming an immune response in an animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal in a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response convaccine, the inserted epitope, and hybrid fimbriae are easy and income converse in an animal converse converse to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.5%; Score 692; DB 3; Length 151; 90.7%; Pred. No. 1.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by GCC'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00233788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity you. Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1994;
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29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                            The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                             Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                          .
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                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                        12; Indels
           Doran JL;
                                                                                                                                                                                                                                                                                                    Score 692; DB 2;
Pred. No. 1.1e-58;
2; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW;
           Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison SK,
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                                                                                                                                               Disclosure, Fig 7B; 95pp; English.
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                                                                                                                                                                                                                                                                                                    88.5%;
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                                                                                                                                                                                                                                                                                                                                        Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis.
           Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA
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                                            WPI; 1994-358275/44.
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N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                              N-PSDB; AAQ87467
                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200060102-A2.
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                                                                                                                                                                                                                                                                                                       Query Match
         Kay ww,
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05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                        86.3%;
ilarity 81.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVTRVVTHEMAHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200060102-A2.
                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                          The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic pacteria for the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITOSGYGNGADVGGADNSTIELTONGFRNNATIDOMNAKNSDITVGOYGG 120
                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                           61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                         Gaps
                                           Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                 87.9%; Score 687; DB 2; Length 151; 90.1%; Pred. No. 3.3e-58; ive 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                           NNPALVNÓTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene r
vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                                                                              Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36349 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-672631/65.
N-PSDB; AAC64625.
          WPI; 1997-309886/28.
                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 136; Conserv
                     N-PSDB; AAT74142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                   Query Match
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back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, to comprising separating an amino acid polymer comprising a recombinant of protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or cheraceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immune adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response cagainst the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                                                                                                                                 The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue filmbrin subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombinant gene into the chromosome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 675; DB 3; Le Pred. No. 4.7e-57; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
                                                                                              Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epictope or antigen. Also described are: (I) use of thin aggregative finbriae (SEPI)/TAF) mucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant had facting recombination of a recombinant one chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal comprising asparating an amino acid polymer comprising are combinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or seful for the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live incomes in a inserted eliciting an immunogenic properties relevant for an efficient live incomes in a important for directing an immunogenic properties are usually strong immunogens, which may be important for directing an immunogenic properties are easy and and inserted elicities elected elicities elicities elected elicities elected elicities elicities elicities elicities elicities elicities elected elicities elicities elicities elicities elicities elimportant for an effected elicities elicities elicities elicities 
                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    id fimbriae are easy and
The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNFNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 617; DB 3; Length 151;
Pred. No. 1.8e-51;
0; Mismatches 0; Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inexpensive to purify in large amount. The pure exemplification of the present invention
                                                                                                       Kay WW;
                                                                                                                                                                                                                                                                                                                                     English
                                                                                                       Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36346 standard; protein; 151 AA.
05-APR-1999; 99US-0127888P
                                                                                                                                                                                                                                                                                                                               Disclosure; Page 138; 139pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.9
Best Local Similarity 73.6
Matches 128; Conservative
                                                (UYVI-) UNIV VICTORIA
                                                                                                       Doran JL,
                                                                                                                                                     2000-672631/65
                                                                                                                                                                             N-PSDB; AAC64630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
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                                                                                                    White AP,
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence, which encodes a foreign epitope or antigen. Also described are: (3) use of thin aggregative fimbriae (SET)TAPE) mucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the protein containing a replacement segment or acarrier or diluner. (1) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation containing accordance in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immune, the carrier fimbrial subunit protein possesses both the immune, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against, the inserted epitope, and hybrid fimbriae are easy and immunosensive to purify in large amount. The present sequence is given in the expression of the present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.5%; Score 614; DB 3; Length 151;
80.8%; Pred. No. 3.5e-51;
ive 6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inexpensive to purify in large amount. The porthe exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                  Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                    Collison SK,
                                                                                                                                                                                                                                              99US-0127888P.
                                                                                                                                                                                                 2000WO-CA000356.
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                   Salmonella enteritidis.
                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-672631/65.
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                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC64622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                         WO200060102-A2.
                                                                                                                                                                                               05-APR-2000;
                                                                                                                                                                                                                                            05-APR-1999;
                                                                                                                                                    12-OCT-2000.
                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                    White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
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Best Local
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120

RESULT 9

vaccine; immune response; immunogen.

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEP1/7AE) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of fimbriae compitising recombinant AgfA. CsgA and AgfA.homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene homologue fimbrin subunits, respectively; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal; copy of that gene; and (4) eliciting an immune response in an animal; copy of that gene; areplacement segment to resements of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the collymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for the containing a replacement an animal; in a fimbrial presentation and an animal; in a fimbrial presentation and animal in an animal; in a fimbrial presentation and animal and animal and animal and animal animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.3%; Score 612; DB 3; Length 151; 81.5%; Pred. No. 5.5e-51; ive 5; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                            AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immune response; immunogen.
                                    AAB36347 standard; protein; 151 AA.
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Conservative
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64623.
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Best Local Similarity
Matches 123; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                       AAB36347;
AAB36347
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: sequence which encodes a foreign epitope or antigen. Also described are: or seembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; seplacing the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finhbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                              61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system the heterologous antigens are presented in high numbers (up to 550,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                           151
                                                                                                                                   121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                 AAB36352 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
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N-PSDB; AAC64628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
Synthetic.
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MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ

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RESULT 12
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                                                                                                                                       61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination and the back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                               1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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0
                                                 Length 151;
                                                                     23; Indels
                                               Score 609; DB 3;
Pred. No. 1.1e-50;
4; Mismatches 23
                                                                                                                                                                                                     amino acid sequence SEQ ID NO:22.
the exemplification of the present invention
                                                                                                                                                                                      NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collison SK,
                                                                                                                                                                                                                                                                      AAB36351 standard; protein; 151 AA
                                             77.9%;
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                                                                                                                                                                                                                                                                                                                    (first entry)
                                                       al Similarity 82.1
124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
Escherichia coli.
Synthetic.
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N-PSDB; AAC64627.
                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060102-A2
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                                             Query Match
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                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVIRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Best Local Similarity 81.5%; Pred. No. 6.3e-50;
Matches 123; Conservative 4; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36355 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-672631/65.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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N-PSDB; AAC64631
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Escherichia coli
N-PSDB; AAC64624.
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assembly system of strains of Salmonella, Escheridia coli and assembly system of strains of Salmonella, Escheridia coli and ansembly system of strains of Salmonella, Escheridia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Gene into the chromosome of the Chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of sequences grown on a Salmonella, E. coli or chromosome chromosome of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbria protein possesses both the immunogens, which may be important for directing an immune response in an animal munogens, which may be important for directing an immunogens, which may be important for directing an immunogens, which may be important for directing an easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                            76.7%; Score 600; DB 3; Length 151; 81.5%; Pred. No. 7.8e-50; ive 4; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Matches 123; Conservative
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of the gene can described are:

(1) use of thin aggregative fimbrine (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and casembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant configuration of a recombinant gene into the chromosome of the homologous species, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an emino acid polymer comprising a replacement segment or segments of foreign main.

(C) copy of that gene; and (4) eliciting an immune response in an animal, comprising sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or colymer into the animal in conjunction with a carrier or dilutent. (1) is polymer into the animal in conjunction with a carrier or dilutent. (1) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/Cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response capaning the present for directing an immune response in an animal. The present sequence is given in inexpensive to purify in large amount. The present sequence is given in
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
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Pred. No. 1.3e-47;
5; Mismatches 24
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                                                                                                                                                                                       Disclosure, Page 136, 139pp, English
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80.8%;
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Best Local Similarity 80.8
Matches 122, Conservative
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Plasma protein; immune response; antibacterial; vaccine; gene therapy

Escherichia coli.

WO2003064446-A2 07-AUG-2003

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbried (SEFI/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and comprising recombination of submologues pecies, (3) directing recombinant gene into the chromosome of the homologue species, respectively; (2) directing recombinant gene into the chromosome of the homologue species, replacing the native copy of that gene; and (4) eliciting an immon of a propriet separating a main of a limmune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino grad sequence or sequences grown on a Salmonella, E. coli or Enterobacteriace host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is electing an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrin protein sare usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and innexed in hyper animal in conjuncting in home and sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                         Kay WW;
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                                                                                                                                                                                                                                                                                                        Disclosure; Page 135; 139pp; English.
                                                                                                                     Collison SK,
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05-APR-2000; 2000WO-CA000356.
                                         99US-0127888P
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Matches 104; Conservative
                                                                              (UYVI-) UNIV VICTORIA
                                                                                                                       Doran JL,
                                                                                                                                                              2000-672631/65.
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                                       05-APR-1999;
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ABR82651
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New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.

Disclosure; Page 41-42; 42pp; English.

Herwald H;

Wikstroem M,

Bjoerck L, Olsen A,

WPI; 2003-646136/61. N-PSDB; ACF36153.

30-JAN-2003; 2003WO-EP000943. 31-JAN-2002; 2002GB-00002275 (HANS-) HANSA MEDICAL RES AB

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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642. ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
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Matches 103, Conservative
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68.9%; Pred. No. 2e-42;
ive 18; Mismatches 29; Indels
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9

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Indels

66.2%; Score 518; DB 7; Length 151; 68.2%; Pred. No. 6.2e-42;

Mismatches

18;

2, 2004, 14:48:28 completed: August

E. coli CsgA subunit 15 kDa protein.

(Olden) Andla seport sint

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3739, Ap
Sequence 5130, Ap
Sequence 18, Appl
Sequence 53, Appl
                                                        August 2, 2004, 14:40:48 ; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                US-09-543-407-26
782
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                          389414
                                                                                                                                                                                                                                                                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                   389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length D
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78.5
78
77.5
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                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                   Database :
                                                                                                                       Sequence:
                                                                                                                                                                        Searched:
                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
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Sequence 9, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 5434, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 17, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli		DETECTION	Length 151; Indels 0; Gaps 0;
28 77 9.8 1338 2 US-08-728-470-9 31 77 9.8 1529 3 US-08-719-641-9 31 77 9.8 1529 3 US-08-719-641-10 32 77 9.8 1529 3 US-08-719-641-10 33 77 9.8 1599 2 US-08-617-697-9 34 77 9.8 1600 2 US-08-617-697-9 35 76.5 9.8 363 1 US-09-458-023B-5 36 76.5 9.8 435 2 US-08-458-023B-5 37 76.5 9.8 435 2 US-08-458-023B-5 38 76.5 9.8 435 3 US-09-168-406A-2 39 76.5 9.8 941 4 US-09-336-447A-9 40 76.5 9.8 1612 1 US-07-792-259-17 41 76 9.7 1385 1 US-07-876-280-2 42 76 9.7 1385 1 US-07-876-280-2 44 76 9.7 1385 1 US-08-158-232-2 45 76 9.7 1385 1 US-08-158-232-2 45 76 9.7 1385 1 US-08-158-232-2	ALIGNMENTS	RESULT 1  US-08-233-788A-59  Sequence 59, Application US/08233788A  Sequence 59, Application US/08233788A  Sequence 59, Application US/08233788A  Sequence 59, Application US/08233788A  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, Karen S.  APPLICANT: Collinson, METHODS AND COMPOSITIONS FOR ITILE OF INVENTION: OF SALMONBLLA NUMBER OF SOURNCES: 61  CORRESPONDENCE ADDRESS:  ADDRESSEE: Seed and Berry  STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: U.S.A.  ZIP: 188104-700 Columbia Center, 701 Fifth Avenue STATE: Washington COUNTRY: Seattle STATE: Washington COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Defending MELOS OFFRANCE: Seed and Berry  SOFFWARE: PAPPLICATION DATA: APPLICATION: APPLICATION: 48.000  FILING DATE: 26-APR-1994  CLASSIFICATION NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REFERENCE/DOCKET NUMBER: 35,570  REGINENCE CHARACTERISTICS: LENGTH: 151 amino acids  TYPEL AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO acid  TYPE: AMINO a	Query Match 87.9%; Score 687; DB 1; Le Best Local Similarity 90.1%; Pred. No. 7e-60; Matches 136; Conservative 2; Mismatches 13;

1 MKLLKVAAPAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60

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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 VVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADV
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PATCHOLONY:
APPLICANT: NEWATION:
APPLICANT: Collinson, Faren S.
APPLICANT: Collinson, Faren S.
APPLICANT: Collinson, Faren S.
APPLICANT: Collinson, Faren S.
APPLICANT: Collinson, Faren S.
APPLICANT: Collinson, Faren S.
APPLICANT: Collinson, Faren S.
APPLICANT: Collinson, Faren S.
APPLICANT: OF SALMONELLA
NUMBER OF SEUTHORS: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: Ason Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: Washington
COUNTRY: U.S.A.
ALTOS SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: Detentin Release #1.0, Version #1.25
CORPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CORPATION SYSTEM: BC-ADS-1994
CLASSIFICATION NUMBER: US/08/233,788A
FILING DATE: Z6-APR-1994
CLASSIFICATION NUMBER: 35,570
REGISTRATION NUMBER: 35,570
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
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TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: MADER SEDIANBERRY
TENER: 3723836 SEEDANBERRY
NAME: LEMETHONE SEDIANDER SEDIANBERRY
NAME: LEMETHONE ASSED IN NO. 57: SEQUENCE HARACTERISTICS:
LEMETHONE ASSED IN NO. 57: SEQUENCE HARACTERISTICS:
LEMETHONE ASSED IN NO. 57: SEQUENCE HARACTERISTICS:
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Pred. No. 2.1e-42;
2; Mismatches 12; Indels
                                                                                                                                                                                          121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.5%;
Matches 98; Conservative
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amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-233-788A-57
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US-09-056-556-204
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; Sequence 204, Application US/09056556; Patent No. 6350456; GENERAL INFORMATION:

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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN----
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Houghton, Raymond
Vodvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.8%; Score 100; DB 4; Length 943; Best Local Similarity 26.0%; Pred. No. 0.2; Matches 40; Conservative 12; Mismatches 52; Indels
                                                                                                                           ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTRY: USA
ZIF: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLEASSFICATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INPORMATION POR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIA NUMBER OF SEQUENCES: 350 CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
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Patent No. 6458366
GENERAL INFORMATION:
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Dillon, Davin C.
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16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Davin C.
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houdarickson, Ronald C.
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES, 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN--
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                                                                                         GYGNGADVGOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN
                                          571 GSGNIGVENVGSGSLCNYNIGSGN-----LGIYNIGFGNVGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Tale PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT: APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                     122 ---NAALVNOTASDSSVM---VROVGFGNNATAN 149
                                                                                                                                                                                                                          661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.8%; Score 100; DB Best Local Similarity 26.0%; Pred. No. 0.2; Matches 40; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Sequence 204, Application US/09072967
Patent No. 6592877
GENERAL INSPENTION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION UNDRER: 21015
REFERENCE/DOCKET NUMBER: 21015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 943 amino acids amino acid
                                                                                                                                        611 GFGNAGDFNQGFANT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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US-09-072-967-204
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| Sequence 131, Application US/09477135A
| Patent No. 6572865
| GENERAL INFORMATION:
| APPLICANT: Nano, Francis
| TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding:
| TITLE OF INVENTION: immunostimulatory Peptides
| TITLE OF INVENTION: immunostimulatory Peptides
| TITLE OF INVENTION: immunostimulatory Peptides
| TITLE OF INVENTION: immunostimulatory Peptides
| FILE REPERENCE: 52888
| CURRENT APPLICATION NUMBER: US/09/477,135A
| PRIOR APPLICATION NUMBER: US/010375
| PRIOR FILING DATE: 1995-06-15
| PRIOR FILING DATE: 1995-06-15
| NUMBER OF SEQ ID NOS: 169
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN------ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.8%; Score 100; DB 4; Length 943; 26.0%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Indels
                                                                                                                                                         SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, DAVIG J.
REFERENCE/DOCKET NUMBER: 210121.417C9
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
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US-09-477-135A-131
                                          ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 943 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 26.0%
Marches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.0°
Matches 40; Conservative
STATE: Washington
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US-09-072-596-199
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Gaps

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Sequence 4764 pplication US/09328352

Sequence 4764 pplication US/09328352

Sequence 4764 pplication US/09328352

GENERAL INFORMATION:

APPLICANT: GATY L. Batton et al.

APPLICANT: GATY L. Batton et al.

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

LENGTH: 975

LENGTH: 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 ----GNGADVGQGADNSTI--ELTQNGFRNMATIDQWMAKNSDITVGQYG---GNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 NSFTLIGNSS---SSSVNTAPTITSNTVNDNDTID--NGNSGGTGSGSGNGSGDGLLNGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 -----YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 GGGNHN------GGGNSS---GPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Gaps
                                                                                                                                                       APPLICANT: AEBI, CHRISTOPH
APPLICANT: AEBI, CHRISTOPH
APPLICANT: ACBI, CHRISTOPH
APPLICANT: ACBI, CHRISTOPH
APPLICANT: MACIVEL, ISOBEL
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FEBDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT APPLICATION NUMBER: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATCHIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 975;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDTNDANG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.9%; Score 93; DB
ilarity 27.7%; Pred. No. 0.89
Conservative 14; Mismatches
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11.7%; Score 91.5; D
Best Local Similarity 27.4%; Pred. No. 1.4;
Matches 37; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 V----NQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AGGSHNQATGEGSF---AAGVENKANAN 218
                                                                             Sequence 5, Application US/09336447A Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), ORGANISM: Acinetobacter baumannii
US-09-328-352-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 41; Conserv
                                                                                                                                     GENERAL INFORMATION:
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US-09-328-352-4764
                                                     JS-09-336-447A-5
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                                                                                                                                                                                                                                                                     APPLICANT: KINIO NAKASHINA et al.

APPLICANT: KINIO NAKASHINA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED TERREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

TITLE OF INVENTION: TO SAID POLYPEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TRVVTHEMAHAGYGNGADVGQGADNSTIELTQ----NGFRNNATIDQWNAKNSDITVGQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1850.....

GITY: TSU-city

STATE: Mi-prefecture

COUNTRY: JAPAN

ZIP: 514-01

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage

COMPUTER: Law Compatible

OPERATING SYSTEM: Microsoft Windows 95

COMBUTER: Law Compatible

OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: May 28, 1997

APPLICATION NOTABER: US, 08/864,038A

FILING DATE: May 28, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 8-184459

FILING DATE: 15-0419-1996

ATTORNEY/AGENT INFORMATION:

NAME: C. Eruce Hamburg

REFERENCE/DOCKET NUMBER: P-5610

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 YGGNNAALVNQTASDSS-----VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 LGGGSAAAAAAAAAAGGGGRALRRALRROMRGGGSAAA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GGGGGGNGGGNGGGGG-
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                                                  554 GIGNSGLFNSGINNVGIFNAGIGNVGIANSGIGN 587
122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
12.6%; Score 98.5; DE
Best Local Similarity 28.1%; Pred. No. 0.2;
Macches 45; Conservative 11; Mismatches
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IDENTIFICATION METHOD: E (by experiment)
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CELL TYPE: mantle epithelial cell
                                                                                                                                                                                           Sequence 3, Application US/08864038A
Patent No. 6001592
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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                                                                                                                                     RESULT 7
US-08-864-038A-3
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                    RESULT 13
US-09-841-835-8
US-09-841-835-8
Sequence 8, Application US/09841835
Pacent No. 6506587
GENERAL INFERMATION:
APPLICANT: de Lange, Titia
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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486 GANIGSGASGITVVQ--SQNGANIGSGASGISVVQSQSG 522
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATENIN PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Ver
CURRENT.APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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INFORMATIÓN FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 34; Conservative
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TYPE: amino acid
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USA
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US-09-196-387-8
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Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6167
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11.3%; Score 88; DB '
Best Local Similarity 28.5%; Pred. No. 0.6;
Matches 43; Conservative 19; Mismatches
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              393 ASGNGEHNYGIGNGN 407
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US-09-252-991A-26438
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                                                                                                                                                    RESULT 10
US-09-328-352-6167
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE: 100/196,387
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 201-343-1684
                        09/095,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09841835
Patent No. 6506587
                   APPLICATION NUMBER: 09/095, FILING DATE: June 10, 1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 133521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 949 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-196-387-10
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 34; Conserv
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQL--- 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.5%; Score 82; DB 4; Length 673; Best Local Similarity 29.6%; Pred. No. 7.4; Matches 34; Conservative 14; Mismatches 59; Indels
                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMCPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600-1-230 CIP1
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTBRISTICS:
LENGTH: 673 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-841-835-8
                                                                     New Jersey
USA
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CLASSIFICATION:
                                                                                         COUNTRY: U
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 GVSSTAPLGPGAÁGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
TITLE OF INVENTION: OF USE THEREOF
TORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                               10.5%; Score 82; DB 3; Length 949; 29.6%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REBERENGCE/DOCKET NUMBER: 600-1-230 CIP1
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERESTICS:
IRNGTH: 949 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600-1-230 CIP1
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TOPOLOGY: linear

Wollectur Type: protein
US-09-841-835-10

Query Match
Best Local Similarity 29.6%; Pred. No. 12;
Matches 34; Conservative 14; Mismatches 59; Indels 6; Gaps 4;

G VAAFAI-VVSGSALAGVVPQWGGGGNSGPDSTLSIYQYGSANAALYDQL--- 61

OY 6 VAAFAI-VVSGSALAGVVPQWGGGSNNSPSSSSPTS: SSSSPSSPGSSLASSPSPA 157

OY 62 -VTRVVTHEMAHAGYGNGAPNPAGSGSNNSPSSSSPTSS-SSSSPGSSLASSPEA 157

OY 62 -VTRVVTHEMAHAGYGNGADVGGADNSTIELTGONG--FRNNATIDQWNAKNSDI 113

Db 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKOM 212

Search completed: August 2, 2004, 14:58:36
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(0108N) YUD18 860d S141

us-09-543-407-26.rapb

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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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782
1 MKLLKVAAFAAIVVSGSALA.......bSSVMVRQVGFGNNATANQY
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  1291235 seqs, 313682936 residues
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Sequence 146, App	Sequence 131, App	Seguence 131, App	Sequence 131, App	Sequence 199, App	Sequence 204, App	Sequence 64369, A	Sequence 20619, A	Sequence 49412, A	Semience 5 Annli
	QH	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-09-793-306-146	US-09-996-634-131	US-09-997-182-131	US-09-997-181-131	US-10-193-002-199	US-10-084-843-204	US-10-282-122A-64369	US-10-369-493-20619	US-10-282-122A-49412	US-09-952-267-5
	DB	12	12	12	12	15	σ	თ	10	10	14	14	12	15	12	10
	Query Match Length	151	151	131	131	445	597	943	943	943	943	943	3300	486	186	892
₩	Query Match	66.5	66.5	56.5	56.5	14.9	13.4	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.3	11.9
	Score	520	520	442	442	116.5	105	100	100	100	100	100	100	98.5	96	69
	Result No.	-	71	М	4	w	ω	7	æ	σ	10	11	12	13	14	15

Sequence 114193,	equence 625	equence 21,	quence 193	equence 1623	23,	equence 11, 7	equence 64573	equence 44999	62472	equence 6	equence 6775(	equence 10, A	equence 11, 7	equence 998,	equence 20397		equence 18460,	equence 12420,	equence 64364,	15	49	28, 7	e 148	e 80,	105	e 1529	e 120	487	1ce 553
US-10-437-963-114	US-10-282-122A-6254	US-09-820-843A-2	US-10-437-963-19306	US-10-437-963-16	US-10-233-553-23	US-10-233-553-1	US-10-282-122A-6457	US-10-282-122A-4499	US-10-282-122A-624	US-10-282-122A-6779	US-10-425-114-6775	US-10-185-990-10	US-10-185-990-1	US-10-408-765A-998	US-10-424-599-20	-10-479-670-164	US-10-369-493-1846	US-10-369-493-124	US-10-282-122A-6436	US-10-424-599-2151	US-10-425-114-49	09-810-264-28	US-10-437-963-1	US-10-479-670-80	US-10-437-963-10541	US-10-437-963-15292	US-10-437-963-1201	0-424-599-14844	US-10-425-114-5533
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 5 11.8	2,5 11.8 1	92 11.8	92 11.8	1.5 11.7	5 11.7	1:5 11.7	91 11.6	1 11.6	1 11.6 1	1 11.6 6	8.5 11.3	8.5 11.3 1	8:5 11.3 1	88 11.3 1	7:5 11.2	7.5 11.2	7.5 11.2 1	87 11.1	6.5 11.1 2	86 11.0	5.5 10.9	5.5 10.9	85 10.9	4:5 10.8	4 10.7	4 10.7	4 10.7	4 10.7	4 10.7
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#### ALIGNMENTS

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Sequence 4, Application US/09741873B
Publication No US20020081722A1
GENERAL INFORMATION:
APPLICANT:
Olsen, Arne
APPLICANT:
Olsen, Arne
TITLE OF INVATION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT APPLICATION NUMBER: US 88/104-04
PRIOR APPLICATION NUMBER: US 88/104-04
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1991-11-06
PRIOR PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1992-11-06
PRIOR FILING DATE: 1994-01-28
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; ORGANISM: Escherichia coli
US-09-741-873B-4
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ö Query Match
66.5%; Score 520; DB 12; Length 15
Best Local Similarity 68.2%; Pred. No. 2.2e-44;
Matches 103; Conservative 19; Mismatches 29; Indels

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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60

3 10:54:42 2004

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56.5%; Score 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT , ORGANISM: Escherichia coli US-09-741-873B-2
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US-09-741-873B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 GFGNNATANOY 151
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US-V9-V41-8/58-9

Sequence 4, Application US/09741873B

Publication No. US2004009565A9

GENERAL INFORMATION:
APPLICANT: Olsen, Arne
APPLICANT: Olsen, Arne
TITE OF INVENTION: Piblicancetin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012089-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US/08/741,873B

CURRENT APPLICATION NUMBER: US/08/73-1

PRIOR APPLICATION NUMBER: US/08/73-1

PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: US/07/347,189

PRIOR FILING DATE: 1991-11-06

PRIOR APPLICATION NUMBER: US/07/789,437

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

NUMBER OF SEQ ID NOS: 10

SOFTWARRE: Patentin Version 3.0

SOFTWARRE: Patentin Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09741873B
Publication No. US20020081722A1
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
                                                                             LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                Escherichia coli
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US-09-741-873B-2
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US-09-741-873B-4
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APPLICANT: Novement, Content Anne TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
PRIOR PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PRING DATE: 1989-11-06
PRIOR PRING DATE: 1989-11-06
PRIOR PLING DATE: 1991-11-06
PRIOR PLING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PLING DATE: 1994-01-28
PRIOR PLING DATE: 1994-01-28
PRIOR PLING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Version 3.0
SOFTWARE: PatentIn Version 3.0
SET UND SET OF SEQ ID NOS: 10
SET OF SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBER: US SECTION NUMBE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
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56.5%; Score 442; DB 12;
Best Local Similarity 64.9%; Pred. No. 1.3e-36;
Matches 85; Conservative 18; Mismatches 28;
PRIOR APPLICATION NUMBER: SE 8801/23-1
PRIOR FILING DATE: 1998-05-06
PRIOR PLING DATE: 1998-05-06
PRIOR PLING DATE: 1997-11-26
PRIOR PLING DATE: 1997-11-26
PRIOR PELICATION NUMBER: US 07/347,189
PRIOR PELICATION NUMBER: US 07/789,437
PRIOR PELICATION NUMBER: US 07/789,437
PRIOR PLING DATE: 1991-11-06
PRIOR PLING DATE: 1991-11-03
PRIOR PLING DATE: 1992-11-03
PRIOR PLING DATE: 1994-01-08
PRIOR PLING DATE: 1994-01-08
PRIOR PLING DATE: 1994-01-08
PRIOR PLING DATE: 1994-01-08
PRIOR PLING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PARCHAIN OF SEQ ID NOS: 10
SOFTWARE: PARCHAIN VERSION 3.0
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Length 131;

DB 12;

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387 GFGNAGDINTGFGNAGD--TNTGFGNAGFFNWGIGNAGNEDMGVGNGGSFNVGVGN--AG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 LTGDNLVGIGALNSGIGN-LGFGNSG--NNNIGFFNSGNNNVGFFNS-----GNNNF 386
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Sequence 131, Application US/09996634

GENERAL INFORMATION:

APPLICANT Non-US20020172684A1

SERREAL INFORMATION:

TITLE OF INVENTION: Immunostimulatory Peptides

TITLE OF INVENTION: Immunostimulatory Peptides

TITLE OF INVENTION: Immunostimulatory Peptides

TITLE OF INVENTION: Immunostimulatory Peptides

TITLE OF INVENTION: Immunostimulatory Peptides

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TITLE OF INVENTION: Immunostimulatory Peptides

TITLE OF INVENTION: Immunostimulatory Peptides

TITLE OF INVENTION: Immunostimulatory Peptides

PRIOR FILING DATE: 1990-01-03

PRIOR FILING DATE: 1996-06-14

PRIOR FILING DATE: 1995-06-15

NUMBER OF SEQ ID NOS: 169

SEQ ID NO: 131

LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNNAALVNQTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His US-09-793-306-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.4%; Score 105; DB 9; Length 597; llarity 29.0%; Pred. No. 0.065; Conservative 18; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%; Score 100; DB 9; Length 943; 26.0%; Pred. No. 0.37; ive 12; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN-
TITLE OF INVENTION: Of Tuberculosis FILE REFERENCE: 014058-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-25
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR APPLICATION NUMBER: US 60/223,828
NUMBER OF SEQ ID NOS: 164
SOFTWARE: PARENTIN Ver: 2.1
SEQ ID NO 146
ILBNGTH: S97
TYPE: PARENTIN STATE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 DSSVMVRQVGFGNNATAN 149
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REPERENCE: 38-203-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-22
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
                                                                                                                                                                              VGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                               51 GSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GNSNSVGRD-----IQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                      9
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Patent No. US20020098200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
                                                                                                              21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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Best Local Similarity 27.5%; Pred. No. 0.0032;
Matches 46; Conservative 20; Mismatches 60; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 DPGVFNKITQDSSSNGSKVSVIQDGKNNVFSIKQGNTGNSTSVNQIG 176
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        Pred. No. 1.3e-36;
3; Mismatches 28; Indels
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DAME/KEY: unsure

LOCATION: (1): (445)

OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20638
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20638, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rhodopseudomonas palustris
                                  18;
     64.98;
                                85; Conservative
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                                                                                                                                                                                                                                                                                  141 GFGNNATANQY 151
        Best Local Similarity
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US-10-369-493-20638
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US-09-793-306-146
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US-10-193-002-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 131, Application US/09997181
| Publication No. US20030049269A1
| Publication No. US20030049269A1
| SEQUENCE 131, Application No. US20030049269A1
| SEQUENCE 1 INFORMATION: Mycobacterium Tuberculosis DNA Sequences Encoding
| TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences FILE REFERENCE: 61257
| TITLE OF INVENTION: immunostimulatory Peptides
| FILE REFERENCE: 61257 | SEQUENCE: 61257 | SETTION OF INVENTION: immunostimulatory Peptides
| FILE REFERENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 61267 | SEQUENCE: 1996-06-14 | SEQUENCE: PATENTION NUMBER: 60/000,254 | SEQUENCE: PATENTION PATE: 1995-06-15 | NUMBER OF SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTION PATE: 1995-06-15 | SEQUENCE: PATENTI
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences
FILE REFERENCE: 61286
CURRENT APPLICATION NUMBER: US/09/997,182
CURRENT FILING DATE: 2001-11-28
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1996-06-14
PRIOR FILING DATE: 1996-06-14
PRIOR FILING DATE: 1996-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.0
SSETURE: DATENTING DATE: 1000-131
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12.8%; Score 100; DB 10; Length 943;
Best Local Similarity 26.0%; Pred. No. 0.37;
Matches 40; Conservative 12; Mismatches 52; Indels 5
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122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                         661 GTGNSGLFNSGTNWGIFNAGTGNVGIANSGTGN 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-997-182-131
                                                                                                                                                                                                                                                                             Sequence 131, Application US/09997182 Publication No. US20030049263A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-997-181-131
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                                                                                                                                                Gaps
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Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
Hendrickson, RombonnDs AND METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: COMPONDS.
                                                                                                                                             50;
                                                                                          12.8%; Score 100; DB 10; Length 943; 26.0%; Pred. No. 0.37; ive 12; Mismatches 52; Indels 5:
                                                                                                                                                                                                                                                571 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY----
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                 74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                        122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 210121.417C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-WAY-1998
ĀTTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-997-181-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 199, Application US/10193002
Publication No. USZ0030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-49
TELEFAX: (206) 682-6031
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SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       611 GFGNAGDFNQGFANT----
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                                                                                                    Query Match
Best Local Similarity 26.01
Matches 40; Conservative
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---NV 503
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  GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
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                                                                                                 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN
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                                              GSGNIGVENVGSGSLGNYNIGSGN----LGIYNIGFGNVGDY---
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                                                                                                                                                                                             122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                                                                                                                                                                                                           554 GIGNSGLFNSGINNVGIFNAGIGNVGIANSGIGN 587
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PRING DATE: 2000-03-21
PRIOR PLING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-29
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                               Sequence 64369, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis
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SEQ ID NO 64369
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Ohlsen, Kari
Zyskind, Judith
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Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 26.0°
Matches 40; Conservative
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Zamudio, Carlos
Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carlos
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Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                        Publication No. US200
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      RESULT 12
US-10-282-122A-64369
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ORGANISM:
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                                                                                                                                                                                                                                              504 GFGNAGDFNQGFANT-----GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553
                                                                                                 73
                                                                                                 16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
                                                     Gaps
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
Query Match 12.8%; Score 100; DB 14; Length 943; Best Local Similarity 26.0%; Pred. No. 0.37; Matches 40; Conservative 12; Mismatches 52; Indels 5
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                                                                                                                                            164 GSGNIGVENVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
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                                                                                                                                                                                                                                                                                            122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                     554 GIGNSGLFNSGINNVGIFNAGIGNVGIANSGIGN 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-10-084-843-204
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-084-843-204
; Sequence 204, Application US/10084843
; Publication No. US20030143243A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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57 LYDQLVTRVVTHEMAHAGYGNGADVG--QGADNST-IELTQNG-----FRNNAT 102
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PRIOR FILING DATE: 2000-03-21

PRIOR PADLICATION NUMBER: 60/206,848

PRIOR PAPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/200,335

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-01-02-3

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-26

PRIOR PILING DATE: 2000-12-26

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 IDOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Indels
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Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 96; DB 12
29.3%; Pred. No. 0.12;
tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
, ORGANISM: Moraxella catarrhalis
US-09-952-267-5
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27.7%;
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Best Local Similarity
Matches 49; Conserv
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Best Local Similarity
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US-10-282-122A-49412
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                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Alater, Steven C.

APPLICANT: Gldman, Barry S.

APPLICANT: Chen, Xianfeng

ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)8

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT PLING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20619
                                                                          630 GFGNAGDFNQGFANT-----GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 -----VIIHTAAVGGRPRGALISQG--NLLI-----AQSSLVDAWRLTEADVNLGM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Forsyth, R. APPLICANT: Xu, H. TILLE OF INVENTION: Identification of Essential Genes in Microorganisms TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL
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25.7%; Pred. No. 0.23;
tive 22; Mismatches 50; Indels
                                                                                                                                                 122 ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                                                                                                                                                                 680 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure

: LOCATION: (1).:(486)

: OTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-20619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 ----QYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 LPLFHVTGLGLMLTLQQAGGAŠVI 212
                                                                                                                                                                                                                                                                                                                        RESULT 13
US-10-369-493-20619
; Sequence 20619, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Garr, Grant
APPLICANT: Carr, Grant
APPLICANT: Famamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.73
Matches 37; Conservative
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US-10-282-122A-49412
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Sequence 5, Application US/0995267

Publication No. US2003003272A1

GENERAL INFORMATION:

APPLICANT: HANSEN, ERIC J.

APPLICANT: ABSI, CHRISTOPH

APPLICANT: COPE, LESLIE D.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FISKE, MICHAEL J.

APPLICANT: FOR J.

APPLICANT: FOR J.

APPLICANT: POSPERIOR SOSS A.

TITLE REFERENCE: ANCY:024

CURRENT FILING DATE: 2001-09-12

CURRENT FILING DATE: 2001-09-12

PRIOR FILING DATE: 1999-06-21

NUMBER OF SEQ ID NOS: 98

SOFTWARE PARENTE PARENTIN VET: 2.1

SEQ ID NO S.
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(0,10/sn) 4UD/8 @60d s/4/

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sequence 24, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 30, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 24, Appli
Sequence 34, Appl
Sequence 34, Appl
Sequence 5834, Ap
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Sequence 5834, Appli
Sequence 32, Appli
Sequence 32, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 5833, Ap
Sequence 5833, Ap
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US-09-543-407-26

US-09-543-407-26

US-09-543-407-26

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: RAY, William W.

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

CURRENT FILING DATE: 2000-4.05

CURRENT FILING DATE: 2000-04-05

CURRENT FILING DATE: 2000-04-05

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 151
                           Sequence 20, P
Sequence 5, Ap
Sequence 57, Ap
Sequence 18, P
Sequence 28, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 199,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 204
Sequence 199
                                                                                                                                                                  Sequence 14,
Sequence 24,
Sequence 31,
Sequence 22,
                                                                                                                                              Sequence
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19 US-09-543-407-26
19 US-09-543-407-20
19 US-09-543-407-20
19 US-09-543-407-18
19 US-09-543-407-18
19 US-09-543-407-14
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266
201.5
                                                                                                                                                                         August 2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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                                                                                                                                                                                                                                                                   US-09-543-407-26
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1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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1: /cgn2 6/ptodateJ2/paa/PCTUS_COMB.pep: *

2: /cgn2 6/ptodateJ2/paa/BCTUS_COMB.pep: *

3: /cgn2 6/ptodateJ2/paa/US07 COMB.pep: *

4: /cgn2 6/ptodateJ2/paa/US081 COMB.pep: *

6: /cgn2 6/ptodateJ2/paa/US081 COMB.pep: *

6: /cgn2 6/ptodateJ2/paa/US082 COMB.pep: *

7: /cgn2 6/ptodateJ2/paa/US084 COMB.pep: *

8: /cgn2 6/ptodateJ2/paa/US084 COMB.pep: *

10: /cgn2 6/ptodateJ2/paa/US085 COMB.pep: *

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11: /cgn2 6/ptodateJ2/paa/US086 COMB.pep: *

12: /cgn2 6/ptodateJ2/paa/US087 COMB.pep: *

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14: /cgn2 6/ptodateJ2/paa/US089 COMB.pep: *

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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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                                                                                                                 1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                   1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
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                                                                               Gaps
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinaon, S. Karen
APPLICANT: Collinaon, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga, of OTHER INFORMATION: sequence containing the replacement fragment, OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-20
                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.7%; Score 709; DB 19; Length 151; ilarity 89.9%; Pred. No. 1.3e-67; Conservative 0; Mismatches 0; Indels 16
                                                                             Indels
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                                   Query Match 100.0%; Score 782; DB 19; Best Local Similarity 100.0%; Pred. No. 1.8e-75; Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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ORGANISM: Artificial Sequence
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Matches 143; Conserv
US-09-543-407-26
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US-08-213-642A-57
i Sequence 57, Application US/08233642A
j Sequence 57, Application US/08233642A
j GENERAL INFORMATION:
APPLICANT: Clouthier, S. March
APPLICANT: Clouthier, S. March
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: DORING AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: MEASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
ADDRESSE: Seed and Berry
ADDRESSE: Alon Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                          Query Match 88.5%; Score 692; DB 19; Length 1
Best Local Similarity 90.7%; Pred. No. 8.7e-66;
Matches 137; Conservative 2; Mismatches 12; Indels
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COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                       NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
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TELECOMUNICATION INFORMATION:
TELEPHON: (206) 622-6900
TELEFAX: (206) 682-6031
TELEFAX: 372384 SEEDANBERRY
INFORMATION FOR SEO ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           ) ORGANISM: Salmonella enteritidis
US-09-543-407-5
2000-04-05
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ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
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amino acid
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STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local S.
Matches 122
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| Sequence 28, Application US/09543407 |
| Sequence 28, Application US/09543407 |
| GENERAL INFORMATION: |
| APPLICANT: White, Aaron P. |
| APPLICANT: Octan, James L. |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Experiment Present Collinson, S. Karen |
| TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
ITILE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
ITILE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
ITILE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESO for Windows Version 4.0
SEQ ID NO 18
LENGTH: 151
TYPE: PRT
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86.3%; Score 675; DB 19; Length 151;
Best Local Similarity 81.9%; Pred. No. 5.9e-64;
Matches 136; Conservative 0; Mismatches 0; Indels 30
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 92043.407
CURRENT APPLICANION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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TYPE: PRT
CRGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
CTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-28
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                                                                                                                                                                                  Score 617; DB 19;
Pred. No. 1e-57;
0; Mismatches 0;
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Pred. No. 2.2e-57;
6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                       61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
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US-09-543-407-12
Sequence 12, Application US/09543407
GENERAL INFORMATION:
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80.8%;
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Best Local Similarity 73.6
Matches 128; Conservative
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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Description 16.9%; Score 601; DB 19; Length 151;
Best Local Similarity 81.5%; Pred. No. 5.5e-56;
Matches 123; Conservative 4; Mismatches 24; Indels
Matches 123; Conservative 4; Mismatches 24; Indels
                                                                                                                                                                   US-09-543-407-31
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US-09-543-407-22
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LENGTH: 131
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Sequence 24, Application US/09543407
Sequence 24, Application US/09543407
SEQUENCANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Ray, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTER M.
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASCESO for Windows Version 4.0
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OTHER INFORMATION: sequence containing the replacement fragment.
OTHER INFORMATION: encoding FT3 from GP63 of Leishmania major.
US-09-543-4407-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
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ORGANISM: Artificial Sequence
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123; Conservative
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US-09-543-407-24
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09543407
GENERAL INFORMATION:
APPLICANT: Wither, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: SOO: S. Karen
APPLICANT: SOO: SOO: SOO: Collinson
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                              APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DAPER: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA p. OTHER INFORMATION: sequence containing the replacement fragment orther INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.4%; Score 605; DB 19; Length 131; 89.3%; Pred. No. 1.7e-56; ive 2; Mismatches 12; Indels (
121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                      Sequence 31, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 117; Conserv
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US-09-543-407-7
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US-09-543-407-7
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FEATURE:
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                                                                           120
                                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REPERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16
                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALALQ
                                                                           61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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APPLICANT: White, Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.7%; Score 600; DB 19; Length 151; Best Local Similarity 81.5%; Pred. No. 7e-56; Matches 123; Conservative 4; Mismatches 24; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                              121 NNAALVNQTASDSSVWVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                 Sequence 30, Application US/09543407 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-09-543-407-16
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US-09-543-407-30
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US-09-543-407-30
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US-08-978-878-4
US-08-978-878-4
Sequence 4, Application US/08978878
SEQUENCE 4, Application US/08978878
SEQUENCE 4, APPLICANT NORMARK, Staffan
APPLICANT NORMARK, Staffan
TITLE 0F INVENTION FIREONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT PILING DATE: 1997-11-26
SALLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                 09
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                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                               1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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APPLICANT White, Aames L.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT RAY, William W.
TITLE OF INVENTION: BACETERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT PALLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTHARE: FASLESCE for Windows Version 4.0
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Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                    Length 151;
                                                                                                                                  73.8%; Score 577; DB 19; Length 15
80.8%; Pred. No. 2.1e-53;
tive 5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Indels
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68.9%; Pred. No. 1.4e-47;
tive 18; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 68.9%
Matches 104; Conservative
                                                                                                                                          Query Match 73.85
Best Local Similarity 80.85
Matches 122; Conservative
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     CTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-543-407-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.5%; Score 520; DB 13; Length 151; Best Local Similarity 68.2%; Pred. No. 2.9e-47; Matches 103; Conservative 19; Mismatches 29; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/18,519
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTING DATE: 1955-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTING DATE: 1955-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTING DATE: 105-06-28
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Escherichia coli
US-08-978-878-4
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Query Match
Best Local Similarity 69.2%
Matches 103; Conservative
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US-09-741-873C-4
  US-09-741-873C-4
SEQ ID NO 4
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Sequence 5, Appli
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Sequence 124, Appli
Sequence 124, App
Sequence 574, App
Sequence 574, App
Sequence 571, App
Sequence 571, App
Sequence 602, App
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                                                                     2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                             US-09-543-407-26
782
1 MKLLKVAAFAAIVVSGSALA.......bSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                       Pending_Patents_AA_New:*

1: /cgn2 6/ptcdata/2/paa/USO5_NEW_COMB.pep:*

3: /cgn2 6/ptcdata/2/paa/USO5_NEW_COMB.pep:*

4: /cgn2 6/ptcdata/2/paa/USO3_NEW_COMB.pep:*

5: /cgn2 6/ptcdata/2/paa/USO3_NEW_COMB.pep:*

5: /cgn2 6/ptcdata/2/paa/USO3_NEW_COMB.pep:*

7: /cgn2 6/ptcdata/2/paa/USO3_NEW_COMB.pep:*

7: /cgn2 6/ptcdata/2/paa/USO3_NEW_COMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-9741-873C-2
US-09-9741-873C-2
US-09-952-768-5
US-10-872-768-5
US-10-425-115-312468
US-10-425-115-312468
US-00-566-425-574
US-60-566-425-574
US-60-566-425-570
US-60-566-425-570
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US-60-576-812-603
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                                                                                                                                                                                        601315 seqs, 104695340 residues
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                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
                                                                                                                                                                    , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Gapop 10.0 ,
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                                                                                                                Title:
Perfect score:
                                                                                                                                                          Scoring table:
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                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                           Database
                                                                       Run on:
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No.
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1991-481-834C-4

Sequence 4, Application US/09741873C

GENERAL INFORMATION:
APPLICANT:
Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPRENCE 10289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT APPLICATION NUMBER: US 8801723-1
PRIOR PAPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1995-11-06
PRIOR PELLOR DATE: 1995-11-06
PRIOR PELLOR NUMBER: US 07/789,437
PRIOR PELLOR UNMBER: US 08/187,665
PRIOR APPLICATION NUMBER: US 08/187,665
PRIOR APPLICATION NUMBER: US 08/187,665
PRIOR APPLICATION NUMBER: US 08/187,665
PRIOR APPLICATION NUMBER: US 08/187,665
PRIOR PILING DATE: 1994-01-28
PRIOR PILING DATE: 1994-01-28
PRIOR PILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Version 3.0
                                       Sequence 30330, Sequence 193207, Sequence 193207, Sequence 7905, Ap Sequence 7906, Ap Sequence 7006, Ap Sequence 11109, A Sequence 21256, Sequence 3168, Ap Sequence 9168, Ap Sequence 226699, Sequence 741, App Sequence 741, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App 
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              Sequence
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68.2%; Pred. No. 5.5e-38;
ive 19; Mismatches 29; Indels
US-60-579-062-7907
US-10-425-115-1300390
US-10-425-115-1300390
US-60-565-632-7905
US-60-579-062-7906
US-60-579-062-7906
US-60-579-062-7906
US-60-565-632-1109
US-60-565-632-11109
US-60-565-632-11109
US-60-565-632-11109
US-60-565-632-11109
US-60-565-632-11109
US-10-172-115-219256
US-10-172-115-2168
US-10-170-2058-741
US-60-578-062-9168
US-10-170-2058-741
US-60-578-062-9168
US-10-170-2058-741
US-10-170-2058-741
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR PAPPLICATION NUMBER: US 8801723-1
PRIOR PAPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-11-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1991-11-03
PRIOR FILING DATE: 1991-11-03
PRIOR PELING DATE: 1991-11-03
PRIOR PELING DATE: 1994-00-05
PRIOR SPELICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Version 3.0
SOFTWARE: PatentIn Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD 80
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEB1, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: MACTVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
FILE REFERENCE: AMCY: 0.24
CURRENT FILING DATE: 2001-09-12
PRIOR PILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VET: 2.1
SECTIVE SECTION OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VET: 2.1
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.5%; Score 442; DB 5;
64.9%; Pred. No. 2.8e-31;
live 18; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09952267B GENERAL INFORMATION:
                                       Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Moraxella catarrhalis
US-09-952-267B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.9%
Matches 85; Conservative
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                                                                                           APPLICANT: Normark, Staffan
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US-09-952-267B-5
RESULT 2
US-09-741-873C-2
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                                                                                                                                                                                                                                    138 YSRAIGDSSTIGGGYYNQATGEXSTVAGGRNN----QATGNNSTVAGGSYNQATGNNSTV 193
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| GENERAL INFORMATION:
| APPLICANT: HANSEN, ERIC J.
| APPLICANT: ARBI, CHRISTOPH
| APPLICANT: ARBI, CHRISTOPH
| APPLICANT: OPE, LESLIE D.
| APPLICANT: FISSE, MCHAREL J.
| APPLICANT: FISSE, MCHAREL J.
| APPLICANT: FISSE, MCHAREL J.
| APPLICANT: FISSE, MCHAREL J.
| APPLICANT: FISSE, MCHAREL J.
| TITLE OF INVENTION: USPAI AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
| FILE REFERENCE: AMCY:024
| CURRENT FILING DATE: 2004-06-21
| FRIOR PILING DATE: 1999-06-21
| FRIOR FILING DATE: 1999-06-21
| NUMBER OF SEQ ID NOS: 999-06-21
| SOFTWARE: PATENTIN VET: 2.1
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                                                                                             28 GGGNHN-----GGGNSS---GPDSTLSIYQYGSANAALYDQLVTRVVTHEWAHAGY
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                                                  Gaps
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Sequence 5, Application US/10872769
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: COPE, LESLIE D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
FILE REPERENCE: AMCY:024
FILE REPERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/10/872,769
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
                                                  44;
11.9%; Score 93; DB 5; Length 892; llarity 27.7%; Pred. No. 5.7; Conservative 14; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 27.7%; Pred. No. 5.7;
Matches 41; Conservative 14; Mismatches 49; Indels
                                                                                                                                              89 GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDTNDANG---
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                                                                                                                                                                                                                                                                                              126 V----NOTASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                       194 AGGSHNOATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Moraxella catarrhalis
                              Best Local Similarity
Matches 41; Conserv
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US-10-872-769-5
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US-10-872-768-5
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            Query Match
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67 THEMAHAGYGNG----ADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----TVGQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        776 ISAF-HSGVGNTDSQLAGFMRNAAGGT--LFNFGFANDGTLNLGNANLGDYNVGSGNVGS 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 GADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVWV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVV 66
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.8%; Score 92; DB 6; Length 1459;
Best Local Similarity 25.0%; Pred. No. 12;
Matches 38; Conservative 20; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 574, Application US/60566425
GENERAL INFORMATION:
APPLICANT DOMON, BOLON DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001522-PROV
CURRENT APPLICATION NUMBER: US/60/566,425
CURRENT FILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
SOFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 91.5; DB 7; 27.1%; Pred. No. 7.7;
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                            CURENT APPLICATION NUMBER: US/10/482,706
CURENT FILING DATE: 2004-01-02
PRIOR APPLICATION NUMBER: PCT/GB02/03052
PRIOR FILING DATE: 2002-07-04
PRIOR FILING DATE: 2001-07-04
PRIOR FILING DATE: 2001-07-04
PRIOR FILING DATE: 2001-07-04
PRIOR FILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 282
SOFTWARE; Patentin version 3:1
SOFTWARE; Patentin version 3:1
LENGTH: 1459
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GENERAL INFORMATION:
APPLICANT: DOMON, Bruno
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874 SQGGYGRNA 882
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Best Local Similarity
Matches 35; Conserv
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US-60-566-425-574
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US-60-576-812-606
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
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GENERAL INFORMATION:
APPLICANT: James, Baian William
APPLICANT: March, Philip
APPLICANT: Hampshire, Tobias
TITLE OF INVENTION: Mycobacterial Antigens Expressed During Latency
                                                                                                                                                                                                                      Query Match
11.9%; Score 93; DB 6; Length 892;
Best Local Similarity 27.7%; Pred. No. 5.7;
Matches 41; Conservative 14; Mismatches 49; Indels
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11.8%; Score 92; DB 6; Length 295;
Best Local Similarity 25.3%; Pred. No. 2;
Matches 37; Conservative 13; Mismatches 40; Indels
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US-10-425-115-312468
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                                                                                                                         TYPE: PRT ORGANISM: Moraxella catarrhalis
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 892
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-60-566-425-578
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US-60-566-425-575
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                    SEQ ID NO 571
LENGTH: 894
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11.7%; Score 91.5; DB 7; Length 894;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 47
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11.7%; Score 91.5; DB 7; Length 891;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 4
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GENERAL INFORMATION:
APPLICANT: DOMON, Bruno et al.
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001522-PROV
CURRENT FILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
SOFTWARE: FactSEQ for Windows Version 4.0
ERQ ID NO 570
LENGTH: 894
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TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
FILE REPERENCE: CL001522-PROV
CURRENT APPLICATION NUMBER: US/60/566,425
CURRENT FILING DAIE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
    TITLE OF INVENTION: COLON DISBASE TARGETS AND USES THEREOF FILE REFERENCE: CL001527PROV CURRENT APPLICATION NUMBER: US/60/576,812 CURRENT FILING DATE: 2004-06-04 NUMBER OF SEQ ID NOS: 1501 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 606
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US-60-256-425-571
Sequence 571, Application US/60566425
GENERAL INFORMATION:
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877 SQGGYGRNA 885
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874 SQGGYGRNA 882
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CRGANISM: Homo sapiens
US-60-566-425-570
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ORGANISM: Homo sapiens
US-60-576-812-606
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US-60-566-425-570
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                                                                                               11.7%; Score 91.5; DB 7; Length 894; ilarity 27.1%; Pred. No. 7.7; Conservative 15; Mismatches 32; Indels 47
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GENERAL INFORMATION:
APPLICANT: DOMON, Burno et al.
APPLICANT: DOMON, Burno et al.
APPLICANT: DOMON, Burno et al.
APPLICANTION: COLON DISEAE TARGETS AND USES THEREOF;
FILE REFERENCE: CLO01522-ROV
CURRENT APPLICATION NUMBER: US/60/566,425
CURRENT FILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
SEQ ID NO 578
LENGTH: 894
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GENERAL INFORMATION:
APPLICANT: DOMON, Bruno et al.
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CLOOL522-RROV
CURRENT APPLICATION NUMBER: US/60/566,425
CURRENT FILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 575
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US-60-566-425-575
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ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Homo sapiens
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Matches 35; Conserv
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11.7%; Score 91.5; DB 7; Length 894;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 47; Gaps
                                                                              Gaps
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                                    11.7%; Score 91.5; DB 7; Length 894; 27.1%; Pred. No. 7.7; ive 15; Mismatches 32; Indels 4
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11.7%; Score 91.5; DB 7; Length 894;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 602, Application US/60576812
GENERAL INFORMATION:
APPLICANT DOMON, Bruno
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/60/576,812
CURRENT FILING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 1501
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence (603, Application US/60576812
GENERAL INFORMATION:
APPLICANT DOMON, Bruno
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001527PROV
CURRENT PELING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 1501
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 894
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Best Local Similarity 27.18
Matches 35; Conservative
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ORGANISM: Homo sapiens
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US-60-576-812-603
US-60-566-425-578
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US-60-576-812-602
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US-60-576-812-603
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us-09-543-407-26.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec Run on:

US-09-543-407-26 782 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY

151

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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30	31	32	33	34	32	36	3.7	38	39	40	41	42	43	44	45	

#### ALIGNMENTS

 RESULT 1 JC6639 finbrin protein ac C;Species: Salmone C;Date: 31-Dec-195 C;Accession: UC603 R;Collinson, S.K., J. Bacteriol, 178, A,Title: Salmonell A,Reference number A,Accession: UC603 A,Molecule Lype: A,Residues: 1-15: A,Residues: 1-15: A,Residues: 1-15: A,Residues: 1-15:	PESULT 1  Indicates a standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard of the standard
A, Accession: PC60 A, Rosidues: 175: 18, Residues: 175: 18, Residues: 175: 18, Rocallinson, S.K., J. Bacteriol: 173, A, Title: Purificat A, Reference number: 27655 A, Accession: A4488 A, Residues: 27655 A, Residues: 27655 A, Residues: 27655 A, Residues: 27655 A, Residues: 27655 A, Residues: 27655 A, Residues: 27655 A, Residues: 27655 A, Residues: 27655 A, Residues: 21-33	Alacession: PC601 Alacession: PC602 Alacession: PC602 Alacession: PC602 Alacession: PC602 Alacession: PC602 Alacession: 21-52 <cc2> Alacession: Alacession: Alacession and characterization of thin, aggregative fimbriae from Salmonell Alacession: A44898 Alacession: A44898 Alacession: A4898 Alacession: A4898 Alacession: A4898 Alacession: A4898 Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession: Alacession</cc2>
 A, October 3 and M, Genetics: A, Gene agfa C, Function: A, Description C, Keywords: F, 1-20/Domain	Afforms agfA.  C,Genetics: A,Gene agfA.  A,Gene agfA.  A,Gene agfA.  A,Gene agfA.  A,Description: major component of thin aggregative fimbriae  A,Description: major component of pasminogen, tissue plasminogen activator  C,Keywords: fimbria  F,1-20/Domain: signal sequence #status predicted <sig> F,1-20/Domain: signal sequence agfA #status experimental <mat></mat></sig>
 Query Match Best Local Matches 13 Qy 1	Ouery Match Best Local Similarity 90.7%; Pred. No. 3.6e-51; Matches 137; Conservative 2; Mismatches 12; Indels 0; Gaps 0; MALLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
 os es os	61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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60 QLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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NyAlternate names: csgA protein, major curlin protein

Cipscales: Escherichia coli

Cipscales: Escherichia coli

Cipacesion: 207088; G4846; S31202; S34560; S34559

Cipacesion: 570788; G4846; S31202; S34560; S34559

RiHammar, M.; Arnqvist. A.; Bian, Z.; Olsen, A.; Normark, S.

Mol. Microbiol. 18, 61-670, 1995

A;Accession: 570788; MUD:9614468; PMID:8817489

A;Accession: 570788; MUD:96414468; PMID:8817489

A;Accession: 570788; MUD:9614468; PMID:8817489

A;Accession: 570788; MUD:9614468; PMID:8817489

A;Accession: 570788; MUD:9614468; PMID:8817489

A;Accession: 570788; MUD:91147558; PIDN:CAA62282.1; PID:91147564

A;Accession: 570788; MUD:91147558; PIDN:CAA62282.1; PID:91147564

A;Accession: Source: strain K12, substrain Willo

A;Residues: 1-151 cAMA.

A;Cross-reference rumber: A64720; MUD:97426617; PMID:9278503

A;Accession: G4846

A;Cross-reference number: A64720; MUD:97426617; PMID:9278503

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                                                                                                                                                                                                                               major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Typin (5)Species: Salmonella enterica subsp. enterica serovar Typin (5)Species: Salmonella enterica subsp. enterica serovar Typin (5)Species: Salmonella enterica subsp. enterica serovar Typin (5)Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (5)Accession: Al0635 (6) Tames, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R.; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, K.; T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; O'Gaora, P. (6) Tames, M.; Simmonds, M.; Skelton, J.; Stevens, K.; Althors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Alter encomplete genome sequence of a multiple drug resistant salmonella enterica serov A; Reference number: AB0502; MUID:21534947; PMID:11677608 A; Residues: 1-151 cPAR>
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A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Genetics: A, Gene
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Pred. No. 3.6e-51;
2; Mismatches 12;
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NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Matches 137; Conservative
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A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csg;
A;Reference number: S31202; MUID:93211294; PMID:8459772
A;Accession: S31202
A;Redidues: 1-6, 'V', 8-151 < OLS1>
A;Coss-references: EMBL:L04979
A;Coss-references: EMBL:L04979
A;Residues: 121-42;44-50 < OLS2>
A;Residues: 21-42;44-50 < OLS2>
B;Olsen, A.N.; Armqvist, A.M.
Submitted to the EMBL Data Library, October 1992
A;Recersion: S34559
A;Recersion: S34559
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
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A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
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A Modecule type: DNA
A Modecule type: DNA
A Meeddues: 1-152 KHAY>
A Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:913360880; GSPDB:GN00154
A Cross-references: GB:BA001007; PIDN:BAB34843.1; PID:91360880; GSPDB:GN00154
A CROSS-references: GB:BA001007; PIDN:BAB34843.1; PID:91360880; GSPDB:GN00154
A CROSS-references: GB:BA001007; PIDN:BAB34843.1; PID:91360880; GSPDB:GN00154
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68.9%; Pred. No. 5.3e-37;
cive 18; Mismatches 29
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QY 3 LLKVAAFAAIVYSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANA 55  DD 1 MIRKSFIASALVALVGLSAAABAMANDVRIEQYGWSNSAGGAQEGYGNRITYQNGGYN- 59  QY 56 ALYDQLVTRVHPRAHAGYGNGADNSTIELTQNGFRNATIDQWNARNSDITV 115  DD 60RIVOHQYGRHNLSAVQSEGHDNYGSTTQNGRRNVAGI 96	Oy 116 GQYGGUNAALVNQTASDSSVAVYRQVGFCRNATANQ 150  Db 97 GQFGSNHTTILTQDCNGNIAAGVQGFGCSANVSQ 131  RESULT 7  H99144  FOR CALL 228 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens (strain C58, Cere C; Species: C; Alinae, M.) Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M.; Blanchard, M	Oy 116 GCYGGNNAALWNOTASDSSVMVRQVGFGNNATANO 150
	RESULT 5 H856LS  Hypothetical protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C; Speciale: Escherichia coli C; Speciale: Scherichia coli C; Speciale: Scherichia coli C; Speciale: Scherichia coli C; Speciale: Scherichia coli C; Speciale: Scherichia coli C; Speciale: Scherichia coli R; Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B; Glasner, J.D; Rose, D.J.; Mayhew Nature 409, 529-533, 2001 A; Recension: H856S A; Reterance number: A85480; MUD:21074935; PMID:11206551 A; Recension: H856S A; Reterance number: A85480; MUD:21074935; PMID:11206551 A; Recension: H856S A; Reterance number: A85480; MUD:21074935; PMID:11206551 A; Recension: H856S A; Reterance number: A85480; MUD:21074935; PMID:11206551 A; Reterance number: A85480; MUD:21074935; PMID:11206551 A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Genterohemorrhagic Escherichia coli 0157:H7. A; Residence: Gente	RESULT 6 AD3143  CONSERVED Hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain C5 C, Species: Agrobacterium tumefaciens C, Species: Agrobacterium tumefaciens C, Species: Agrobacterium tumefaciens C, Accession: AD3143 C, Accession: AD3143 C, Accession: AD3143 C, Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I F, Rarp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A, Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A, Title: The Ganome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A, Acterior number: AB2577; MUID:21608550; PMID:11743193 A, Status: prellminary A, Molecule type: DNA A, Status: prellminary A, Molecule type: DNA A, Status: prellminary A, Molecule type: DNA A, Status: prellminary A, Molecule type: DNA A, Crose-references: GB.AE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN0187 A, Experimental source: strain C58 (Dupont) C, Generics: A, Gene: Atu4768 A, Mat position: linear chromosome Query Match Best Local Similarity 25.2%; Pred. No. 0.0088; Matches 39; Conservative 26; Mismatches 59; Indels 31; Gaps 4;

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C.Accession: C50806
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Sasawata, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90806
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                                                                                                                  - Escherichia coli (strain 0157:H7, subs
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C;Species: Brwinia ananas
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 26-Aug-1999
                                                                                                              minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O. C. Species: Escherichia coli
C. Species: Bscherichia coli
C. Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR--
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0.015;
ches 49;
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ilarity 29.8%; Pred. No. 0.015;
Conservative 17; Mismatches 4
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Best Local Similarity
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ses 34; Conserv
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NyAlternace names: cagB protein; curlin nucleation component; minor curlin protein
Cipbete: 12-Peb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
Cipate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
Cipate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
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Cipate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
Cipate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
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A.; Residues: 1-13. 4-May
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                                                                                                                                                                                                         Length 2174;
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A,Reference number: A96039; MUID:21368234; PMID:11474104
A,Contents: annotation
C,Generics:
A,Gene: SMb21548
A,Genome: plasmid
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ilarity 29.8%; Pred. No. 0.015;
Conservative 17; Mismatches 4
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                                                                                                                                                                                                                                                                       Conservative
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Nature 413, 848-852, 2001
A,Authors: Pairy, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A,Authors: Pairy, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A,Authors: Pairy, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A,Accession; AHG635
A,Accession; AHG635
A,Accession; AHG635
A,Status: preliminary
A,Nolecule type: DNA
A,Residues: 1-151 - PAR.
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A;Residues: 1-1034 <MIC>
C;Comment: This protein
C;Superfamily: ice nucleation protein
F;161-993/Region: R-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ice_nucleation active protein - Erwinia uredovora (strain KUIN-3)
C;Species: Erwinia uredovora
C;Species: Erwinia uredovora
C;Accession: 30-58p-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C;Accession: JC2143 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
R;Michigami, Y:; Watabe, S:; Abe, K:; Obata, H:; Arai, S.
B:osci: Biorechnol. Biochem: 58, 762-764, 1994
A;Title: Clohing and sequencing of an ice nucleation active gene of Erwinia uredovora. A;Reference number: JC2143; MUID:94264407; PMID:7764866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYG----GNNAALV----NQTASDSSVM 136
                                                                                                                                                                                                                                                                                                      A;Cross_references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
C;Genetics:
A;Gene: STY1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 ----LTA-GYGSTQTAQE----NSDLTTG-YGSTSTAGYDSSLIAGYGSTQTAGYHSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 RNNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.9%; Pred. No. 0.39;
Matches 40; Conservative 19; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                              13.7%; Score 107; DB 2; Length 151; 30.4%; Pred. No. 0.039; ive 17; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GSANAALYD--QLVTRVVTHEMAHAGYGNGADVGQ-GADNST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2, 2004, 14:56:25
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T--AGYGSTQTAQE 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Conservative
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e : 10.4 secs
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Best Local(Similarity
Matches 35; Conserv
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#H0635

nucleation component of curlin monomers [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: #H0635
                                                                                                        Sequence similarity to those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Accession: JC6040
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A;Reference number: JC6039; MUID:96146512; PMID:8550497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Description: minor component of thin aggregative fimbriae
A,Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 QNGFRNNATIDQWNAKNSDITVGQYG----GNNAALV----NQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-131 <COL>
A,FResidues: 1-131 <COL>
A,Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A,Experimental source: strain 276755-3b
A,Genetics:
A,Genetics:
C,Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Gaps
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                                              RiAbe, K.; Watabe, S.; Emori, Y.; Watanabe, M.; Arai, S.
FEBS Lett. 258, 297-300, 1989
A;Title: An ice nucleation active gene of Erwinia ananas. Sequence similary Reference number: S07053; MUID:90092494; PMID:2599095
A;Reference number: S07053
A;Status: not compared with conceptual translation
A;Molecule type: DAA
A;Residues: 1-1322
A;Cross-references: GB:X17316; NID:9296095; PIDN:CAA35194.1; PID:9296096
C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                          Length 1322;
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Fj22-151/Product: fimbrin protein agfB #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                              21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933 GSTSTAGPDSSL-IAGYGSTQTAGYNSILT------AGYGS---
                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                          ; Score 107.5; DB; Pred. No. 0.38; 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
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29.9%;
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Best Local Similarity 30.4%;
Matches 35; Conservative 1'
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Rest Local Similarity 29.9%
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1014 SSQTARE 1020
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec Run on:

US-09-543-407-26 782 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: 7 Sequence:

Scoring table: BLOSUM62 Gapext 0.5

141681 segs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		escherichi	escherichi	escherichi	P20469 pantoea ana	Q8z7m3 salmonella	salmonel	pantoea	o)	×	Q9kka3 r outer mem	P51521 drosophila	Ω	006653 r outer mem		È		Q10778 mycobacteri	P06620 pseudomonas	P49687 saccharomyc	P43150 leishmania	pseudomon	pseudomon	leishmani	leis	Sac	schi	Q47502 escherichia	Q44052 arthrobacte	P14914 rickettsia	r outer	mycobacte	095271 homo sapien
	CI	CSGA SALTY	CSGA_ECOLI		CSGB_ECOLI		CSGB_SALTI	CSGB_SALTY	ICEN_PANAN	ICEN_ERWHE	ICEN XANCT	OMPB_RICCN	OVO DROME	ICEV PSESX	OMPB_RICJA	GP63_LEICH	YK98 MYCTU	ILF3_HUMAN	YF48 MYCTU	ICEN PSESY	N145 YEAST	GP63_LEIME	ICEK_PSESX	ICEN_PSEFL	GP63_LEIMA	GP63_LEIDO	N100 YEAST	YDHE_SCHPO	CEAK_ECOLI	IMD ARTGO	120K RICRI	OMPB_RICRI	Y442 MYCTU	TNK1_HUMAN
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Q01646 plasmodium Q9utk4 schizosacch P07909 drosophila Q10540 mycobacteri Q8w234 arabidopsis P27692 saccharomyc P24785 drosophila P18431 drosophila P2674 oryza sativ P51989 xenopus lae Q9k0k9 neisseria m
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### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 21-151 FROM N.A.
SPECIES-S.enteritidis, STRAIN=77655-3B;
MEDLINE=9401373; PubMed=8104955.
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA,
the structural gene for thin, aggregative fimbriae.",
J. Clin. Microbiol. 31:2263-2273(1993).
                                                                                                           SEQUENCE FROM N.A.
SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96.46512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAJOR CURLIN SUBUNIT.
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; B7DAC0D16B621359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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PIR; JC6039; JC6039.
Stydene; SG1068; CsgA.
Fimbria; Signal; Complete proteome.
                                                             Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                                                                                                                                              Bacteriol. 178:662-667(1996).
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EMBL, AAD08749, AAL20074.1, -
EMBL, AL627269, CAD08268.1, -
EMBL, AE016840, AA069399.1, -.
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MEDLINE=91310586; PubMed=1677357;

MEDLINE=91310586; PubMed=1677357;

Collinean S.K., Emcedy L., Trust T.J., Kay W.W.;

Collinean S.K., Emcedy L., Trust T.J., Kay W.W.;

Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).

-I. FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                        SHEAIN-KIZ / W3110;
NFDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A.;
"The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding curli in
                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE 59414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of
fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97061202; PubMed=8905232;
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
"A TAB-kb DAN sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-RIZ / MGG1655;
MEDIJNE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / YMEL;
MEDLINE-93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.;
"The Crl protein activates cryptic genes for curli formation and fibronectin binding in Escherichia coli HBIOL.";
Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of Escherichia coli K-12.";
                              01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28 FEB-2003 (Rel. 41, Last annotation update)
 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 18:661-670(1995).
                                                                                      Major curlin subunit precursor.
CSGA OR B1042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence Science 277:1453-1474(1997).
STANDARD;
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
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                                                                                                                        Escherichia coli
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ECOLI
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FIBRONECTIN.

us-09-543-407-26.rsp

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                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=0157.H7 / ATCC 41895;
MEDINE=21218556; PubMed=11319125;
Muthich G.A., Keen J.E., Bilder R.O.;
"Mutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli 0157:H7.";
Appl. Bnviron. Microbiol. 67:2367-2370(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=O157:H7 / EDD933 / ATCC 700927;
STRAIN=O157:H7 / EDD933 / ATCC 700927;
STRAIN=O157:H7 / EDD933 / ATCC 700927;
PEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melon R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSGA ECOST STANDARD; PRT; 152 AA.

033UZ4;
031UZ4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.

Major curlin subunit precursor.

GSGA OR ECS1420.

Escherichia coli 0157:H7.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                           66.9%; Score 523; DB 1; Length 151; 68.9%; Pred. No. 4.1e-37; ive 18; Mismatches 29; Indels
                                                                                                                                                                                                                                         MAJOR CURLIN SUBUNIT.
A -> E (IN REF. 1).
C003470D208D395F CRC64;
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 104979; AAA23616.1; EMBL; X90754; CAA62282.1; EMBL; AE000205; AAC74126.1; EMBL; D90741; BAA35840.1; EMBL; D7742; BAA35840.1; EMBL; S70788; S70788. Ecodene; EG1489; CmgA. Fimbria; Signal; Complete proteome. SIGNAL
                                                                                                                                                                                                                                                                     151 AA; 15049 MW;
                                                                                                                                                                                                                                                                                                             Best Local Similarity 68.9
Matches 104; Conservative
                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                           Similarity
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PSOURNEE FROM N.A.

STAIN-CLESTHY / RIMD 0509952;

X MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MAYASHI T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohteubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

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Ruhara S., Shiba T., Hattori M., Shihagawa H.;

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Ruhara S., Shiba T., Hattori M., Shihagawa H.;

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Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa H.;

Ruhara S., Shiba T., Hattori M., Shihagawa K.,

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Ruhara S., Shiba T., Hattori M., Shihagawa K.,

Ruhara S., Shiba T., Hattori M., Shihagawa K.,

Ruhara S., Shiba T., Hattori M., Shihagawa K.,

Ruhara S., Shiba T., Pubmara M., Shihagawa K.,

Ruhara S., Shiba T., Hattori M., Shihagawa K.,

Ruhara S., Shiba T., Pubmara M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba M., Shiba
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Anquist A., Bian Z., Olsen A., Normark S.;
Hammar M., Anquist A., Bian Z., Exprisesion of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
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01-FEB.1995 (Rel. 31, Created)
01-FEB.2003 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor outlin subunit precursor.
CSGB OR(B1041 or 216/75 OR ECS1419.
Escherichia coli, and
Bacherial oli/197:47.
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriacee, Escherichia.
Enterobacteriaceee, Escherichia.
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21 152 MAJOR CURLIN SUBUNIT.
152 AA; 15099 MW; BE2D2D94DDE91243 CRC64;
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Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95157246; PubMed=7854117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X90754; CAA62281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-21 FROM N.A. STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                         O157.H7 and genomic comp
DNA Res. 8:11-22(2001).
                               / MG1655;
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                                                                                                      SEQUENCE FROM N.A.
                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   [5]
SEQUENCE FROM N.A.
                                                         Gregor J., David
                                STRAIN=K12
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15882 MW; B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                        MINOR CURLIN SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                  14.3%; Score 112; DB
29.8%; Pred. No. 0.00
ive 17; Mismatches
                                                                                                                                                                                                                                                                                       POTENTIAL.
EMBL; AE000205; AAC74125.1; -...
EMBL; D90741; BAA35831.1; -...
EMBL; AE005315; AAG5557.1; -...
EMBL; AP002554; BAB34842.1; -...
PIR; C90806; C90806.
PIR; S70787; S70787.
ECOGene; EG12621; csgB.
Fimbria; Signal; Complete proteome.
SIGNAL
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Best Local Similarity 29.88
Matches 34; Conservative
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P20469;
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"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-: PUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURRACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic Escherichia coli (Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;

MEDLINE=97061202; PubMed=8905232;

MEDLINE=97061202; PubMed=8905232;

Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,

Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                  MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Mayhaw G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfei G., Hackett J., Kink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.",
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yano M., Horiuchi T.; "Annow of the Escherichia coli K-12 genome "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                   Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                          Mol. Microbiol. 18:661-670(1995)
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                                                                                                                                        51 GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR-----
                                                                     Gaps
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                                                                                                                                                                                                                                                                            99 -NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                         14;
Length 151;
                                                                     49; Indels
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Ice nucleation; Repeat; Outer membrane.

DOMAIN 162 1281 OCTAPEPTIDE PERIODICITY.
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MEDLINE=90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
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H
                                 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ice nucleation protein inaA.
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HSSP; P06620; INA.
HTGAFDO; IPRO00258; ICe_nucleatn.
Pfam; PF00818; ICe_nucleatin.
69.
PRINTS; PR00327; ICENUCLEATN.
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Fimbria; Signal; Complete proteome SIGNAL 1 21 POTEN
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CTIS.";
                                                                                                                                                                                                                        GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                  DB 1; Length 1322;
                                                                                                                          Indels
      1322 AA; 131094 MW; 89B0EE24AA837039 CRC64;
                                                                                                                       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Indoor curlin subunit precursor.
CSGB OR STY1180 OR F1777.
                                                              n
Similarity (29.9%; Pred. No. 0.22;
38; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AA
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                                                                                                                             38; Conservative
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            SEQUENCE
                                                                  Query Match
                                                                                                 Local
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                                                                                                                             Matches
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J. Bacteriol. 178:662-667(1996).
J. Bacteriol. 178:662-667(1996).
J. BACTON: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLIDED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
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SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                   SPECIES_S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling.U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                       Gaps
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SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE-96146512: Pubmed-8550497;
Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS5226 Annual Simulator, Fri, 131 An.
PS5236 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Minor curlin subunit, precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFE OR STM143.
Salmonella typhimurium, and
Salmonella typhimurium, and
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                       16;
                                                                                                                                     1; Length 151;
                                                                                                                                                                                                       47; Indels
                                                                                                                                                                                                                                                                    51 GSANAALYD--QLVTRVVTHEMAHAGYGNGADVGQ-GADNST----
21 POTENTIAL.
151 MINOR CURLIN SUBUNIT.
16254 MW; 161C54326E573495 CRC64;
                                                                                                                                  13.7%; Score 107; DB 1, 30.4%; Pred. No. 0.022;
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                                                                                                                                                                                                          17; Mismatches
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                                                                                                                                                                                                          Conservative
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                                       151
                                                                        151 AA;
                                                                                                                                                                      Local Similarity
les 35; Conserv
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                                                                        SEQUENCE
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DOMAIN

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                                                                                                                                                                                                                                                                                                     51 GSANAALYD--QLVTRVVTHEMAHAGYGNGADVGQ-GADNST-----IELTQNGF 97
                                                                                                                                                                                                                                                                                                                                           76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosci. Biotechnol. Biochem. 58:762-764(1994).

-! FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-! SUBCELLULAR LOCATION: Outer membrane.

-! SUBCELLULAR LOCATION: Outer membrane.

-! DOMAIN: CONTAINS IMPERECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

-! MISCELLANGOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

-! SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                             77 NNRAKVDQ---AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                               98 RNNATIDOWNAKNSDIT-VGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94264407; PubMed=7764866;
Michigami Y., Watabe S., Abe K., Obata H., Arai S.;
"Cloning and sequencing of an ice nucleation active gene of Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                       13.7%; Score 107; DB 1; Length 151; 30.4%; Pred. No. 0.022; tive 17; Mismatches 47; Indels
                                                                                                                                                                                         COFC5430E6DD361D CRC64;
                                                                                                                                                   POTENTIAL.
MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1034 A.A.
or send an email to license@isb-sib.ch)
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Pfam, PF00818; Ice_nucleation; 51.
PRINTS; PR00327; IČENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 34.
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                                                                                                         Stydene, SG10609, csgB.
Fimbria, Signal, Complete proteome
SIGNAL 1 21 POTEN
                                   EMBL; AJ002301; CAA05316.1; -. EMBL; AE008749; AAL20073.1; -.
                                                                                                                                                                                       151 AA; 16182 MW;
                                                                       ; U43280; ÅAC43598.1; ~.
JC6040; JC6040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ice nucleation protein inaU.
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                                                                                                                                                                                                                                             Local Similarity 30.4 es 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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HSSP, P06620, 11NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=KUIN-3;
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Matches
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                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                          576 ----LTA-GYGSTQTAQE----NSDLTTG-YGSTSTAGYDSLIAGYGSTQTAGYHSIL 624
                                                                                                                                                                                                                                                                                                                    531 GYGSTSTAGANSS-----LIAGYGSTQTASYNSVLT------AGYGSTQTAREGSD 575
                                                                                                                                                                                                                                                                                                                                                                                            87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYG----GNNAALV----NQTASDSSVM 136
                                                                                                                                                                                                                                                   86
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"The consensus sequence of ice nucleation proteins from Erwinia
"The consensus sequence of ice nucleation proteins syringae.";
Gene 85:239-242(1989).
-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate
crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS 126 IMPERECT REPEATS OF A CONSENSUS OCTAPEPTIDE
A-G-Y-G-S-T-X-T; PURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE
                                                                                                                                                                                                                                                   27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGAD
                                                                                                                                                                           38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE ICE
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--- MISCELANBOUSE.
NUCLEALANBOUSE. A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                      Length 1034;
                                                                                                                                                                               Indels
162 993 OCTAPEPTIDE PERIODICITY.
1034 AA; 103378 MW; FA222523D333EADD CRC64;
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                                                                                                      13.6%; Score 106; DB 1; Le ilarity 29.9%; Pred. No. 0.22; Conservative 19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; MZ6882; AAA24823.1; --
PIR; JQ0188; JQ0188.
HSSP; P06620; IINA.
InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice nucleation; 65.
PRINTS; PR00327; ICENUCLEATION; 45.
PROSITE; PS00314; ICE NUCLEATION; 45.
ICE nucleation; Repeat; Outer membrane.
DOMAIN 162 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=M1;
MEDLINE=90152370; PubMed=2515997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 VRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             625 T--AGYGSTQTAQE 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce nucleation protein.
                                                                                                                                        Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=549;
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                                  SEQUENCE
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                                                                                                              Query Match
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ICEN ERWHE
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DB 1; Length 1258;

13.4%; Score 104.5; DE 29.5%; Pred. No. 0.36;

Best Local Similarity

Query Match

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1105 TGTAGADSSLIAGYGSTQTAGYGSTQTAREDSSLTAG-YGSTSTAGHDSSLI 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF0208659; AAL03623.1; -.
EMBL, AF123721; AAF74124.1; -.
EMBL, AF123726; AAF74129.1; -.
EMBL, AF149110; AAD99533.1; -.
PIR, E97835; E97835.
Interpro; IPR006515; Autotransport.
Interpro; IPR005546; Autotransporter.
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE (
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    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GQGADNSTIE---LTQN-GFRNNATI----DQWNAKNSDITVGQYG-----GNNAALV 126
                                                     773 GSTSTAGADSSL-IAGYGSTQTAGYHSILT-----AGYGSTQTAQERSDLTTGYGS 822
                                                                                               --GA
                                                                                DVGQGADNSTIE---LTQN-GFRNNATI----DQWNAKNSDITVGQYG-----GNNAALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN-----GADV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomones campestris print the incention gene into from Xanthomones campestris print the incention gene from Cenet. 223:163-166(1990).

-!-FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-!-SUBCELLUIAR LOCATION: Outer membrane (By similarity).

-!-DOMAIN: CONTAINS 153 IMPEREGY REPRAINS OF THE CONSENSUS OCTAPERTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

-!-MISCELLANGOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

-!-SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                     Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 1567;
                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao J., Orser C.S.; "Conserved repetition in the ice_nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001258; Ice nucleatn.
Pfam; PF00818; Ice nucleation; 81.
PRINTS; PR00327; ICENUCLEATIN.
PROSITE; PS00314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
    Indels
                            34 GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN-
 37;
                                                                                                                                                                                                                                                     (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                              PRT; 1567 AA
  Mismatches
                                                                                                                                  127 ----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                   882 AGYGSTQTAGYNSILT--AGYGSTQTAQE 908
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=X568;
MEDLINE=91080859; PubMed=2259339;
 23;
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    Conservative
                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                              Ice nucleation protein.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=343;
                                                                                                                                                                                                                                       P18127;
01-NOV-1990 (
01-NOV-1990 (
16-OCT-2001 (
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  44;
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Stenos J., Walker D.;
Stenos J., Walker D.;
Stenos J., Walker D.;
The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
layer with hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                           OMPB RICCN STANDARD; PRT; 1655 AA.

O9KKA3; Q9KK98; Q9XC45;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 41, Last sequence update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (CompB)
(Comp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen)
OMPB OR; RC1085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB)."; Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
MEDLINE=21442074; PubMed=11557893;
Ogata H; Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae, Rickettsiae, Rickettsia.
NCBI_TaxID=781;
                                                      1164 AGYGSTQTAGYNSILT--TGYGSTQTAQE 1190
----NQTASDSSVMVRQVGFGNNATANQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 -----GGNGYINCGGVG-GPNNS---LDGNNLLNPASVSNYNESNSKFHNHHHHHHHH 152
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                                                                                                                                                                                                                                                                                                                                    HSSP; P07248; ZADR.
TRANSFAC; T00669; -.
Flybase; Fggn0003028; ovo.
InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 3.
SWART; SM00355; ZnF C2H2; 4.
PROSITE; PS00028; ZINC_FINGER C2H2_1; 3.
PROSITE; PS00029; ZINC_FINGER C2H2_2; 3.
Zinc-finger; Metal_binding; DNA-binding; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> R (IN REF. 2).
D7068BB2BC0F6F77 CRC64;
PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS. -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
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C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
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EMBL; X59772; CAB36921.1; ALT_SEQ.
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43; Conserva
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 GGGNHNG--GGNSSGPDSTLSIYQYGSANAALYDQLVTR-----VVTHEMAHAGYGNGA 79
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-I-FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-I-SUBCELLULAR LOCATION: Nuclear (Potential).

-I-DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OGGENBEIS. STORED IN THE EGG, BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.;
"Multiple products from the shavenbaby.ovo gene region of Drosophila melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                            TYPHUS).
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Eddopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                       TIGREAMS; TIGRO1414; autotrans barl; 2.
Antigen; S-layer; Cell wall; Complete proteome.
CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.
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G -> S (IN REF. 3).
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                                                                                              32 kDa BETA PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSI51; OSXZU4;
01-OCT-1996 (Rel. 34, Created)
01-OCT-2003 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
OVO protein (Shaven baby protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 102.5; DE 26.8%; Pred. No. 0.73; iive 18; Mismatches
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MEDLINE=95021209; PubMed=7935398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.8
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 GADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMV
Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen S) (Grass) (TompB) (TompB) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρλ
                                                                                                                                                                                                                                                                                                                   Uchiyama T.;
Uchiyama T.;
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3 4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).
                                                                                                                                                                                                                                                                                                                                                                               japonice.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                             Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 kDa SURFACE-EXPOSED PROTEIN. 32 kDa BETA PEPTIDE. POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             layer with hexagonal symmetry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168097 MW; 3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%; Score 95.5; DI
25.0%; Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB003681, BAA20138.1, -
InterPro, IPR005315, Autotransport
InterPro, IPR00546, Autotransporter.
Féan, PP03797, Autotransporter, 1.
TIGRFAMS; TIGR01414; autotrans_bar1; 2.
Antigen; S-layer; Cell wall.
CHAIN 1339 1656 32 kDa BETA E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1320 TNAQLDVAKDIQAQLGNRLGALRY 1343
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25.0%; F...
21; '
                                                                                                                                 Rickettsia japonica.
Bacteria, Proteobacteria,
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36; Conserv
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=35790;
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P15706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to nucleate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas syringae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular organisation of the ice nucleation protein InaV from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
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W; C9E9974CB1731E68 CRC64;
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(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
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Last annotation update)
  PRT; 1196 AA
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Pfam; PF00818; Ice_nucleation; 61.
PRINTS; PR00327; ICENUCLEATN.
PROSITE, PS00314; ICE NUCLEATION; 42.
Ice_nucleation; Repeat; Outer_membrane.
                                                                                                                                                                                                                                                                                                                                                  STRAIN=INAS;
MEDLINE=97462815; PubMed=9323042;
Schmid D., Pridmore D., Capitani
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  STANDARD;
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                                                                                                                                    nucleation protein.
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                                                                                                                                                                                                                                                                        NCBI_TaxID=317;
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30-MAY-2000
16-OCT-2001
                                                   15-DEC-1998
                                                                                15-DEC-1998
                                                                                                       16-OCT-2001
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006653;
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RESULT 14

Best Loc Matches

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Query Match
Best Local Similarity 54.8%; Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                  Wilson M.E.;

"Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishhania donovani chagasi promastigores to an infectious form.";

"Elol. Chem. 267:1888-1895(1992).

-! FUNCTION! Has an integral role during the infection of macrophages in the mammalian host.

-! CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-|-COPACTOR: Binds 1 zinc ion per subunit (By similarity).

-! SUBSELLUIAR LOCATION: Attached to the membrane by a GPI-anchor.
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REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                 Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=44271;
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
GPT-anchor amidated asparagine (By
                                                                                                            MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks an
Arg-Gly-Asp sequence.";
Mol. Biochem. Parasitol. 39:267-274(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, A44951, HAMBER PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PR
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(BY SIMILARITY)
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ZINC (CATALYTIC)
ZINC (CATALYTIC)
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=92112918; PubMed=1370484;
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EMBL; M28527; AAA29235.1; -.
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                                                                                          SEQUENCE FROM N.A.
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        Matches
        23;
        Conservative
        5;
        Mismatches
        8;
        Indels
        6;
        Gaps

        Qy
        52
        SAN-AALYDQLVTRVVTHEMAHA.----GYGNGADVGQGADN
        87

        Db
        244
        AANIASRYDQLVTRVVTHEMAHALGFSVGFFEGARILESISN
        285
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Search completed: August 2, 2004, 14:49:32 Tob time : 6.3 secs

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August 2, 2004, 14:39:17; Search time 29.7 Seconds (without alignments) 1604.150 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Database :

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5: sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	033802 salmonella Q7xx43 citrobacter Q7xx40 citrobacter Q8xw63 escherichia Q7xx37 enterobacte Q5465 salmonella Q9s3j5 escherichia Q9s3j5 escherichia Q9s4h4 shewarella Q8u6n9 aprobacteri Q9ung rhizobium m Q7uz1 shigella fl Q8vw64 escherichia Q8vx74 citrobacter Q8xv7 shigella fl Q7xx4 citrobacter Q8p38 xanthomonas	Q8efu3 shewanella
SUMMARIES 1 ID	2 033802 2 07X243 2 07X240 6 QBCW63 2 07X237 2 07X237 2 054069 6 QBS3J5 16 QBEN4 16 QBCN9 16 QBCN9 16 QBCN9 16 QBCN9 16 QBCN9 16 QBCN9 16 QBCN9 16 QBCN9 16 QBCN9	.6 Q8EFU3
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% Query Match	28 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	13.7
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1111 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	44 44 60 44 70

## ALIGNMENTS

SUL 380	-	01-DEC-2001 (TrEMBirel, 19, Last		OS Salmonella typhimurium. OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales:	Enterobacteriaceae; Salmon	[1]	kCM N.A. 0053981; PubMed=9393832;	RA Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D., Ra Normark S.T. Rhen M.	"Expression of thin, aggregative fimbriae promotes inters	RT Salmonella typnimurium SR-11 with mouse small intestinal epithelial RT cells.";	Infect. Immun. 65:5320-5325(	NON_TER 152 152	SQ SEQÜENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	Query Match 87.3%; Score 683; DB 2; Length 152; Best Local Similarity 89.4%; Pred. No. 2.8e-48; Matches 135; Conservative 3; Mismatches 13; Indels 0; Gaps 0;	Qy I MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60	Db 1 MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	Qy 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	DD 61 SDARKSETTITQSGYGNGADVGQGADNSTIELLTQNGFRNNATIDQWNAKNSDITVGQYGG 120	Qy 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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RESULT 2

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                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
                                    61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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Enterobacteriaceae; Enterobacter.
NCBI TaxID=28141;
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia,
NCBI_TaxID=217992,
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67.8%; Pred. No. 4.8e-34;
ive 18; Mismatches 30; Indels
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Last annotation update)
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                                                                                                                                    119 RNGALVNQTASDSNVLIQQVGFGNNATANQH 149
                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
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01-MAR-2003 (TrEMBLrel. 23, Last
Major curlin subunit precursor.
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                               Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 7:1131-4158 (2003).
EMBL, AJS15700; CADS6672.1; -. SEQUENCE 150 AA, 15016 MW; 1D7141B8D6973DC6 CRC64;
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                                                                                                                                                                                                                                                  Cirrobacter sp. Fec2.
Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=546;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 74.2%; Score 580.5; DB 2; Length 150; Best Local Similarity 78.1%; Pred. No. 6.3e-40; Matches 118; Conservative 10; Mismatches 22; Indels 1
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      NCBI_TaxID=562;
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SEQUENCE 5
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Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).
EMBL; AJS15702; CADS6678.1; -.
SEQUENCE 150 AA; 15112 MW; 5D8BS2D872DF15F3 CRC64;
                                                                                                                                                               Gaps
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Enterobacteriaceae; Salmonella.
NOBI_TaxID=592;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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"Virulence of Salmonella enteritidis in chickens correlates with
colony mcrphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U53207; AAA98671.1;
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                                                                                                                         Length 150;
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Pred. No. 1e-17;
2; Mismatches 13; Indels
                                                                                                                                                               Indels
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larity 80.3%;
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01-NOV-1996 (TrEMBLrel. 01,
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SEF17 fimbrin (Fragment).
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0983J5;
01-MAY-2000
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Best Local S
Matches 91
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TRANSPOSON=Insertion sequence IS1;
MEDLINE=99314153; Pubmed=10386375;
MEDLINE=99314153; Pubmed=10386375;
MODLINE=99314153; Pubmed=10386375;
Non-outliation of Escherichia coli 078:K80 isolates associated with
IS1 inserti on in csgB and reduced persistence in poultry infection.";
FEMS Microbiol. Lett. 175:247-253(1999).
NON_TER.
29 29
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MEDLINE=22297686; PubMed=12368813;

MEDLINE=22297686; PubMed=12368813;

Medline: Signification of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of the strength of 
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Alteromonadaceae; Shewanella.
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Pred. No. 0.0022;
1; Mismatches 2; Indels
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D08CA23D6C46B62D CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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502 AA; 52441 MW;
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1 Similarity 89.7%;
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AA; 2789 MW;
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TIGR; SO0865; -.
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56 ALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58."}\,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21608551; PubMed=11743194; Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M., Gordoner B., Tarchouk D., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowl C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; Gurson J., Lomo C., Sear C., Strub G., Gielo C., Slater S.; He plant pathogen and biotechnology agent Science 294:2322-2328(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21668550; PubMed=11743193; Monks D.E., Kitajima J.P., Nocd D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.P. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Katpavin T., Levy R., Li W.-J., McClelland E., Palmieri A., Karpvavin T., Levy R., Li M.-J., McClelland E., Palmieri A. Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Mester E.W.;
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                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu468.
ATU468 OR AGR L 228.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobian/Agrobacterium group; Agrobacterium.
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45 AA; 14984 MW; DEDC870E1713D51A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SMb21548.
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                                      145 AA
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                                   PRELIMINARY;
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PIR; H98144; H98144.
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Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=176299;
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SEQUENCE 14
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Q8U6N9
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738 ----GGYANTANVGFKGLTLTTQGSHAAGIVAQSVGGGGGTGGTASSYSAGIGFTASVAV 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 EMAHAGYGNGADVG------QGADNSTI--ELTQNGFRNNATIDQWNAK---NSDITV
                                                                                                                                                            Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A., "The complete sequence of the 1,683-kb psymB megaplasmid from the N2-
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wei J. Goldberg M.B. Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling M Mau B., Perna M. N.T., Payre S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457F."; Infect. Immun. 71:2775-2786 (2003).
EMBL, AEO10981, AAP16542.1; -. SEQUENCE 151 AA, 15868 MW, 5D5D266B964014A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%; Score 113; DB 16; Length 2174; 27.0%; Pred. No. 2.3; ive 21; Mismatches 51; Indels 36;
Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales; Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     693 AIATAGAGAVGILAQSIGGGGGN---GGNATGGDAGFGSFQIGGGGGG-
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR065546; Autotransporter.
InterPro; IPR062016; Peroxidage.
InterPro; IPR002013; PERs
Pfam; PF03797; Autotransporter; 1.
PROSITE; PS00435; PERCXIDASE 1; 1.
PROSITE; PS00583; PFKB KINASES 1; 2.
PROMITE; PS00581; PFKB KINASES 1; 2.
PROMITE; PS00581; PFKB KINASES 1; 2.
SEQUENCE 2174 AA; 203314 MW; 0068EB68297B44182 CRC64;
                                                                                                                                                                                                                                     fixing endosymbiont Sinorhizobium mellioti.";
Proc. Natl. Acad. 861. U.S.A. 98:9889-9894 (2001).
EMBL; ALG03645; EG49389.1;
PIR; E95965; E95965.
GO; GO:0046821; C:sxtrachromosomal DNA; IEA.
GO; GO:0004601; F:peroxidase activity; IEA.
GO; GO:0006979; P:response to oxidative stress; IEA.
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Last annotation update)
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
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                                                                                                                                 STRAIN=1021;
MEDLINE=21396508; PubMed=11481431;
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25,
25,
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Best Local Similarity 27.03
Matches 40; Conservative
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                                                                                                            SEQUENCE FROM N.A.
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Q7UCZ1;
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Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou
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Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                   46)
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.8%; Pred. No. 0.12;
Matches 34; Conservative 17; Mismatches 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequent
01-0CT-2003 (TrEMBLrel. 25, Last annotati
Nucleation component of curlin monomers
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Bacteria, Proteobacteria, Gammal
Enterobacteriaceae, Citrobacter
NCBI_TaxID=213763;
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NCBI_TaxID=340;
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(TrEMBLrel. 22,
(TrEMBLrel. 24,
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01-OCT-2002
01-JUN-2003
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STRAIN=301 / Serotype 2a;
STRAIN=301 / Serotype 2a;
MEDLINE=2222406; PubMed=12384590;
Min Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
                                                                                                                                     GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR-----
                                                                                                                                                                        51 GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR-----
                                                                            Gaps
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Kasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
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of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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                                                                                                                                                                                                                                                       99 -NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                 SNRAKIDOTGDYNL-AYIDOAGSANDASISOGAYGNTAMIIOKGSGNKANITOY 129
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Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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            Length 151;
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 AA; 16963 MW; 49F68448D979B986 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Minor curlin subunit precursor, similar ro CsgA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit precursor.
CSGB OR C1305.
                                                                            49;
               DB 16;
               ; Score 112; DB 1
; Pred. No. 0.11;
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
               14.3%;
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EMBL; AE016759; AAN79778.1;
                                                                            Conservative
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                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=217992;
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SEQUENCE 160 AA;
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               Query Match
Best Local Simil
Matches 34; C
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QBCW64
QBCW64
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Matches
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"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
"Genome comparison with genomes of Escherichia coli Kl2 and O157.";
hucleic, Acids Res. 30:4432-4441(2002).
EMBL, ABULS131; AAN42658.1; -.
CCMplete proteon.
SEQUENCE 160 AA; 16919 MW; 50269F526BD2A32F CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae isolated from the Human Gastrointestinal Tract.";
Infect.: Immun. 72:4151-4158 (2003).
EMBL, AJS15700; CAD566711.1; -.
SEQUENCE 151 AA, 16158 MM; BD00AF57E1400704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
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                                                                                                                                                                                                         Nature 417:459-463(2002).

BMBL, AR012148, AAM39283.1; -.

GO, GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA. InterPro; IPR000258; Ice_nucleatn.

Ffam, PF00318; Ice_nucleatin, 68.

PRINTS; PR00317; ICENUCLEATIN, 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     951 TQTAGYESTLTAG-YGSTQTAQEISWLTTGYGSTQTAGHGSILT--AGYGSNSTA 1002
                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                DB 16; Length 1333;
                                                                                                                                                                                                                                                                                                              Query Match 13.9%; Score 108.5; DB 16; Length Best Local Similarity 26.3%; Pred. No. 3; Matches 46; Conservative 22; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                           1333 AA; 131306 MW; 326078458D0E4842 CRC64;
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SEQUENCE 1333 AA
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Search completed: August 2, 2004, 14:54:41 Job time : 30.7 secs

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E. coli c Mycobacte Anti-CD38 Arabidops Arabidops Bifidobac

Run on:

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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                           Aab36319 Salmone
Abr82649 B. coli
Aab36328 Salmone
Aab36328 Salmone
Aab36328 Salmone
Aab36329 Prinone
Abv82632 Prinone
Aaw32312 Leishmen
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Abr8268 Arti-CD
Aag29728 Arabido
Abp669842 Human p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgfA::PT3#9 amino acid sequence SEQ ID NO:28
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Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64630.
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Aab36351 AgfA::PT3
Aar74625 AgfA sequ
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                                                                                                               August 2, 2004, 14:35:42 ; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
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                                  Compugen Ltd
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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                                                                                                                                                                                                                                                                                                1586107 seqs, 282547505 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Result è.

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copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (1) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbhrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TARF) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CSA and AgfA, homologue fimbrin shunits, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologue species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment of segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or comprising separating in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the animal in conjunction with a carrier or diluent (1) is useful for the expression of recombinant AgfA protein which is useful for the retrologous antigens are presented in high numbers (up to Sou,000 copies/Cell), the hybrid finbrin protein possesses both the immunelly properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live
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Best Local Similarity 91.1%; Pred. No. 3.3e-61;
Matches 144; Conservative 0; Mismatches 0; Indels
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the exemplification of the present invention
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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterbacteriaceae for the production of fimbriae comprising recombinant of a fracting recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native compositions species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. Coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response in manned the present invention in inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 683; DB 3;
Pred. No. 2.2e-58;
1; Mismatches 14;
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90.1%;
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Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
29-SEP-1997
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Best Local
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AAW23570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                           Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                  The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                               Score 683; DB 2; Length 151;
Pred. No. 2.2e-58;
1; Mismatches 14; Indels
            Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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          Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36341 standard; protein; 151 AA
                                                                                                                                                                                                      Disclosure, Fig 7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                 ttch 88.1%; sal Similarity 90.1%; 136; Conservative
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       Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UYVI-) UNIV VICTORIA.
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                                                        WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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05-APR-2000; 2000WO-CA000356.
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Matches 136; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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                                                                                                                   The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETIITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAXNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                 Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
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0
                                                                                                                                                                                                                                                                                                              Score 678; DB 2; Length 151;
Pred. No. 6.6e-58;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANOY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; immune response; immunogen.
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                                                                                         Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                              87.5%;
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 89.4'
Matches 135; Conservative
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      WPI; 1997-309886/28.
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                     N-PSDB; AAT74142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                   Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               61
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RESULT 6 AAB36350

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA consequence which encodes a foreign entopop or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI7/TAF) nucleation depended assembly system of strains of Salmontella, Escherichia coli and consequence of the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the composition of a recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the correction of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrim protein possesses both the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response community the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the horseon the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the recombinant of the
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81.9%; Pred. No. 2.4e-56;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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protein useful for eliciting immune response in animal.
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                                                                                                            Disclosure; Page 137; 139pp; English
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of the necdess a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbried (SETI/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and directing recombination of finbrials comprising recombination of directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino cortaining an expansion of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial submuit protein are usually strong immunogens, which may be important for directing an immune response conception of the present invention manual sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 138; 139pp; English
                                                                                                    Collison SK,
99US-0127888P
                                             (UYVI-) UNIV VICTORIA.
                                                                                                    White AP, Doran JL,
                                                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64629.
05-APR-1999;
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Sequence 151 AA;

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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAAL--- 57
                                                                                                                                                                          97
                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                          ----- 97
                                                                                                                                                                      58 ------YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGF
                                     46; Gaps
                                                                                                                                                                                                                98 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                    Length 151;
Score 617; DB 3; Length 151;
Pred. No. 5.7e-52;
0; Mismatches 0; Indels
                                                                                                                                            61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA-----
 Query Match 79.6%;
Best Local Similarity 73.6%;
Matches 128; Conservative C
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Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                  AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                        AAB36355 standard; protein; 151 AA
                                                                          (first entry)
                                                                            26-FEB-2001
RESULT 8
AAB36355
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Salmoneila enteritidis. Escherichia coli. Synthetic. 

WO200060102-A2

Kay WW;

12-OCT-2000.

05-APR-2000; 2000WO-CA000356

99US-0127888P

(UYVI-) UNIV VICTORIA

Kay WW; Collison SK, White AP, Doran JL,

WPI; 2000-672631/65.

N-PSDB; AAC64631

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

English. Disclosure; Page 139; 139pp;

The present invention describes a recombinant agfA gene (1) where a segment of a foreign bNA segment of the gene has been replaced by a segment of a foreign bNA segment of the gene has been replaced by a segment of a foreign bNA sequence which encodes a foreign epitope or antigen. Also described are:

CC (1) uses of thin aggregative fimbriae (SETIJ/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant commologue fimbrin subunits. respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, respectively; (2) directing species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or cardiecral containing a replacement segment or segments or dilutent. (1) is protein containing a replacement segment or active or dilutent. (1) is cuseful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/Cell), the hybrid fimbrina are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live companient, the inserted epicope, and hybrid dimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention

Sequence 151 AA;

SDARKSETTITOSGYGNGAD------YDOLVTRVVTHEMAHAFR MKILKVAAFFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ Ouery Match Best Local, Similarity 74.6%; Pred. No. 1.4e-51; Matches 129; Conservative 0; Mismatches 0; Indels 44; Gaps -------GGNNAALVNQTASDSSVWVRQVGFGNNATANQY 151 99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 61

엄 ò 임 δ RESULT 9

AAB36346

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEF1/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprision recombinant dark. CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant denomologues species; (3) directing recombinant gene homologous species; (3) directing recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal; comprising separating an amino acid polymer comprising are combinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and nurroducing the protein containing a replacement segment or segments of coli or acid sequence or sequences grown on a Salmonella, E. coli or Interobacteriaceae host cell, from the host cell and nurroducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expension of recombinant AgfA protein which is useful for useful for the retrier fimbrial submit protein possesses both the system the heterologous antigens are presented in high numbers (up to 500,000 cophes/cell), the hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                         agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.1%; Score 605; DB 3; Length 151
80.1%; Pred. No. 8.3e-51;
ive 5; Mismatches 25; Indels
                                                                                                                             AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                         vaccine; immune response; immunogen.
AAB36346 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-012788BP
                                                                                  (first entry)
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                                                                                                                                                                                                                                    Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC64622
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                                                                                                                                                                                                                                                                                                                       WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1999;
                                                                                    26-FEB-2001
                                                                                                                                                                    Salmonella;
                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000
                                                                                                                                                                                                                                                                                Synthetic.
                                         AAB36346;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TAP) nucleation depended are: (2) use of thin aggregative finbriae (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant CG Buterobacteriaceae for the production of fimbriae comprising recombinant con composines species, (3) directing recombination of a recombinant gene composition species; (3) directing recombination of a recombinant gene composition species; (3) directing recombinant confirmed sequence of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino composition of the composition of a sequence or sequences grown on a Salmonella, E. Coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is collymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful cellciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or coll or 
SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope;
vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                           AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                            Kay WW;
                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 136; 139pp, English.
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                                                                                                                                                                                                                                                            AAB36347 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White AP, Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella;
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AAB36347
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Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            back into the chromosome of them. It is a species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                120
                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SETI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and AbfA, CspA and AgfA-homologue fimbrine subunits, respectively; (2) directing recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologue species; (3) directing recombination of a recombinant gene
                                                                                                           9
                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                               agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                ;
0
                                           Length 151;
                                                               Indels
                                 Score 603; DB 3; Le
Pred. No. 1.3e-50;
                                                                                                                                                                                                                                                                                                                         AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
the exemplification of the present invention
                                                                                                                                                                                           Pred. No. 1.3e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay WW;
                                                                                                                                                                            121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                          vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SK,
                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                       AAB36349 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888P
                                          77.8%;
80.8%;
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-672631/65.
                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                      Sequence 151 AA;
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                                                   Local Simi.
hes 122;
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                                                                                                                                                                                                                                                                                                                                               Salmonella;
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                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                          Query Match
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for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITOSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                               ü
Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to $500,000 copiess/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given it the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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Pred. No. 2e-50;
4; Mismatches 25, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.8 Matches 122; Conservative
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Escherichia colí.
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N-PSDB; AAC64628.
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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant control of a recombinant gene into the chromosome of the homologous species, replacing necombinant gene back into the chromosome of the homologous species, replacing of the chromosome of the homologous species, replacing neman; or comprising separating an aimon acid polymer response in an animal, comprising separating an aimon acid polymer comprising are comprising a replacement segment or segments of foreign animo acid polymer comprising a separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 100,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response in an immune response in an immune response in an immune response in an immune response in an immune response in a manual in the present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 600; DB 3;
Pred. No. 2.5e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36348 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.4%;
81.5%;
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Best Local Similarity 81.5
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPIJ/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enerotacterizacae for the production of fimbriae comprising recombinant of Enerotacterizacae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologue important gene comprising separating a recombinant gene into the chromosome of the homologus species, replacing the native comprising separating an amino acid polymer comprising a recombinant of the comprising separating an amino acid polymer comprising a recombinant of comprising separating an amino acid polymer comprising a recombinant of the comprising separating an amino acid polymer comprising a recombinant of comprising a replacement sequence of sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (T) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are usually strong inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o;
                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%; Score 568; DB 3; ilarity 80.1%; Pred. No. 3.3e-47; Conservative 4; Mismatches 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                          Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB36343 standard; protein; 151 AA
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N-PSDB; AAC64624.
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Best Local Simi:
Matches 121,
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shighla infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
      Plasma protein; immune response; antibacterial; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 41-42; 42pp; English
                                                                                                                                                                                                                                             30-JAN-2003; 2003WO-EP000943.
                                                                                                                                                                                                                                                                                                          31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                                                                                                                                                    (HANS-) HANSA MEDICAL RES
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                                                                Escherichia coli.
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                                                                                                                             WO2003064446-A2
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                                                                                                                                                                                       07-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbries (SEFIT/TAP) nucleation depended assembly system of strains of Salmonella Escharichia coli and comparation of strains of Salmonella Escharichia coli and adgregate the production of fimbriae comprising recombinant contracting recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino comparising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a nation and salmonella, E coli or Enterobacteriace host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is consecut for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to conjunction, the carrier fimbrial subunit proteins are usually strong mumunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier of pubric fimbriae are easy and conjuncted the present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                   Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 135; 139pp; English.
                                                                                                                                                                                Collison SK,
05-APR-2000; 2000WO-CA000356
                                                      99US-0127888P
                                                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                                                Doran JL,
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                                                      05-APR-1999;
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Herwald H;

Wikstroem M,

Olsen A,

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SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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65.0%; Score 504; DB 7; Length 151; 67.5%; Pred. No. 5.5e-41; ive 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                      121 GNGAAVDOTASNSSVNVTQVGFGNNATAHOY 151
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                    Best Local Similarity 67.5
Matches 102; Conservative
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Gaps . 0

Best Local Similarity 68.23 Matches 103; Conservative

Local Similarity

1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGHGGGGGNNSCPNSELNIYQYGGGNSALALQ SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG

E. coli CsgA subunit 15 kDa protein.

(first entry)

04-DEC-2003

8X8X8X8X

ABR82651;

ABR82651 standard; protein; 151

RESULT 15 **ABR82651** 

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121 NNAALVNOTASDSSVMVRQVGFGNNATANQY

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                                                                                                                                                     Sequence 42,
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Sequence
Sequence
                               Sequence
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APPLICANT: Doran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADGRESS:
ADDRESSE: Seed and Berry
STREET: 6300 Collumbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
CITY: Seattle
COMPUTER: Dead of SALMONELLA
MEDIUM TYPE: D.S.A.
ZIP: 98104-7092
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: 26-APR-1994
CLASSIFICATION NUMBER: US/08/233,788A
FILING DATE:
APPLICATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
TELLEPRONE: (206) 622-4900
TELLEPRONE: (206) 622-4900
TELLEPRONE: (206) 622-6031
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US-08-899-575-34
US-08-383-619-16
US-08-129-597-16
US-09-129-597-16
PCT-USS3-08364-16
PCT-USS3-08364-16
US-09-495-880A-22
US-08-553-497A-22
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US-09-219-019-4
US-09-46-6669A-1
US-09-463-668A-1
US-09-463-668A-1
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Pred. No. 4e-61;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
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Best Local Similarity 89.4°
Matches 135; Conservative
     TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                         US-09-543-407-28
775
1 MKLIKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY
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(GGTZ = 6/ptodata/2/iaa/5B_COMB.pep:*

(GGTZ = 6/ptodata/2/iaa/5B_COMB.pep:*

(GGTZ = 6/ptodata/2/iaa/6A_COMB.pep:*

(GGTZ = 6/ptodata/2/iaa/6B_COMB.pep:*

(GGTZ = 6/ptodata/2/iaa/PCTUS COMB.pep:*

(GGTZ = 6/ptodata/2/iaa/PCTUS COMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-233-788A-57

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US-09-056-556-204

US-09-072-596-139

US-09-477-135A-131

US-09-477-135A-131

US-09-477-135A-131

US-09-477-135A-131

US-09-252-991A-30983

US-09-252-991A-30983

US-09-252-991A-30983

US-09-252-991A-36983

US-09-252-991A-26438

US-09-336-44A-5

US-09-336-44A-5

US-09-0257-688-280

US-09-0257-688-280

US-09-0257-688-280

US-08-0336-44A-13

US-08-0336-44A-13

US-08-0336-44A-13

US-08-0336-44A-13

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US-08-1336-11-16

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US-08-1337-16
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                 SDARKSETTITOSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
ALTILE OF INVENTION: OF SALMONELLA.
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 498; DB 1; Length 120;
Pred. No. 4.6e-43;
1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTY: Searchie
COUNTY: U.S.A.
21P: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentln Release #1.0, Version #1.25
COMPUTER: Patentln Release #1.0, Version #1.25
COMPUTER: Patentln Release #1.0, Version #1.25
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COMPUTER: Joshus Release #1.0, Version #1.25
COMPUTER: JOSHUS JOSHUS RESEDANBERRY
INPORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
COMPUTER: JOSHUS PRINTERRY
INPORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
COMPUTER: JOSHUS PRINTERRY
INPORMATION FOR SEQ ID NO: 57:
COMPUTER: JOSHUS PRINTERRY
INPORMATION POR SEQ ID NO: 57:
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COMPUTER POR SEQ ID NO: 
                                                                                                                                                                                                                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4764, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.6%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-233-788A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: Washingt
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-328-352-4764
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: NOVEL POLYPEPTIDE CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: AID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: 812-5 Hiran-
STREED
                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 ALALQSDARKSETTI-----TQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 APTITSNIVNDNDTIDNGNSGGIGSGSGNGSG-DGLLNGAASGNGEH----NYGIGNGNG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 AGNGIA-----SGNGEHNYGIGNGNGDDVDITAPITGVLNISGNSFTLIGNSSSSSVNT 353
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                          11.0%; Score 85; DB 4; Length 975; 25.3%; Pred. No. 4.2; cive 18; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                               15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDSTLSIYQYG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 KNSDIT-----VGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 DDVDITSPITGIFNFSGNSFSLIGNSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F-5610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08864038A
Patent No. 6001592
GENERAL INFORMATION:
APPLICANT: Kunio NAKASHIMA et al.
                                                                                                                                                                                                                                                     ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REPERBUGL/DOCKET UMBER: F-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212)986-2340
(212)953-7733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: ISSUAN.
CITY: Tsu-city
STATE: Me-prefecture
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.33
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                  US-09-328-352-4764
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US-08-864-038A-3
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us-09-543-407-28.rai

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TUBERCULOSIS
504 GFGNAGDFNQ------GFANTGNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                      APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                           ---NAALVNQTASDSSVM----VRQVGFGNNATAN
                                                                                  554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
10.8%; Score 84; DB 4
Best Local Similarity 24.7%; Pred. No. 5.1;
Matches 38; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210121.41709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATCHLIN RELEASE #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USASSON COUNTRY: USASSON ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          Sequence 199, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                          Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hendrickson,
TITLE OF INVENTION: COMP
NUMBER OF SEQUENCES: 350
CARSPONDENCE ADDRESS:
ADDRESSEE: 6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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US-09-477-135A-131
                                                                                                                                                   RESULT 6
US-09-072-596-199
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                                                                                                                                                                                                                                                                                                                          419 LLKSSASASASASASAG----GGGGGGNGGGNGGGG------GGGAGALA---- 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- 121
                                                                                                                                                                                                                                                                                 3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                     Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 204, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ALBERSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYGNGADYDOLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN----
                                                                                                                                                                                          Score 84.5; DB 3; Length 738;
Pred. No. 3.3;
1; Mismatches 22; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 943;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAYLG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEDEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.8%; Score c., 24.7%; Pred. No. 5.1; rive 12; Mismatches
                                                                                                       LOCATION: From 1 to 738
, IDENTIFICATION METHOD: E (by experiment)
US-08-864-038A-3
                  ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
FEATURE:
                                                                                                                                                                                                                                     4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 204: SEQUENCE CHARACTERISTICS: LENGTH: 943 amin-
                                                                                                                                                                                                                                                                                                                                                                                                             ----AALAAAĠAĠĠĠ 471
                                                                                                                                                                                          Query Match
Best Local Similarity 35.5%;
Matches 27; Conservative
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amino acid
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Best Local Similarity 24.7*
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Colur
CITY: Seattle
STATE: Washington
                                                                                  NAME/KEY: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
ORIGINAL SOURCE
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US-09-056-556-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-056-556-204
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
STREET: 115
CITY: New )
                                                                                                                                                                                                                                                                                                                                    US-09-072-967-204
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; Sequence 131, Application US/09477135A
; Patent No. 6572865
; GENERAL INFORMATION:
APPLICANT: Nano, Francis
; TITLE OF INVENTION: immunostimulatory Peptides
; TITLE OF INVENTION: immunostimulatory Peptides
; TITLE OF INVENTION: immunostimulatory Peptides
; TITLE OF INVENTION: immunostimulatory Peptides
; TITLE OF INVENTION: immunostimulatory Peptides
; TITLE OF INVENTION: immunostimulatory Peptides
; TITLE OF INVENTION: immunostimulatory Peptides
; CURRENT APPLICATION NUMBER: US/09/477,135A
; CURRENT FILING DATE: 1997-12-15
; PRIOR FILING DATE: 1997-12-15
; PRIOR PELICATION NUMBER: US/06/000,254
; PRIOR FILING DATE: 1995-06-15
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Lodes, Michael U.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 84; DB 4; Length 943; 24.7%; Pred. No. 5.1; tive 12; Mismatches 54; Indels
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COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 204, Application US/09072967 Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Conservative
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CCUNTX: USA
ZIP: 98104-709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity
Matches 38; Conserv
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STREET: 6300 CC
CITY: Seattle
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MANGESTRATION PROCRACT NUMBER: 1313141411C9

REGISTRATION PROCRET NUMBER: 1313141411C9

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REGISTRATION PROCRET NUMBER: 1313141411C9

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US-09-489-039A-11518

Sequence 11518, Application US/09489039A

Sequence 11518, Application US/09489039A

Sequence 11518, Application US/09489039A

Sequence 11518, Application US/09489039A

Sequence 11518, Application:

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                                                                                                                                              5 KVAAFAAIVVSGSALAGVVPQWGG------GGNHNGGGNSSGPDSTLSIYQYGSANAAL
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                                         Gaps
                                      28;
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APPLICANT Weltrin, Richard A.
APPLICANT Weltrin, Richard A.
APPLICANT Guy, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Wethods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
CURRENT APPLICATION WUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR PILING DATE: 1998-06-19
                                  61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            114 TV----GQYGGNNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 YG--GNNAALVNOTASDSSVMVRQVGFGNNATA 148
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      ; Pred. No. 3.3; 34; Mismatches
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 745
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18-09-338-115C-6
Sequence 6/ Application US/09336115C
Patent No. 6576244
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      20.1%;
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ORGANISM: Helicobacter pylori
Best Local Similarity 20.1%
Matches 31; Conservative
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/094,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30983
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Patent NO. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROITNOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-02-18
PRIOR PLILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32096
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                                                                                                                                                                                                                                            16 GSALAGV-----VPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
                                                                                                                                       Gaps
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                                                                                                                                    34;
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                                                              10.6%; Score 82; DB 3; Length 2123; 25.8%; Pred. No. 24; tive 17; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-252-991A-30983
; Sequence 30983, Application US/09252991A
; Parent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32096
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                                                    Query Match
Best Local Similarity 25.8*
Matches 31; Conservative
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Matches 27; Conservative
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US-09-252-991A-30983
   US-08-968-685A-10
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US-09-222-991A-26438

Sequence 26438, Application US/09252991A

Sequence 26438, Application US/09252991A

Sequence 26438, Application US/09252991A

Sequence 26438

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: USCALLA 1990-12-18

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26438

LENGTH: 1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 ADFAISGO-LKDHASHYGAGGLVGRNRGGLIRSSGSQGTLSLSGGRGMNLGGLVGYSSAGG 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 -RKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN- 121
                                                                                                                                                                                                                                                                                                                       102 AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                                                                                                                                     38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AAIVVSGSALAGVVPOWGGGG--NHNGGG--NSSGPDSTLSIYQYGSANAALALQSDA-- 63
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 RINNATIDQW-NAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 DINGGVYQFCKAKNGSSSSSNGGNGSSTQTTATTTQDGVIITTTYNNNKAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.3%; Score 79.5; DB 4; Length 1415; Best Local Similarity 28.9%; Pred. No. 25; Matches 44; Conservative 17; Mismatches 74; Indels 17
                                                                                                                                                                                         10.3%; Score 79.5; DB 4; Length 745; 20.5%; Pred. No. 11; tive 27; Mismatches 70; Indels 35
                                                                                                                                                                                                                                                                                  -- GGGGNHNGGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 NAALVNQTA-SDSSVMV-RQVG--FGNNATAN 149
                                                                                                           DOCATION: 721
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-115C-6
                                                                                                                                                                                                                                                                                  8 AFAAIVVSGSALAGVVPQW-----
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                                                                                                                                                                                           Query Match
Best Local Similarity 20.5'
Matches 35; Conservative
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(20)
                                                                FEATURE: NAME/KEY: VARIANT
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US-09-841-786-4
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Sequence 4, Application US/09841786
Patent No. 666940
GENERAL INFORMATION:
APPLICANT: NAGARAJA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJEEV K.

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--TIIIQSGYGNGADY---DOLVIRVVIHEMAHAFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 IVVSGSALAGVVPQWGGGG----NHNGGGW---SSGPDSTLSIYQYGSANAALALQSDAR
APPLICANT: CHENGAPPA, M. M.

TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN

TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF

FILE REPERENCE: 30296

CURRENT APPLICATION NUMBER: US/09/841,786

CURRENT FILING DATE: 2001-04-24

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 4

LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.1%; Score 78.5; DB 4; Length 714;
Best Local Similarity 22.8%; Pred. No. 13;
Matches 31; Conservative 16; Mismatches 56; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 2, 2004, 14:58:36
Job time : 12 secs
                                                                                                                                                                                                                                                                                                            ; TYPE: PRT ; ORGANISM: Fusobacterium necrophorum US-09-841-786-4
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151 AGESESQKMDVDVTAY 166
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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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1 MKLLKVAAPAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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| Ggn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| Ggn2_6/ptodata/2/pubpaa/Derror NEW PUB.pep:*
| Ggn2_6/ptodata/2/pubpaa/Derror NEW PUB.pep:*
| Ggn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 186417,	Sequence 50616, A	Sequence 21, Appl	Sequence 3, Appli	Seguence 3, Appli	Seguence 20638, A	Seguence 998, App	Seguence 146, App	Sequence 44999, A	Seguence 64364, A	Sequence 905, App
SUMMARIES		QI	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-437-963-186417	US-10-282-122A-50616	US-09-820-843A-21	US-09-730-374-3	US-10-704-206-3	US-10-369-493-20638	US-10-408-765A-998	US-09-793-306-146	US-10-282-122A-44999	US-10-282-122A-64364	US-09-880-748-905
		DB	12	12	12	12	16	12	10	σ	16	15	16	σ	12	12	10
	* Query	Length	151	151	131	131	400	1074	354	249	249	445	1448	597	974	2204	254
	* Query	Match	65.3	65.3	55.2	55.2	12.3	11.9	11.5	11.3	11.3	11.3	11.3	11.2	11.1	11.0	11.0
		Score	506	206	428	428	95	9	60 60	87.5	87.5	87.5	87.5	87	86	85.5	82
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16   85   11.0   254   12   US-10-293-418-905   Sequence 905, App   18   45   10.9   928   12   US-10-282-122A-54379   Sequence 54647, App   18   41   10.8   943   10   US-09-996-634-131   Sequence 131, App   22   84   10.8   943   10   US-09-997-182-131   Sequence 131, App   23   10   US-09-997-182-131   Sequence 131, App   24   10.8   943   10   US-09-997-182-131   Sequence 131, App   24   10.8   943   14   US-10-193-002-199   Sequence 131, App   25   84   10.8   943   14   US-10-193-002-199   Sequence 131, App   26   10.8   943   14   US-10-193-002-199   Sequence 199, App   26   10.8   10.8   10.9   10.10-103-002-199   Sequence 199, App   26   10.8   10.9   10.10-103-002-199   Sequence 10.9   App   26   10.9   10.9   10.10-103-102-12A-64369   Sequence 10.9   App   27   27   27   27   27   27   27	JS. App	4	4047, A	1379, A	l, App	31, App	31, App	99, App	04, App	4369, A	62284,	83675,	2467, A	0037, A	47748,	2, Appl	3, Appl	, Appli	9412, A	5041, A	75468,	7763, A	Appli	4094, A	94, Ap	46651,	08981,	134, Ap	87064,	3269, A	1,00
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## ALIGNMENTS

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RESULT 1

Sequence 4, Application US/09741873B

Sequence 4, Application US/09741873B

Publication No. US20020081722A1

GENERAL INFORMATION:
APPLICANT Olsen, Arne
TITLE OF INVENION: Fibronectin Binding Protein As Well As I
FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT FILING DATE: 2003-04-04

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1999-11-26

PRIOR FILING DATE: 1999-11-26

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-05

PRIOR FILING DATE: 1994-01-05

PRIOR FILING DATE: 1994-01-05

NUMBER OF SEQ ID NOTE: 1994-01-05

NUMBER OF SEQ ID NOTE: 1994-01-05

NUMBER OF SEQ ID NOTE: 100-05

NUMBER OF SEQ ID NOTE: 100-05

NUMBER OF SEQ ID NOTE: 100-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
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US-09-741-873B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 151
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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SE 8801723-1

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APPLICATION NUMBER:
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US-09-741-873B-2
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                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Publication No. US20040095955A9

Publication No. US2004009595A9

GENERAL INPORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
ITLE OF INVENTYON: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 08/9741,873B

CURRENT APPLICATION NUMBER: US 08/976,878

PRIOR APPLICATION NUMBER: US 08/976,878

PRIOR FILING DATE: 1994-01-12-6

PRIOR PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR PRILING DATE: 1991-11-06

PRIOR PRILING DATE: 1994-01-28

PRIOR PRILING DATE: 1994-01-28

PRIOR PRILING DATE: 1994-10-05

PRIOR PRILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SECOTTMARER: Patentin version 3.0
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                                                           SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                   SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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                                                                                                                                                             121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                      121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 67.5
Matches 102; Conservative
                                                                                                                                                                                                                                RESULT 2
US-09-741-873B-4
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US-09-741-873B-2
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81 YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01288-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
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55.2%; Score 428; DB 12; Length 131;
Best Local Similarity 64.1%; Pred. No. 1.1e-34;
Matches 84; Conservative 15; Mismatches 32; Indels
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-105-04
PRIOR FILING DATE: 1991-11-06
PRIOR PLING DATE: 1991-11-06
PRIOR PLING DATE: 1991-11-06
PRIOR PLING DATE: 1992-11-03
PRIOR PLING DATE: 1994-01-28
PRIOR FILING DATE: 1994-00-05
PRIOR FILING DATE: 1994-00-05
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SSOTUNOS: PRIOR PLING DATE: 1994-11-05
NUMBER OF SEQ ID NOS: 10
SSOTUNOS: PRIOR PLING DATE: 1994-11-05
NUMBER OF SEQ ID NOS: 10
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PRIOR APPLICATION NUMBER: SE 8801723-1

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1999-05-04

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-8

PRIOR FILING DATE: 1994-01-8

SOFTWARE: PATENTING VOMBER: US 08/318,519

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 2
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Sequence 21, Application US/09820843A
Sequence 21, Application US/09820843A
Publication No. US20030039963A1
SEQUENCE INFORMATION
APPLICANT: Council of Scientific and Industrial Research
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTE
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT PILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 21
LENGTH: 354
TYPE: PRT
                                                                                       APELICANT: XU, H.
APELICANT: XU, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR PRIORING NUMBER: 60/257,931
PRIOR PRIING DATE: 2001-12-22
PRIOR PRIING DATE: 2001-12-22
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PRIOR PRIOR DATE: 2001-12-22
PRIOR PRIING DATE: 2001-12-22
PRIOR PRIOR DATE: 2001-12-22
PRIOR PRIOR DATE: 2001-12-22
PRIOR PRIOR DATE: 2001-12-26
PRIOR PRIOR DATE: 2001-02-09
PRIOR PRIOR DATE: 2001-02-06
PRIOR PRIOR DATE: 2001-02-06
PRIOR PRIOR PRIOR DATE: 2001-02-06
PRIOR PRIOR PRIOR DATE: 2001-02-06
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Best Local Similarity 28.1%; Pred. No. 3.5;
Matches 39; Conservative 21; Mismatches
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRICE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 186417
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                                                                                                                                                                                                                                                                     61 VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                      81 YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
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                                                                                                                                                  21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD 80
                                         Gaps
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12.3%; Score 95; DB 16; Length 400;
Best Local Similarity 23.6%; Pred. No. 0.52;
Matches 37; Conservative 20; Mismatches 62; Indels
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_83218C.1.pep
US-10-437-963-186417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 VGQYGGNNAALVNQTASDSSVMVRQVGF--GNNATAN 149
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          Pred. No. 1.1e-34;
                                      15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 186417, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50616, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Manone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Zamudio, Judith
APPLICANT: Trawick, John
          64.1%;
          Best Local Similarity 64.1%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                    GFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                               121 GEGNNATAHOY 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-282-122A-50616
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APPLICANT: Cao, Yorgwei
APPLICANT: Cao, Yorgwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Saveen C.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
TITLE OF INVENTION: ExpRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
TYPE: PRI
CORGANISM: Rhodopseudomonas palustris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 GNSNSVGRDIOGKOSGAGNS-AAIFQEGTGSDVELOOTGT-----SNGAVPSGW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AAFAA-----IVVSGSALAGVVPQWGGGG-----GNSSGPDSTLSIYQY 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 LLISGATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 ALQSDARKSETTITQ--SGYGNGADYDQLVTRVVTHEMA 94
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; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
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                     PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: PCT/US99/12512
PRIOR APPLICATION NUMBER: PCT/US99/12512
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20638, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
     PRIOR APPLICATION NUMBER: 09/730,374
                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 27.3%;
Matches 27; Conservative
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nes 45; Conserv
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US-10-369-493-20638
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Best Local S:
Matches 45,
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Publication No. US20040141982A1
GENERAL INFORMATION:
APPLICANT: Lust, John A.
APPLICANT: Lust, John A.
TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES TO CD38 TO TREAT MULTIPL
FILE REFERENCE: 150.188US2
CURRENT APPLICATION NUMBER: US/10/704,206
CURRENT FILING DATE: 2003-11-07
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---GYVNTSTTSMFGGNSGVLN 300
                                                                                                                                                                                                                                                                                 200 AGDVNSGVGNAGDVNTGLGNSGNINTGGFNPGTLNTGFFSAMTQAGPNS--GFFNAGTGN 257
                                                                                                                                                                                                                                                                                                                                        AALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                   -- NSSGPDSTLSIYQYGSAN 54
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                                                                                                                                                                                    Gaps
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US-09-730-374-3

Sequence 3, Application US/09730374

Patent No. US20010031261A1

Fatent No. US20010031261A1

Fatent No. US20010031261A1

FAPELICANT: INFORMATION:

APPLICANT: LUST, JOHN A.

APPLICANT: Donovan, Kathleen A.

TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES

TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES

TITLE OF INVENTION: US DOF GENETICALLY ENGINEERED ANTIBODIES

TITLE OF INVENTION: US DOF GENETICALLY MULTIPLE MYELOMA

FILE REFERENCE: 150.188US2

CURRENT FILING DATE: 1990-06-04

FRIOR APPLICATION NUMBER: 60/088,277

FRIOR APPLICATION NUMBER: 60/088,277

FRIOR FILING DATE: 1996-08-05

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTESE for Windows Version 4.0

SEQ ID NOS: 4
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1.7;
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                                                                                                                                                                                 63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 11.3%; Score 87.5; DB 9; 1 Similarity 27.3%; Pred. No. 1.6; 27; Conservative 9; Mismatches 32;
                                                                                                                           ch 11.5%; Score 89; DB Similarity 24.1%; Pred. No. 1.7; 38; Conservative 17; Mismatches
                                                                                                                                                                                                                                10 AAIVVSGSALAG-VVPQWGGGGNHNGGG-
                                                                                                                                                                                                                                                                                                                                                                                   258 SGFGHNDPAGSGNSGIONSGFGNS---
) OTHER INFORMATION: PPE
NAME/FRY: misc feature
) THER INFORMATION: gi|1781260
US-09-820-843A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GGGGNHNGGGNSSGPD--
                                                                                                                             Query Match
Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
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358 FGNSGNNNIGFFNSG-NNNVGFFNSGNNNFGFGNAGD-----INTGFGNAGDINT-- 406
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                                                                                                                                                                                                                                                                                                                                                                                                            -----GFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGN--AGNQS-----VGFG 449
                                                                                                                                                               26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLV 85
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

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PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PELING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2001-02-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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DB 9; Length 597;
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11.1%; Score 86; DB 1
Best Local Similarity 26.0%; Pred. No. 12;
Matches 39; Conservative 17; Mismatches
    111.2%; Score 87; DB 9 27.0%; Pred. No. 5.3; ive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44999, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin version 3.1
SEQ ID NO 44999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskiná, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
Query Match
Best Local Similarity 27.0%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 NNATAN 149
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Sequence 146, Application US/09793306

Sequence 146, Application US/09793306

Sequence 146, Application US/09793306

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Ovendale, Pamela

APPLICANT: Ovendale, Pamela

APPLICANT: Ovendale, Pamela

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APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 35; Gaps
                                                                                                           Sequence 998, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Fahy, Edin D.
APPLICANT: Glaso, Bradford W.
APPLICANT: Glaso, Bradford W.
APPLICANT: Glaso, Bradford W.
APPLICANT: Glaso, Bradford W.
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APPLICANT: Glaso, Bradford W.
APPLICANT: Glaso, Bradford W.
APPLICANT: Glaso, Bradford W.
APPLICANT: WARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660088465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 998
SEQ ID NO 998
LENGTH: 1448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 1448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.6*
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-408-765A-998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 TASDSS 134
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                                                        SULT 11
-10-408-765A-998
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299 AGNGIA-----SGNGEHNYGIGNGNGDDVDITAPITGVLNISGNSFTLIGNSSSSSVNT 352
                                                                                                                                                                                               353 APTTTSNIVNDNDTIDNGNSGGTGSGSGNGSG-DGLLNGAASGNGEH----NYGIGNGNG 407
                                                                                                                                      56 ALALQSDARKSETTI-----TQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNA 108
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PRIOR APPLICATION NUMBER: 06/191,078

PRIOR APPLICATION NUMBER: 60/2026,848

PRIOR FILING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2001-02-09

PRIOR PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

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PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 31; Gaps
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                                                                                                                                                                                                                                                                                                                       109 KNSDIT-----VGOYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                      408 DDVDITAPITGVFNFSGNSFSLIGNSSSSS 437
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11.0%; Score 85.5; Di
Best Local Similarity 25.0%; Pred. No. 38;
Matches 34; Conservative 15; Mismatches
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CURRENT APPLICATION NUMBER: US/10/282,122A
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Sequence 64364, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangeu

APPLICANT: Malone, Cheryl

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Chleen, Kari

APPLICANT: Zyskind, Undith

APPLICANT: Tymind, Undith

APPLICANT: Tramick, John
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US-10-282-122A-64364
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Yamamoto, Robert
Forsyth, R.
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ORGANISM:
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US-09-880-748-905

Sequence 905, Application US/09880748

Publication No. US20030059937A1

GENERAL IMPORVATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERSENCE: PFF23

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: PARENTIN Ver. 2.0

SEQ ID NO 905
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11.0%; Score 85; DB 10;
Best Local Similarity 23.0%; Pred. No. 2.9;
Matches 29; Conservative 11; Mismatches 42;
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1997 ----IGFFNSGTGN 2006
134 SVMVRQVGFGNNATAN 149
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CORGANISM: Homo sapiens
US-09-880-748-905
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- protein search, using sw model

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Run on:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Listing first 45 summaries

Database :

Post-processing: Minimum Match 0% Maximum Match 100%

6019581 seqs, 976053577 residues

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Title: Perfect score:

Sequence:

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Sequence 4, Appli
Sequence 2, Appli
Sequence 53, Appli
Sequence 534, Appl
Sequence 5834, Appl
Sequence 5834, Appl
Sequence 5834, Appli
Sequence 2, Appli
Sequence 37, Appli
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Sequence 20, A
Sequence 26, A
Sequence 30, A
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Sequence 14, P
Sequence 18, P
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Seguence 31, 7
Seguence 16, 7
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GENERAL INFORMATION:
APPLICANT Milte, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: RESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543.407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASES for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1
Sequence 6
Sequence 6
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ORGANISM: Artificial Sequence
ORGANISM:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: Sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                        19 US-09-543-407-20

19 US-09-543-407-20

19 US-09-543-407-12

19 US-09-543-407-14

19 US-09-543-407-14

19 US-09-543-407-14

19 US-09-543-407-14

19 US-09-543-407-16

19 US-09-543-407-16

19 US-09-543-407-16

19 US-09-543-407-16

19 US-09-543-407-12

19 US-09-543-407-37

19 US-09-552-691-5834

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10 US-09-733-089-18735

10 US-09-731-1886-5833

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                                                                                                                                                                                 August 2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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775
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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1: /cgn2 6/ptodata/2/paa/USO6 COMB.pep:*

2: /cgn2 6/ptodata/2/paa/USO6 COMB.pep:*

4: /cgn2 6/ptodata/2/paa/USO7 COMB.pep:*

4: /cgn2 6/ptodata/2/paa/USO8 1 COMB.pep:*

6: /cgn2 6/ptodata/2/paa/USO8 1 COMB.pep:*

6: /cgn2 6/ptodata/2/paa/USO8 2 COMB.pep:*

7: /cgn2 6/ptodata/2/paa/USO8 4 COMB.pep:*

8: /cgn2 6/ptodata/2/paa/USO8 4 COMB.pep:*

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12: /cgn2 6/ptodata/2/paa/USO8 7 COMB.pep:*

13: /cgn2 6/ptodata/2/paa/USO8 7 COMB.pep:*

14: /cgn2 6/ptodata/2/paa/USO8 7 COMB.pep:*

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17: /cgn2 6/ptodata/2/paa/USO8 7 COMB.pep:*

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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB Length Query Score

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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIUVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kay, William W.
APPLICANT: Colinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James, TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         Query Match 88.1%; Score 683; DB 19; Length 1 Best Local Similarity 90.1%; Pred. No. 9.5e-65; Matches 136; Conservative 1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: 930 COLUMNIA CENTER, 701 FILLIN AVENUE
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFRENCE/DOCKET NUMBER: 920043.403C3
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          920043.403C3
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TELEX: 372836 SEBDAMBERY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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Best Local Similarity 89.4
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA-----DQWNAKNSDI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22, Application US/09543407

Sequence 22, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: UNMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 151
                                                                                                                                Gaps
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US-09-543-407-5
US-09-543-407-5
Sequence 5, Application US/09543407
Sequence 5, Application US/09543407
Septence 7, Applicant White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                Query Match 100.0%; Score 775; DB 19; Length 151; Best Local Similarity 100.0%; Pred. No. 1.2e-74; Matches 151; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
91.9%; Score 712; DB 19; Length 151;
Best Local Similarity 91.1%; Pred. No. 7.2e-68;
Matches 144; Conservative 0; Mismatches 0; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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US-09-543-407-22
         US-09-543-407-28
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TYPE: PRT

FEATURE:

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                        Gaps
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0
Length 151;
                        Indels
87.5%; Score 678; DB 6; Lv
89.4%; Pred. No. 3.3e-64;
live 1; Mismatches 15;
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US-09-543-407-26
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                                                                                            SPARKSETTITQSGYGNGADVGQADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARK-------YDQLVTRVVTHEMAHAGQGADMSTIELTQNGFRNNATIDQ 105
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9
                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                            APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%; Score 662; DB 19; Length 151; larity 81.9%; Pred. No. 1.7e-62; Conservative 0; Mismatches 0; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                 NNPALVNQTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                       121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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US-09-543-407-20
Sequence 20, Application US/09543407
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Simil
Matches 136; (
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US-09-543-407-26
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SNGTH: 151
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                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ------YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT White, Aaron P.
APPLICANT White, Aaron P.
APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                              46;
                                                                            OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                   Length 151;
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                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.1%; Score 613; DB 19; 74.6%; Pred. No. 3.2e-57; iive 0; Mismatches 0;
                                                                                                                                                                                                                   Query Match
Pest Local Similarity 73.6%; Pred. No. 1.2e-57;
Matches 128; Conservative 0; Mismatches 0;
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US-09-543-407-12
; Sequence 12, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James I.
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Matches 129, Conservative
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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ORGANISM: Artificial Sequence
PERTURE:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Orien, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: DRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: UNMER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 151
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APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT PELLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence PEATURE: OPTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.1%; Score 605; DB 19; Length 151; 80.1%; Pred. No. 2.3e-56; ive 5; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
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ORGANISM: Artificial Sequence
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Matches 121; Conservative
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US-09-543-407-14
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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| Sequence 24, Application US/09543407 |
| Sequence 24, Application US/09543407 |
| Sequence 24, Application US/09543407 |
| SEQUENCE 24, Application US/09543407 |
| APPLICANT: White, Aaron P. |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Kay, William W. |
| TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR |
| TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| CURRENT APPLICATION WHORER: US/09/543,407 |
| CURRENT FILING DATE: 2000-04-05 |
| NUMBER OF SEQ ID NOS: 59 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 24 |
| LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    APPLICANT: Dozah, James L. APPLICANT: Collinson, S. Karen APPLICANT: Collinson, S. Karen APPLICANT: Kay, William W. TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 18
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.5%; Score 601; DB 19; Length 151; 80.8%; Pred. No. 6.3e-56; cive 4; Mismatches 25; Indels (
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-543-407-18
Sequence 18, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
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DB 19; Length 151;

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121 NNAALVNQTASDSSWWYRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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Best Local Similarity 68.23
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT;
CRGANISM: Escherichia coli
US-09-543-407-7
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                                                                                                                                                    SDARKSETTITIQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 120
                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGCGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD 60
                                                               1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                      NS-09-543-407-31

Sequence 31, Application US/09543407

Sequence 31, Application US/09543407

Sequence 31, Application US/09543407

Sequence 31, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: CAY, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF SEQUENCE: 920043.406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                        Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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Pred. No. 8.1e-56;
3; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 596; DB 19;
Pred. No. 1.8e-55;
1; Mismatches 14;
                                                                                                                                                                                                                                   121 NNAALVNQTASDSSVMVRQVGFGNNATANOY 151
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US-09-543-407-16
Sequence 16, Application US/09543407
GENERAL INFORMATION:
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; ORGANISM: Salmonella enteritidis
US-09-543-407-31
81.5%;
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Best Local Similarity 88.5%;
Matches 116; Conservative
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ORGANISM: Artificial Sequence
                      123; Conservative
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  Best Local Similarity
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1Sequence 4; Application US/08978878
1Sequence 4; Application US/08978878
1Sequence 4; Application US/08978878
1Sequence 4; Application US/0897878
1Sequence 4; Application NORMARK, Staffan
1Septicant NORMARK, Staffan
1Septicant OLSEN, Arne
1TIRE OF INVENTION: FIBENOECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
1SET IN THE OF INVENTION NUMBER: US/08/978,878
1SEXELIER APPLICATION NUMBER: US/08/978,878
1SEXELIER APPLICATION NUMBER: SE 8801723-1
1SEALIER PILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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| Sequence 7, Application US/09543407
| GENERAL INFORMATION:
| APPLICANT White, Aaron P.
| APPLICANT Collinson, S. Karen
| APPLICANT RAY, Milliam W.
| TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
| TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
| CURRENT APPLICATION NUMBER: US/09/543,407
| CURRENT FILING DATE: 2000-04-05
| CURRENT FILING DATE: 2000-04-05
| SOFWWARE: FastSEQ for Windows Version 4.0
| SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                             26; Indels
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                                                                                                                                              Query Match
73.3%; Score 568; DB 19;
Best Local Similarity 80.1%; Pred. No. 2.2e-52;
Matches 121; Conservative 4; Mismatches 26;
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68.2%; Pred. No. 5e-46;
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 67.5%; Pred. No. 1e-45;
Matches 102; Conservative 16; Mismatches 33; Indels (
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EARLIER PILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER PILING DATE: 1991-11-06
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-01-28
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER PELING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SCOTWARE: PatentIN Ver. 2.0
SEQ ID NO 4
LENGTH: 151
TYPE: PRT
TYPE: PRT
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TYPE: PRT
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2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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1 MKLIKVAAPAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  601315 segs, 104695340 residues
                                                                         OM protein - protein search, using sw model
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Perfect score:
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Pending Patents_AA_New:*

1: /cgn2 6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description	741-873C-4 741-873C-4 741-873C-4 741-873C-2 748-796A-17306 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-701-45603 76-70-70-70-70-70-70-70-70-70-70-70-70-70-
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Result No.	

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Sequence 13, Appl Sequence 13, Appl Sequence 72, Appl Sequence 274032, Sequence 309662, Sequence 34335, Sequence 21471, Sequence 221471, Sequence 1224, A Sequence 1224, A Sequence 1245, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 16, Appl Sequence 15, Appl Sequence 16, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl	Well As Its Preparation	ength 151; Indels 0; Gaps 0;	DSTLSIYQYGSANAALALQ 60  - - - - - - - - - - - - - - - - -	TIDQWNAKNSDITVGQYGG 120  -             :     :   TLDQWNGKNSEMTVKQFGG 120
US-09-952-267B-13 US-10-872-768-13 US-10-872-768-13 US-10-425-115-274032 US-10-425-115-309662 US-10-425-115-31474 US-10-425-115-31478 US-60-581-351-11388 US-60-581-351-11388 US-10-425-115-344789 US-10-425-115-344789 US-10-490-953-13 US-10-490-953-14 US-10-733-981-14 US-10-733-981-14 US-10-733-981-14 US-10-733-981-14 US-10-733-981-14 US-10-733-981-14	ALIGNMENTS 1873C n Binding Protein As 7/99/741,873C 22223-1 8/978,878 7/789,437 7/970,846 8/318,519	; Score 506; DB 5; Le; Pred. No. 6.1e-38; 16; Mismatches 33;	SALAGVVPQWGGGNHNGGGNSSGPDSTLSI'   :	SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGGYGG 
766 55 55 70 70 70 70 70 70 70 70 70 70 70 70 70	-873C-4  -8.1 Application US/05  ANTINOMATION: ANTINOMATION: ANTINOMATION: ANTINOMATION: ANTINOMATION: ANTINOMATION: T APPLICATION NUMBER: T FILING DATE: 1998-05-06-164 APPLICATION NUMBER: US FILING DATE: 1998-05-06-164 APPLICATION NUMBER: US FILING DATE: 1991-11-06-164 APPLICATION NUMBER: US FILING DATE: 1991-11-06-164 APPLICATION NUMBER: US FILING DATE: 1991-11-06-164 APPLICATION NUMBER: US FILING DATE: 1994-10-06-166-166-166-166-166-166-166-166-1	Match 65.3% ocal Similarity 67.5% s 102; Conservative	1 MKLLKVAAFAAIVVSGS; 	61 SDARKSETTITQSGYGNG 
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	RESULT 1 US-09-741-8 Sequence 4 Sequence 4 APPLICANI APPLICANI APPLICANI TITLE OF FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE PRIOR FILE P	Query Mat Best Loca Matches	QQ Dp	Qy

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                                          132 GNQNVGSNSYSPDT-----YGSAIGTLGVQEKTAPAVIGIHSKGIG-AAAYPELT--- 180
                                                                                                                                    ---NAGNTGLAKGTAPASTSATYGESPSADYSKSGATGVVPATYLN 223
30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVV 89
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APPLICANT: Gray. Kevin
APPLICANT: McCann, Ryan
APPLICANT: McCann, Ryan
APPLICANT: McCann, Ryan
APPLICANT: Gerendash, Joel
APPLICANT: Janssen, Giselle
APPLICANT: Janssen, Giselle
APPLICANT: Dahod, Samun
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: 104-04-03
PRIOR APPLICATION NUMBER: 60/480,842
PRIOR PILING DATE: 2003-04-04
PRIOR PILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Obtained from an environmental sample
                                                                                            90 THEMAHAFRNNATIDOWNAKWSDITVGOYGGNNAALVNQTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                               224 TSGAPTGSLNTAGVVGGAGFGDNSNTSSY 252
                                                                                                                                                                                   132 -----DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                     Sequence 38, Application PC/TUS0410229 GENERAL INFORMATION:
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; CTHER INFORMATION: Catalytic domain PCT-US04-10229-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
PCT-US04-09388-9
; Sequence 9, Application PC/TUS0409388
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Best Local Similarity 26.9%
Matches 36; Conservative
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Solbak, Arne
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FEATURE:
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FEATURE:
NAME/KEY: DOMAIN
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NAME/KEY: SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                 Sequence 2, Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
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Best Local Similarity 64.1%; Pred. No. 5e-31;
Matches 84; Conservative 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Indels
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11.5%; Score 89.5; DB 5;
Best Local Similarity 22.1%; Pred. No. 3.6;
Matches 33; Conservative 17; Mismatches 44;
                                                                                                                                      THILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/978,1878
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-04
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PRILING DATE: 1994-01-28
PRIOR PRILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATEURIN VEYSION 3.0
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ORGANISM: Escherichia coli
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US-09-248-796A-17306
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Sequence 320950, Application US/10425115
GENERAL INFORMATION:
APPLICANT La Rosa, Thomas J.
APPLICANT Zhou, Yihua
APPLICANT Zhou, Yihua
APPLICANT Zhou, Yihua
APPLICANT Zhou, Yihua
APPLICANT Zhou, Yihua
APPLICANT SHOUNDIN: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRESENCE: 38-21(2322)B
CURRENT APPLICATION NUMBER: 2003-04-28
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 320950
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133 IRLLEERAQEAILASCRDVLRASGFRFEDAWAKVIPGSDEGVYAWVAANYALGRLGGDPN 192
                                                                                                                                                                                                                                                                                                                                                                                                    61 GXYGEAGGSGXAYAQGGGQGGGGGGQYGGSG-------SGYGSGSGYG 102
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                                                                                                                                                                                                                                                                                                                                          ----QYGSANAALALQSDARKSETTITQSGYGNGADYD
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                                                                                                                                                                     65;
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                                                                                                              Length 234;
                                                                                                                                                                     Indels
               ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep
US-10-767-701-45603
                                                                                                                                                                                                                            1 MKLLKVAAFAAIVV - - SGSALAGVVPOW - - - GGGGNHNGGGN - - -
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US-10-425-115-320950
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NAME/KEY: unsure
LOARION: (1)..(511)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                           Query Match 10.9%; Score 84.5; DB Best Local Similarity 24.2%; Pred. No. 5.5; Matches 39; Conservative 11; Mismatches
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Best Local, Similarity 23.3
Matches 44, Conservative
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US-10-425-115-339993
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FEATURE:
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      APPLICANT: TRAN, Uyen K.; YANG, Yonghong G.;
APPLICANT: TRAN, Uyen K.; YANG, Yonghong G.;
APPLICANT: TRAN, Uyen K.; YANG, Yonghong G.;
APPLICANT: TRAN, Uyen K.; YANG, Yonghong G.;
APPLICANT: TRAN, Uyen K.; YANG, Yonghong G.;
APPLICANT: ADAGE, Usoi; MANG, Jonathan T.;
APPLICANT: ELLIOTT, Vicki S.; CHIEN, David;
APPLICANT: ELLIOTT, Vicki S.; CHIEN, David;
APPLICANT: SILIOTT, Vicki S.; CHIEN, David;
APPLICANT: SILIOTT, Vicki S.; CHIEN, David;
APPLICANT: FAVERO, Kristin D.; RICHARDSON, Thomas W.,
APPLICANT: FAVERO, Kristin D.; RICHARDSON, Mariah R.,
APPLICANT: FAVERO, Kristin D.; BAUGHN, Mariah R.,
APPLICANT: PAVERO, Kristin D.; BAUGHN, Mariah R.,
APPLICANT: PAVERO, Kristin D.; WILSON, Amy D.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND D.; PRICE REFERENCE: PP-1531 PCT
CURRENT FILING DATE: 2004-04-04
PRIOR APPLICATION NUMBER: US 60/455,568
PRIOR FILING DATE: 2003-03-24
PRIOR PELING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: US 60/476,135
PRIOR APPLICATION NUMBER: US 60/476,583
PRIOR APPLICATION NUMBER: US 60/476,583
PRIOR FILING DATE: 2003-06-06
NUMBER OF SEC ID NOS: 40
PRIOR PELING DATE: 2003-06-06
NUMBER OF SEC ID NOS: 40
PRIOR PERMARE: PERL PROFIAM
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GENERAL INFORMATION:
APPLICANT: Covalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1082 -- MOEGWGSGGD-----WINTASOWEDEEGDV----WINDASOES 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 87.5; DB 1; Length 1905; 28.6%; Pred. No. 35; tive 16; Mismatches 39; Indels 35
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LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7525307CD1
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Matches 36, Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-10-767-701-45603
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104 -- DOWNAKNSDITVGOYGGNNA
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
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TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 QSGYGNGADYDQLV-
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us-09-5

"FILE OF INVENTION: Plants
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION NUCLEIC ACID MOLECULES
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 339993
LENGTH: 276
TYPE: TITLE THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO THE TITLE TO T
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GENERAL INFORMATION: Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cano, Yongwei
TITLE OF INVENTION: Uplants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DAITS: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Length 276
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US-10-425-115-193207
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; OTHER INFORMATION: Clone ID: MRT4577_73240C.1.pep
US-10-425-115-339993
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 24.6%
Matches 34; Conservative
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ORGANISM: Zea mays
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LOCATION: (1)..(2
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APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock Diagnostics and THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: 02 09 09 07 4, 725
PRIOR APPLICATION NUMBER: US 60/074, 725
PRIOR PELING DATE: 1998-02-13
PRIOR PELING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
SEQ ID NO 26659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GSALAGVVPQWGGGGNHNGGGNSS----GPDSTLSIYQYGSANAALALQSDARKSETTIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TRVVTHEMAHAFRNN--ATI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/10/805,394
CURRENT FILING DATE: 2004-03-22
PRIOR PLING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 4894
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.5%; Score 81;
Best Local Similarity 24.6%; Pred. No. 1
Matches 35; Conservative 19; Mismatch
                                                                                                                                                                                                                                                                                            APPLICANT: IXEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26659, Application US/09248796A GENERAL INFORMATION:
Sequence 4894, Application US/10805394 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Corynebacterium glutamicum
US-10-805-394-4894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 AGDDEDAKNALITDVNAGGLDA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40; Conservative
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Best Local Similarity
Matches 40; Conserv
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Sequence 16659, Application US/10170205E

SEQUENCE 16659, Application US/10170205E

GENERAL INFORMATION:
APPLICANT; ADAMS, MATK
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEVICES, ABBUTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40112
SEQ TYMARE: Patentin version 3.2
SEQ ID NO 16659
LENGTH: 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NS-10-425-115-312468

Sequence 312468, Application US/10425115

Sequence 312468, Application US/10425115

GENERAL INFORMATION: Thomas J.

APPLICANT: Exercity Yahua

APPLICANT: Zhou, Yahua

APPLICANT: Zhou, Yahua

APPLICANT: Zhou, Yahua

APPLICANT: Zhou, Yahua

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APPLICANT: Zhou, Yahua

APPLICANT: Zhou, Yahua

APPLICANT: Zhou, Yahua

APPLICANT: Zhou, Yahua

FILE REFERENCE: 38-21(5322)

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF, SEQ ID NOS: 369326

SEQ ID NO 312468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 TRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62j AAAAKSGHAWSGAANDEDKSPTWGEPPKPKSQHWGDGQRSNPAWSAGGDWADSSSVLGH 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 YQYGSANAALALQSDARKS----ETTIT-QSGYGNGADYDQLVTRVVTHEMAHAFRN-N 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TNTKANPGTNWG 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . ---- DGYGNGYSGGGYSSG-GYAANGYGVGSGSGNYSNASGGGYSGS----DGYGNGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- WGGGGNHN-----GGGNSSGPDSTLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       681 LGDGKKNGS-GWDADSNRSGSGWNDTTRSGNSGWGNS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ATI-----DQWNAKNSDITVGQYGGNNAALVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            729 ETLKPGPQQNWASKPQDNNVSNWGG--AASVKQTGT 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
US-10-425-115-312468
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 80; DB 6;
Pred. No. 1.4e+02;
5; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 79; DB 6; 25.4%; Pred. No. 23; iive 13; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AAIVVSGSALAGVVPQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                           10.3%;
26.3%;
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Best Local Similarity 25.4%
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.33
Best Local Similarity 26.33
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-170-20SE-16659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | |
220 SYPNPY 225
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Steer, Brian
APPLICANT: Steer, Brian
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Pealey, Shaun
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: GUCCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN
TITLE OF INVENTION: THEM
FILE REFERENCE: 564462005540
CURRENT APPLICATION NUMBER: 60/484,725
PRIOR APPLICATION NUMBER: 60/484,725
PRIOR APPLICATION NUMBER: 60/484,725
NUMBER OF SEQ ID NOS: 518
SOFTWARE: Patent In version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSTASGDGN-CEY----IVSNEWNTGFTGAIRITNEGSSAINGWNVSWSYSDGTSVTS 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITQSGYGNGADYDQLVTRVVTHEMAHAF-----RNNATIDQWNAK------ 109
                                                          289 SSEFLASLINGLGSGGGGGGGSNINSYKNHSTISTISKYFNSSSIATKLSSSKSIYSNS 348
                                                                                                                                                                       349 İTSRSSLSVSSSSTDGGGGANLFGLLINSVAAVSRTLAAESTLSTGTTTTSDSANSNTKD 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
                          --GPDSTLSIYQYGSANAALALQSDARKSET
                                                                                                                          TITOSGY-----GNGADYDQL-----VTRVVTHEMAHAFRNNATIDQWNAKNSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----NSDITVGQYGGNNAALVNQTASDSSVMVRQVGF-GNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
10.5%; Score 81; DB 1; Length 568;
Best Local Similarity 20.7%; Pred. No. 32;
Matches 35; Conservative 22; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(39)
FEATURE:
NAME/EXP: DOMAIN
LOCATION: (46)...(307)
OTHER INFORMATION: Cellulase (glycosyl hydrolase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: DOMAIN

DOCATION: (385)...(413)

COTATION: Callulose or protein binding domain

PCT-US04-21492-458
                                                                                                                                                                                                                                                                      409 YS--SYSGIITSFPSTTGSLS-----GDGNKLIGGNKY 439
                                                                                                                                                                                                                         113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT-ANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Obtained from environmental sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: DOMAIN
LOCATION: (470) ... (567)
OTHER INFORMATION: Cellulose binding domain
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 458, Application PC/TUS0421492 GENERAL INFORMATION:
                             SGSALAGVVPQWGGGGNHNGGGNSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGGGGNHN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                   RESULT 12
PCT-US04-21492-458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 458
LENGTH: 568
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RESULT 13

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Sequence 402, Application PC/TUS0421492
| Sequence 402, Application PC/TUS0421492
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Diversa Corporation
| APPLICANT: Callen, Walter
| APPLICANT: Healey, Shaun
| APPLICANT: Healey, Shaun
| TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN TITLE OF INVENTION: THEM
| TITLE OF INVENTION: THEM
| TITLE OF INVENTION: THEM
| FILE REFERENCE: 564462009540
| CURRENT APPLICATION NUMBER: PCT/US04/21492
| CURRENT FILING DATE: 2003-07-02
| NUMBER OF SEQ ID NOS: 518
| SEQ ID NO 402
| SEQ ID NO 402
| LENGTH: 1010
| LENGTH: 1010
| LENGTH: 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GADY-----DQLVTRVVTHEMAHAFRNNATIDQW 106
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-----YQNSLYRANW 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.2%; Score 79; DB 1; Length 1010; Best Local Similarity 20.8%; Pred. No. 96; Matches 32; Conservative 27; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: DOMAIN
COCATION: (39)...(300)
OTHER INFORMATION: Cellulase (glycosyl hydrolase family 5)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: DOMAIN

LOCATION: (610)...(959)

OTHER INFORMATION: Glycosyl hydrolases family 6

FRATURE:
NAME/KEY: DOMAIN

LOCATION: (493)...(521)

OTHER INFORMATION: Cellulose or protein binding domain

PCT-US04-21492-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :||||
368 SSGSTGGGNCAGVNVYPNWTARDWSGGAYNHANAGDQMV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 ---NAKNSD---ITVGQYGGNNAALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417 YTNSVPGSDASWTSLGACGGNGSTTSSSSSSSSS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: DOMAIN
LOCATION: (393)...(428)
OTHER INFORMATION: Carbohydrate binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: August 2, 2004, 15:29:55 Job time: 17.8 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Bacteria
PEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 TITQSGYGN-
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Gencore version 5.1.6

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OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:39:53; Search time 9.4 Seconds

(without alignments)
1545.204 Million cell updates/sec

Title:
US-09-543-407-28

Perfect score:
775
Sequence:
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 200000000

Maximum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database:
PIR 78:*
1: Pirl:*
2: pirl:*
3: pirl:*
4: pirl:*
4: pirl:*
4: pirl:*
4: pirl:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein a	major curlin chain	curlin protein csg			hypothetical glyci	cnjB protein - Tet	fimbrin protein ag	probable PPE prote	leishmanolysin (EC	F3F19.21 protein -	probable PPE prote	curlin nucleator p	minor curlin subun	curlin minor chain	ice nucleation pro	ce nucleatic	PPE pr	cal	dise	rrt	ice nucleation pro	probable PPE prote	conserved hypothet	hypothetical prote	on cc	manoly	able PPE prot	ble PPE p
SUMMARIES	CI	33	33	S70788	8	9	96	13	7	32	22	56	99	78	8	99	9	57	99	9	88	14	18	4	7,4	<b>***</b>	063	A45621	960	7052
	DB	7	8	7	N	7	N	N	N	C)	Н	~	~	N	7	7	7	7	7	7	N	7	7	~	7	N	N	Н	~	7
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ď	Query Match	im	æ.	65.7	ď	ď	m.	ď	ď	ď.	÷.	4	Ϊ,	Ϊ.	ä	Η.	ä	ä	ä	ä	ä	ä	ä	ä	ä	ä	ä	ų.	ä	i.
	Score		ထ	509	87.		0	σ	94.5	94	91.5	91	91	ο,	σ.	89.5	ω,	o,	α 0	89	۲.	87.5	۲.	87	ė.	86.5	è.	98	85.5	ď.
	Result No.		7	٣	4	ιŋ	<b>v</b>	7	۵	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

conserved hypothet hypothetical prote	leishmanolysin (EC probable lipoprote	probable lipoprote	leishmanolysin (EC	leishmanolysin (EC hemolysin A - Serr	probable PPE prote	probable FE proce hypothetical cell	hypothetical prote	related to take zi hrotein E39D8.1b {	hypothetical prote	SINEX			la enteritidis	-Dec-1996 #text_change 08-Oct-1999	, J.L.; Banser, P.A.; Kay, W.W.	eron encoding thin addregative fimbriae.	MID:8550497		12; PIDN:AAC43599.1; PID:g1184714				rust, T.J.; Kay, W		r chin, aggregacive rimbirae from 41D:1677357				bone (NCBIP:45936)			gative fimbriae	nogen, tissue piasminogen a	predicted <sig> #status experimental <mat></mat></sig>	83; DB 2; Length 151;		1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
AF2959 H98323	S19916 C81265	D81411	12666/ B42049	A44951 A28182	D70575	F/06/5	T05221	T51024	T21998	ALIGNMENTS			Salmonel	rision 31	398 2.; Doran	orfBac on	.96146512		ID:911847	)		555-3b	ler, K.H	91	:91310586				MCBI backbone	100		f thin ag	ctin, pla	status pr n agfA #s	Score 6	Pred. N 1; Mism	LAGVVPQWG
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1052	646 928	9 7 8 9	0 0 0 0 0	599 1608	3300	287	343	940	945	-			recurso	anceric	26015; uthier,	-667, 1 - pritid	5039; M		.U43280	1	Ξ,	strain	dy, L.;	3-4781,	and cna 4898; M			in	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	1		omponen	zo ilbr	sequenc rin pro	88.	90 ativ	FAAIVVS
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31 31	32	) (U) (	36	37	6.6	4. 4 O t-	4.2	443	4 4 4 73		=	JC6039	fimbrin	C; Specie C; Date:	C;Access R;Collin	J. Bacte	A; Refere	A; Molecu	A; Residu	A; Access	A;Molecu A;Residu	A; Experi	R;Collin	J. Bacte	A;Title: A:Refere	A; Conten	A; Access	A; Molecu	A;Residu	C;Geneti	A, Gene:	A;Descri	A;Note:	Fil-20/Domain: signal sequence #status predic F;21-151/Product: fimbrin protein agfA #stati	Query	Best L Matche	δy

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A, Description: major component of wild-type curli; interaction between CsgA and CsgB transloce: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20,Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
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A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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W3110
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A;Title: The RpoS sigma factor relieves H-N3-mediated to A;Reference number: S31202; MUID:93211294; PMID:8459772 A;Accession: S31202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 68.2%; Pred. No. 1.1e-36; Matches 103; Conservative 15; Mismatches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Reatidues: 1-133, RQRDSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424;
A;Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 21-42,44-50 <OLS2>
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library,
A,Reference number: S34559
                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-6,'V',8-151 <OLS1>
A,Cross-references: EMBL:L04979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: csgA
A,Map position: 23.15
C,Function:
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                      A; Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S34559
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                                                                                                                                                                                                                                         major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Typin C.Species: Salmonella enterica subsp. enterica serovar Typin A;Note: this species has also been called Salmonella typhin C.Species: Salmonella enterica serovar Typin A;Note: this species has also been called Salmonella typhin C.Species has also been called Salmonella typhin Sate Anov-2002 C;Accession: Alfo55 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Atthores: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Atthores: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; Atthores: Darry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, A; Accession: Al0635
A; Accession: Al0635
A; Accession: Al0635
A; Residues: Drainhaary
A; Molecule type: DNA
A; Residues: 1-151 PRR>
A; Construction: Drainhaary
A; Construction: C; Ganetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 683; DB 2;
Pred. No. 1.4e-51;
1; Mismatches 14
                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 90.1%;
Matches 136; Conservative
                    121
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syalls curing protein - Tetrahymena thermophila C;Species: Tetrahymena thermophila C;Species: Tetrahymena thermophila C;Species: Tetrahymena thermophila C;Species: Tetrahymena thermophila C;Date: 19-Mar-1997 #sequence revision 18-Jul-1997 #text_change 07-Dec-1999 C;Date: 19-Mar-1997 #sequence revision 18-Jul-1997 #text_change 07-Dec-1999 C;Accession: 42136; 842135; 803550 D.W.

R;Taylor; F.M.; Martindale, D.W.
A;Residence: 1-1748 <-TRX>
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A;Genetic code: SGC5
A;Introns: 85/3: 136/1: 157/3: 201/2: 290/2: 327/3: 499/1: 573/2: 607/3: 708/3: 777/3:
C;Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1722
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------CQSNVQES-TTTSSGGWGSSGSG 1684
                                                                                                                                                                                                                                                                                                           SETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAK---NSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                 AIATAGAGAVGILAQSIGGGGGN---GGNATGGDAGFGSFQIGGGGGGGGGANTANVGFK
                                                                                                                                                                   AIVVSGSALAGVVPQ---WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR----K
                                                                                             Gaps
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                                                                                             22;
                       Length 2174;
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                                                                                                 Indels
                                                                                             61;
                   13.8%; Score 107; DB 2; 26.2%; Pred. No. 0.62; ive 21; Mismatches 61
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A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
A;Cross-references: EMBL:X06462
C;Genetics:
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Filt64-1450/Region: zinc finger CCHC motif
Filt78-1454/Region: zinc finger CCHC motif
Filt78-1514/Region: zinc finger CCHC motif
Filt78-1554/Region: zinc finger CCHC motif
Filt78-1558/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
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                                                                                                        Conservative
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Best Local S
Matches 36
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                               Query Match
Best Local S:
Matches 37
                                                                                                                                                                                                                                                        693
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                                                                                                                                                                                                                                                                                                                          hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) maga CiSpecies: Sinorhizobium meliloti (ciSpecies: Sinorhizobium meliloti (ciSpecies: Sinorhizobium meliloti (ciSpecies: Sinorhizobium meliloti (ciSpecies: Sinorhizobium meliloti (ciSpecies: Sinorhizobium meliloti (ciSpecies: Sinorhizobium meliloti (ciSpecies: Sinorhizobium meliloti (ciSpecies: Manan, T.M., Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Accession: Ses, 98, 9889-9894, 2001
A,Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A,Reference number: A98842; MUID:21396508; PMID:11481431
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A; Molecule type: DNA
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A;Coss.references: GB.AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z16
A;Experimental source: strain O157:H7; substrain EDL933
C;Genetics:
A;Gene: csgA
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62.9%; Score 487.5; DB 2;
Best Local Similarity 66.4%; Pred. No. 7.6e-35;
Matches 101; Conservative 16; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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C,Genetics:
A,Gene: SMb21548
A,Genome: plasmid
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--RNNATIDQWNAKNSDITV-

Assatus: significant sequence differences
Ashalecule type: DNA
Ashalecule type: DNA
Ribouvier, J.; Bordier, C.; Vogel, H.; Reichelt, R.; Etges, R.
Mol. Biochem. Parasitol. 37, 235-246, 1989
Astitle: Characterization of the promastigote surface protease of Leishmania as a membra
A;Reference number: A60648; MUID:90114330; PMID:2608099 A; Molecule type: protein A; Residues: 101, E',103-118, SV',121-123 <BOU> A; Residues: 101, E',103-118, SV', 121-123 <BOU> A; Depertmental Source: Strain LEMS13 R; Schlagenhauf, E.; Erges, R.; Metcalf, P. submitted to the Brookhaven Protein Data Bank, March 1997 A; Reference number: A68135; PDB:1LML A; Contents: annotation; X-ray crystallography, 1.86 angstroms, residues 100-407,412-498, C; Complex: homodimer leishmanolysin (EC 3.4.24.36) precursor [validated] - Leishmania major
NyAlcernate names: promastigote surface proteinase; surface endopeptidase glycoprotein of Species: Leishmania major
C;Dete: Leishmania major
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 15-Sep-2000
C;Date: 16-Sep-1992 #soquence_revision 16-Sep-1992 #text_change 15-Sep-2000
R;Button, L.L., McMaster, W.R.
J. Exp. Med. 171, S89, 1990
A;Reference number: PL0221
A;Contents: erratum
A;Contents: erratum
A;Accession: PL0221 70 ITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129 7 --NVGFGNSGSYN-------FGFGNTG-----NNNIGIGLTGSNQIGFGGLN 369 69 11 AIVVSGSALAGVVPQWGGGGNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT Gaps ----GNANIGLGNVGDG--of Leishmania A,Molecule type: DNA A,Residues: 1-602 - ABUT> A,CYGSS-references: GB:Y00647; NID:g9554; PIDN:CAA68673.1; PID:g9555 A,Note: this is a revision to the sequence from reference A27598 21; DB 1; Length 602; 12; Indels Button, L.L.; McMaster, W.R. Exp. Med. 167, 724-729, 1988 JTILLE: Molecular cloning of the major surface antigen Neference number: A27598; MUID:88154764; PMID:3346625 Score 91.5; DB Pred. No. 3; 2; Mismatches 294 AVPTPGNGNVGI ----GNGGNGNFGGGNT----SGSGN----IGFGNSGTGN 384 130 ASDSSVMVRQVGFGNNATAN Local Similarity 41.7%; tes 25; Conservative 11.8%; A; Accession: A27598  $\overset{\lambda}{\circ}$ 셤 ď ò 염 RESULT 9
P70825
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C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C,Accession. F70825
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70825
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: DASCOLS A; Residues: 1-645 <COL>
A; Cross-references: GB.AL021958; GB.AL123456; NID:g3261536; PIDN:CAA17522.1; PID:e125329
C; Genetics:
A; Gene: PPE Cyacession: JC6040

R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
Jacteriol. 179, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A;Reference number: JC6039; MUID:96146512; PMID:8550497
A;Recession: JC6040
A;Molecule type: DNA
A;Residues: 1-151 «COL»
A;Residues: 1-151 «COL»
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A;Residues: 1-1 aggregative fimbriae. 4 -----AIIQKGSGNKANIT--QYGTQKTAVVVQK 140 ITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129 58 ARVRQEGSKLLSVISQ--EGGNNRAKVDQAGNYNFAYİEQTGNAN------DAS 103 10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 69 fimbrin protein agfB precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 C;Accession: UC6040 B;Oclinson, S.K.; Clouthier, S.C.; Dorgan T. Gaps 12.2%; Score 94.5; DB 2; Length 151; 26.9%; Pred. No. 0.34; cive 17; Mismatches 41; Indels 37

Best Local Similarity 26.9 Matches 35; Conservative

Query Match

| :: | | 141 QSHMAIRVTQ 150

104 ISQSAYGNSA----130 ASDSSVMVRQ 139

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Curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
NyAlternate names: csgB protein, curlin nucleation component; minor curlin protein
C;Species: Bscherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: 570787; F64846
R;Hammar, M;Arnqvist, A; Bian, Z; Olsen, A; Normark, S.
R;Hammar, M;Arnqvist, A; Bian, Z; Olsen, A; Normark, S.
A;Title: Expression of two csg operons is required for production of fibronectin- and C
A;Reference number: 570783; MUID:96414468; PMID:8817489
A;Reference number: 570783; MUID:96414468; PMID:8817489
A;Residues 1131 c4AA>
A;Residues indieic acid sequence not shown; translation not shown
A;Residues: 1-13 c4AA>
A;Residues indieic acid sequence was submitted to the EMBL Data Library, August 1995
A;Experimental source: strain K12, substrain W110
A;Cross-reference: strain K12, substrain W110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
A;Esperimental source: strain K12, substrain W110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Residues: nucleic acid sequence not shown; translation not shown
A;Residues: 1-15 c4LAA
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F;1-21/Domain: signal sequence #status predicted <&IG>
F;22-151/Product: minor curlin chain #status predicted <MAT>
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Escherichia coli (strain O157:H7, subs C;Species: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Esch
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A;Experimental source: strain K-12, substrain MG1655
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401
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365 SGTGNIG----FGNSGNNNIGFFNSG-DGNIGFFNSGDGN-
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                                                                                                                                                                                                                                                                                                                                                                132 DSSVMVRQVGFGNNATAN
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Cispecies: Arabidopsis thaliana (mouse-ear cress)

Cispecies: Arabidopsis thaliana (mouse-ear cress)

Cist. 2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001

Cist. 2001 C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Saxao, H.

A; Authors: Anner, J.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, kar; M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reterence number: A86141; MUD:21016719; PMID:11130712

A; Rosidues: 1573 <STO>

A; Cross-references: GB:AE005172; NID:G4850402; PIDN:AAD31072.1; GSPDB:GN00141
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() Species: Mycobacterium tuberculosis

() Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003

() Accession: E70663

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Perthill, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seegers, S.; Reders, S.; Seguares, S.; Ayuthors Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A;Cross-references: GB:Z83860; GB:AL123456; NID:g3261681; PIDN:CAB06165.1; PID:e290763; A;Experimental source: strain H37Rv C;Genetics: A;Genetics: A;Generics: A;Genetics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;
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                  YDQLVTRVVTHEMAHALGFSGPFFEDARIVANVPNVRGKNFDVPVINSSTAVAKAREQYG 313
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A,Status: preliminary, nucleic acid sequence not shown, translation not shown
A,Molecule type: DNA
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Best Local Similarity 22.5%; Pred. No. 3.4;
Matches 31; Conservative 14; Mismatches 47; Indels
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Best Local Similarity 26.9<sup>5</sup>
Matches 36; Conservative
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Curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain O157:H7 C.Species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Esp
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A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90806
A;Accession: C90806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics: A;Gene: ECS1419
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21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
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11.5%; Score 89.5; DB 2; Length 151;
Best Local Similarity 28.1%; Pred. No. 0.92;
Matches 32; Conservative 15; Mismatches 62; Indels
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11.5%; Score 89.5; DB 2; Length 151;
Best Local Similarity 28.1%; Pred. No. 0.92;
Matches 32; Conservative 15; Mismatches 62; Indels
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J. Bacteriol. 173:4773-4781(1991).
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN 12 THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
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SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDIJNS=91310586; PubMed=1677357;
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SEQUENCE S. enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                             SEQUENCE OF 21-151 FROM N.A.
SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE=9401373; PubMed=8104955;
Doran J.L., Collinson S.K., Buffan J., Sarlos G., Todd E.C.D.,
Murco C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.1%; Score 683; DB 1; Length 151; 90.1%; Pred. No. 1.3e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B7DAC0D16B621359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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StyGene; SG10608; csgA.
Fimbria; Signal; Complete proteome.
                                      Bacteriol. 185:2330-2337(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REF.
                                                                                                                                                                                            Bacteriol. 178:662-667(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL627269; CAD08268.1; -. EMBL; AE016840; AAC69399.1; -. EMBL; U43280; AAC43599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ002301; CAA05317.1; -. EMBL; AE008749; AAL20074.1; -.
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151
151
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es 136; Conserv
                                                                                                                                                                         fimbriae."
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BECCETIOI 173:4773-4781(1991).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96414468; PubMed=8817489; Hammark S.; Arnqvist A., Bian Z., Olsen A., Normark S.; Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Bscherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-31.
MEDLINE-91310586; PubMed=1677357;
Collinson S.K., Emody L., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
                                                                                                                                                                                                                                     STRAIN-KI2 / W3110;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A.;
"The RpoS sigma factor relieves H-NS-mediated transcriptional
renression of csg*, the subunit gene of fibronectin-binding curli in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97061202; PubMed=8905232;
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Alba H., Baba T., Fujita K., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Kajihara M., Kanai K., Kashimoto K.,
Ikemoto S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
A. 718-kb DNA sequence of the Escherichia coli K-12 genome
Corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=9426617, PubMed=9278503;
Blatcher F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE=93023873; PubMed=1357528; Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.; Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.; "The C'rl protein activates cryptic genes for curli formation and fibronectin binding in Bscherichia coll HBlOl."; Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
                                01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
CSGA OR B1042
151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-K12 / MC4100;
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE OF 21-40.
                                                                                                                                Escherichia coli
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN
ECOLI
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                    00005±±±55565±±±555055±±±55555±5±555555±5±555555
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SEQUENCE FROM N.A.
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                              61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Major curlin subunit precursor.
Major curlin subunit precursor.
ESGA OR 21676 OR ECS1420.
ESCharichia coli 0157.H7.

Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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0
                                                                                                                                                                                                        65.7%; Score 509; DB 1; Length 151; 68.2%; Pred. No. 8.7e-37;
                                                                                                                                                                                                                          33; Indels
                                                                                                                                                                    21 151 MAJOR CURLIN SUBUNIT.

7 7 A -> E (IN REF. 1).

151 AA; 15049 MW; C003470D208D395F CRC64;
-!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY,
                                                                                                                                                                                                                                                                                                                 121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                            121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                152
                                                                                                             EMBL; D30742; BAA32.

EMBL; D90742; BAA32.

PIR; S70788; S70788; S70788.

EcoGene; EG11489; csgA.

Fimbria; Signal; Complete proteome.

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7 A J S A G034
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                                                                                    EMBL; L04979; AAA23616.1; -.
EMBL; X90754; CAA62282.1; -.
EMBL; AE000205; AAC74126.1; -.
EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
                                                                                                                                                                                                                          103; Conservative
                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                               Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Orgalete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Reg. 8:11-22(2001).

- FRONGTION: CUBLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLIED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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MEDLINE=8817058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Escherichia coli with respect to operon structure and regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.9%; Score 487.5; DB 1; Length 152; 66.4%; Pred. No. 6e-35; 1ive 16; Mismatches 34; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-027-1996 (Rel. 34, Created)
01-027-1996 (Rel. 34, Last sequence update)
01-027-1996 (Rel. 34, Last sequence update)
Minor cúrlin subunit precursor (Fimbrin SEF17 minor subunit)
CSGB OR AGRE OR STM1143.
Salmonella typhimurium, and
Salmoneila enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EE2D2D94DDE91243 CRC64;
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EMBL; AE005315; AAG55788.1; -.
EMBL; AP005254; BAB34643.1; -.
EMBL; AP00606; D30006.
PIR, D900606; D30006.
PIR, H85665; H85665.
Fimbria; Signal; Complete proteome.
SIGNAL
21 152 MAJOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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[3]
SQUENCE FROM N.A.
STRAIN-O157:H7 / RIMD 0509952;
MEDLINE=21155231; PubMed=11259796;
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nes 101; Conserv
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us-09-543-407-28.rsp

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leishmanolysin.";
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                                                                                                                                                                                                                                                                                                                                                                                              finbriae.";
J. Bacteriol. 178:662-667(1996).
-(- FUNDTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI. CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES=S.typhimurium; STRAIN=IT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES-S. enteritidis; STRAIN=27655-3B;
SPECIES-S. enteritidis; Dubmed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
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MINOR CURLIN SUBUNIT.
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PIR, JC6040, JC6040.
StyGene, SG10609; csgB.
Fimbria, Signal, Complete proteome
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  J. Bacteriol. 180:722-731(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ002301; CAA05316.1; -. EMBL; AE008749; AAL20073.1; -.
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                                                                                                                                                                                                                                                       Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.9<sup>3</sup>
Matches 35, Conservative
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ID GP63_LEIMA
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E Structure 6:1035-1046(1998).

C -!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

C -!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

C -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr- |-Leu-Lys-Lys-.

C -!- CORACTOR: Binds 1 zinc ion per subunit.

C -!- PTM: THE PHOSPHATIDYINOSITOR MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINIX C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0, C16:0,
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PRINTS; PRO0782; LSHMANOLYSIN.
PROSITE; PRO0742; ZINC PROTEBASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Tydrolase; Metalloprotease; Glycoprotein; Metal-binding; Lipoprotein.
Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.
SIGNAL
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95406217; PubMed=7675788; Schlagenhauf E., Edges R., Metcalf P.; diffraction studies of "Crystallization and preliminary X-ray diffraction studies of leishmanolysin, the major surface metalloproteinase from Leishmania
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MEDLINE=98416698; PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
                                                                                                                                                                                                                                                                                                                                    Button L.L., McMaster W.R.;
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
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LEISHMANOLYSIN.
REMOVED IN MATURE FORM.
                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDLINE=88154764; PubMed=3346625;
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InterPro, IPR001577, Peptidase M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Button L.L., McMaster W.R.;
J. Exp. Med. 171:589-589(1990).
[3]
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CSGB ECCL1
CSGB ECCL1
AC D39828;
DT 01-FEB1-1995 (Rel. 31, Last sequence update)
DT 01-FEB1-1995 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DS Minor cutlin subunit precursor.
GN CSGB OR B1041 OR Z1675 OR ECS1419.
OS Escherichia coli (157:H7.
OS Escherichia coli (157:H7.
OS Escherichia Forteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI TaxID=562, 83334;
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MEDLINE=S44468; PubMed=8817489;
MEDLINE=S6414468; PubMed=8817489;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Bscherichia coli Kr.12.";
Mol. Microbiol. 18:661-670(1995).
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STRAIN=KIZ / MGJ655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gragor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.8%; Score 91.5; DB 1; Length 602; 41.7%; Pred. No. 1.6; ive 2; Mismatches 12; Indels 2
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Best Local Similarity 41.7
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"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
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MEDLINE=211562319; PubMed=1258796;
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MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
Ikemoro K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
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Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
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Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12-28.0 min region on the linkage map.";
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Nature 409:529-533(2001)
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
STRAIN=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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Fimbria, Signal, Complete proteome.
SIGNAL 1 21 POTENT
CHAIN 22 151 MINOR
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EMBL; AE00315; AAG55787.1; -.
EMBL; AP002254; BAB34842.1; -.
PIR; C90806; C90806.
PIR; S70787; S70787.
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Science 277:1453-1474(1997)
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DNA Res. 8:11-22(2001).
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MINOR CURLIN SUBUNIT.

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                                                                                                                                                                                                                       21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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MEDLINE-90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
Imp. ice nucleation active gene of Erwinia ananas. Sequence similarity to those of Pseudomonas species and regions required for ice
                                                                                                                                                                       38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- FUNCTION: Item nucleation proteins enable bacteria to nucleate orystallization in supercooled water.
-:- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-:- DOMAIN: CONTAINS MANY IMPERPECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FUNTHER ON A 16-RESIDUE AND A RECIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-:- SIMILARITY: Belongs to the bacterial ice nucleation protein
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Enterobacteriaceae; Pantoea.
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                                                         Length 151;
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InterPro; IPR00258; Ice nucleatn.
Pfam; PF00818; Ice nucleation; 69.
PRINTS; PR0037; ICENUCLEATION; 49.
PROSITE; PS00314; ICE NUCLEATION; 49.
Ice nucleation; Repeat; Outer membrane.
DOMAIN
162 1281 OCTAMENTION GOTAMENTION COTAMENTION SEQUENCE 1322 As, 131094 MW; 89B0EE24AA837039 CRC64;
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151 AA; 15882 MW; B18D266B964014B8 CRC64;
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                                                                                                             62;
                                                         DB 1;
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                      11.5%; Score 89.5; DE 28.1%; Pred. No. 0.5;
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FEBS Lett. 258:297-300(1989).
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                                                                                                                      32; Conservative
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Best Local Similarity
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STANDARD;
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                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                             NCBI_TaxID=553;
                                                                                                                                        Pantoea ananas
                                                                                                                                                                                                       SEQUENCE
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VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 Q-----SDARKSETTITQSGYG----NGAD-----YDQLVTRVVTHEMAHAFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLTAGYGSTQTAQEGSRLISGYGSTATSGSDSAVISGYGSTQTAGSESSLTAGYGSTQT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 VSGSALAG-----VVPQWGG---GGNHN-----GGGNSSGPDSTLSIYQYGSANAALAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 IDQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 A----RKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESLT--AGYGSTQTARK 374
                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).

-! FUNCTION: Ice nucleation porterins enable bacteria to nucleate crystallization in supercooled water.

-! SUBCELUIAR LOCATION: Outer membrane (By similarity).

-! OWAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSOS OCTAPERPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PRRIODICITY IS SUGGESTED IN WHICH THE ICH NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

-!- MISCELLANBOUS: A SITUATIONAL PROPERIOR DISPLAYED TO THAT OF ICE.

-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Indels
                                                                                                                                                                                                                                                                                                                                          Zhao J., Orser C.S., "Conserved repetition in the ice_nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                              (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 89.5; DE 26.4%; Pred. No. 7.2; ive 23; Mismatches
                                                                                                                                                                                                                                                                                                               STRAIN=X56S;
MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52970; CAA37140.1; -. HSSP; P06620; 11NA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Conservative
                                                                                                                                     STANDARD;
                                                                                                                                                                                                       Ice nucleation protein.
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1014 SSQTARE 1020
                                        144 NNATANO 150
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                                                                                                                                                                                                                                                                          NCBI_TaxID=343;
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01-NOV-1990
16-OCT-2001
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P18127;
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               967
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TOTGMKGSDLTAG- 243
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-! FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-! SUBCELLUIAR LOCATION: Outer membrane.

-! SUBCELLUIAR LOCATION: IMPERED REPEATS OF A CONSENSUS OCTAPERTIDE A-G-Y-G-S-T-X-T; PURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

-! NESCELLAMBOSED.

-NUCLEATION PROTEIN DISELAYS A SYMMETRY RELATED TO THAT OF ICE.

-! SIMILARITY: Belongs to the bacterial ice nucleation protein
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Michigami Y., Watabe S., Abe K., Obata H., Arai S.;
"Cloning and sequencing of an ice nucleation active gene of Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea
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                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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PIR; JC2143; JC2143.
HSSP; P06620; INA.
InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 51.
PRINTS; PR00327; ICENUCLEATION
PROSITE; PS00334; ICE NUCLEATION; 34.
ICE nucleation; Separat; Outer membrane.
DOMAIN 162 993 OCTAPEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Erwinia uredovora).
ICEN PANAN STANDARD; ID ICEN PANAN STANDARD; ID ICEN PANAN STANDARD; ID ICEN IS, Created) DT 01-NOV-1997 (Rel. 35, Last sequent of the icent of the icent of the icent of the icent of the icent of the icent of the icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent of icent 
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                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS------GPDSTLSIYQYGSANAAL 57
                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        1258 AA; 125084 MW; 590E8A130077FBD4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.3%; Score 87.5; DE
25.2%; Pred. No. 8.2;
tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 -----GEESSQMAGYGS------
                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 65.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; P800314; ICE NUCLEATION; 45.
Ice_nucleation; Repeat; Outer membrane.
                                                                                                         STRAIN=M1;
MEDLINE=90152370; Pubmed=2515997;
  Created)
                                                                                                                                                                                                                                                                                                                                                      EMBL; M26382; AAA24823.1; -.
                                                                    Enterobacteriaceae; Pantoea
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(Rel. 14, I
(Rel. 40, I
                             ce nucleation protein.
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Best Local Similarity
                                                 Erwinia herbicola
                                                                             NCBI_TaxID=549;
 01-APR-1990 (
01-APR-1990 (
16-OCT-2001 (
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28-FEB-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAILE-TY2 / ATCC 700931,
BOTRAILE-172 / ATCC 700931,
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 185:2330-2337 (2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Backer S., Basham D., Brocks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Larsen E.S., Eamonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%; Score 86.5; DB 1; Length 151; 26.2%; Pred. No. 0.89;
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MINOR CURLIN SUBUNIT.
; 161C54326E573495 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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GP63 LEIDO
ID GP63 LEIDO STANDARD; PRT; 590 AA.
AC P23223;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Mismatches
                                                                                                                                                                                                           MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fimbria; Signal; Complete proteome
                                    Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AA069400.1; -.
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Matches 34; Conserv
                                                                                                                                          SEQUENCE FROM N.A.
                                                                        NCBI_TaxID=601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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73
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-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1, and basic residues at P2 and P3'. A model nonapeptide is P1, and basic residues at P2 and P3'. A model nonapeptide is COFACTOR: sinds 1 zinc lon per subunit (By similarity).

-!- SUBCELIULAR LOCATION: Attached to the membrane by a GPI-anchor.

-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                           Leishmania donovani.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5661;
                                                                                                                                                                                                                                                                                                        Webb J.R., Button L.L., McMaster R.W., "Heterogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.", 48:173-184(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REMOVED IN MATURE FORM (BY SIMILARITY) ZINC (CATALYTIC) (BY SIMILARITY).
10.-OCT-2003 (Rel. 42, Last annotation update)
Leibmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface endopeptidase).
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InterPro; IPR006125; Pept M Zn BS.
InterPro; IPR001577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8: 1.
PRINTS; PR001782; ISHMANOLYSIN.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPT-anchor; Lipoprotein.
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ZINC (CATALYTIC) (BY SIMILARITY).

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Pred. No. 4.7;
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                                                                                                                                                                                                                                                       STRAIN=LV9;
MEDLINE=92107220; PubMed=1762629;
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Best Local Similarity
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

STRAIN=MYC/BZ/62/3739;

MEDLINE=33149206; PubMed=8426614;

Medina-Acosta B. R., Rassell D.G.;

Medina-Acosta B. R., Rassell D.G.;

Medina-Acosta B. R., Rassell D.G.;

Structurally distinct genes for the surface protease of Leishmania mexicana are developmentally regulated.";

Mol. Biochem. Parasitol. 57:31-46(1933).

1. FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

1. CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala-Tyr-1-Lu-Lys-Lys-.

2. COFACTOR: Bands 1 zinc ion per submuit (By similarity).

2. DEVELOPMENTAL STAGE: Expressed in both the promastigote and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on the EMBL outstations on the European Bioinformatics Institute. There are no restrictions on the use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      Leishmania mexicana.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCB. TaxID=5665;
GP63_LEIME STANDARD; PRT; 646 AA.

PP3150;
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
10-CCT-2017 (Rel. 42, Last annotation update)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface endopeptidase)
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ACTIVATION PEPTIDE (POTENTIAL).
LIESHMANOLYSIN C1.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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PROSTE; PRO0782; LEMMANOLYSIN.
PROSTE; PS00142; ZINC_PROTEASE; 1.
PROSTE; PS00142; ZINC_PROTEASE; 1.
Zymogen; Signal; Cell adhesion; Multigene family.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amastigote forms. SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, S19916; S19916.
HSSP; P08148; 1LML.
MEROSE; MOS 1001;
InterPro; IPR006025; Pept M.Zn.BS.
InterPro; IPR001607; Pept M.Zn.BS.
InterPro; IPR001677; Peptidase M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X64394; CAA45733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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263 MAHA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLYA_SERMA
ID HLYA_SERMA
AC P15320;
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"Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishmania donovani chagasi

"Three distinct RNAs for the Surface protease gp63 are differentially promastigores to an infectious form.";

"Deal Chem. 267:1888-1895(1992)."

"FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

"CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala Tyr-|-Leu-Lys-Lys-

"COFACTOR: Binds 1 zinc ion per subunit (By similarity).

"SUBSCELLULAR LOCATION: Actached to the membrane by a GP1-anchor.

"STMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                        YDQLVTRVVTHEMAHAFRNNAT------IDQWNAKNSDITV------GQYG 119
                                                                                                                                               256 YDQLVTRVVTHEMAHAVGFSGTFFGAVGIVQEVPHLRRKDFNVSVITSSTVVAKAREQYG 315
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 nolecule implicated in cellular adhesion lacks an Arg-Gly-Asp sequence.";
Mol. Biochem. Parasitol. 39:267-274(1990).
                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last amotation update)
Leishmanolysin precursor (EC 33.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
(GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL).
                                                                                                 21;
                                                                         Score 84.5; DB 1; Length 646; Pred. No. 6.9;
                                                                                                 7; Mismatches 12; Indels
                                          LINKED (GLUNAC. . .) (P)
FE448DDC78C10B0A CRC64;
                                                                                                                                                                                                                                                              599 AA.
 N-LINKED
N-LINKED
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InterPro; IPR001577; Peptidase_M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=92112918; Pubmed=1370484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M80672; AAA29238.1; -. EMBL; M28527; AAA29235.1; -.
                                                                         10.9%;
                                                   69054
                                                                          Query Match
Best Local Similarity 36.55
Matches 23; Conservative
                                                                                                                                                                                                                                                                STANDARD;
   433
445
466
501
              445
466
501
646 AA;
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                                                                                                                                                                          120 GNN 122
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MEROPS; M08.001;
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                        CARBOHYD
CARBOHYD
SEQUENCE
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   CARBOHYD
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GP63_LEICH
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                                                                                                                                                                                                                                                                                                         ACTIONALM PEPTIDE.
LEISHMANOLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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Poole K., Schiebel B., Braun V.;
"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
-e!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      defined.
PUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE BRYTHROCYTE MEMBRANE. SHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Serratia.
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9
PFON457; Peptidase M8; 1.

PROSTE; PRO0782; LSHMANOLYSIN.

PROSTE; PSO0142; ZINC PROTEASE; 1.

PHydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.

SIGNAL 1 39 PROPEP 40 97 ACTIVATION PEPTIDE.
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-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 31-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemolysin precursor.
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ENBL, M22618; AAA56323.1; -.

PIR; A28182; A28182; A28183 act.

PHemplysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                      88 VVTHEMAHAFRNNAT----IDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SPZ | SKARAKLDATGVINDIGGIGAPNVGLDIGAQGGSS----EKRSSSSQAVVSSVQA 947
                                                                                                                                                                                                                                                                                                                                                                29 GGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYD-QLVTR 87
                                                                                                                                                                                                                                                                                                                            53; Indels 20; Gaps
                                                                                                                                                                                                                                                                                    Query Match 10.8%; Score 84; DB 1; Length 1608; Best Local Similarity 27.0%; Pred. No. 22; Matches 33; Conservative 16; Mismatches 53; Indels 2
                                                                                                                                                                                                                                 CHAIN 31 1608 HEMOLYSIN.
SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
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Search completed: August 2, 2004, 14:49:32 Job time : 5.3 secs

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077855 prochloroco
025275 leishmania
078241 citrobacter
09saf2 arabidopsis
07tyr8 mycobacteri
09683 shewanella
0884145 campylobact
078238 enterobacte
                                                                       Q86wd6 mycoplasma
Q814r8 oryza sativ
Q8cmj0 shewanella
Q8cw64 escherichia
Q7ULC5 mycoblasma
Q7ULC5 mycobacteri
O53818 mycobacteri
Q8mny9 leishmania
Q88my9 leishmania
Q88my9 leishmania
Q83397 cyprinus ca
Q43994 leishmania
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089ji6 bradynhizob
083ru7 shigella fl
08pf38 xanthomonas
08pf72 xanthomonas
P95248 mycobacteri
033801 salmonella
Q89ji5 bradyrhizob
Q94821 tetrahymena
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98053981; PubWed=9293832; Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D., Normark S.J., Rhen M.; "Expression of thin, aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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88.7%; Pred. No. 1.1e-47;
ive 2; Mismatches 15; Indels
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Infect. Immun. 65:5320-5325(1997).
EMBL, AJO00514; CAA04151.1; -.
NON TER 152 AA; 15401 MW, 9DA7DADC2364B006 CRC64;
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Last annotation update)
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Cyzz40 citrobacter
C9x240 citrobacter
C9cx237 enterobacte
C54069 salmonella
C98914 bradythizob
C8914 ralstonia s
C8xsd6 ralstonia s
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C8ctb3 shewanella
C9cuu8 rhizobium m
C8etb3 shewanella
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C8etb4 shewanella
C9cuu8 rhizobium m
C8etb4 shewanella
C8etb3 shewanella
C9cuu8 rhizobium m
C8etb4 shewanella
C8ctb5 synechococc
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB
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Result 8

Q7X243;

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RESULT 2 Q7X243

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61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                        59 SDARKSDVTITQHGRGNGAVVGQGADDSTISLKQTGFQNSATIDQWNAKNADISVTQFGG
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STRAIN=06:HI / CFT073 / ATCC 700928;
STRAIN=06:HI / CFT073 / ATCC 700928;
WEDLINE=22388234; PubMed=12471157;
Welch R.A. Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhew G.F., T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacter sakazakii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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66.4%; Pred. No. 3.4e-32;
ive 15; Mismatches 35; Indels
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NCBI_TaxID=217992,
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SEQUENCE 152 AA;
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Matches
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Q7X237
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
Zogation Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriace Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515701; CAD56675.1; -.
SEQUENCE 149 AA; 15260 Ww; 946DD52017F648FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL, AJ515700; CAD56672.1; -.
SEQUENCE 150 AA; 15016 FWW; 1D7141B8D6973DC6 CRC64;
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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76.8%; Pred. No. 6.5e-39;
iive 10; Mismatches 24
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Matches 116; Conservative
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Curlin-csgA F
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15.7%;
89.7%;
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Blis299, protein.
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Best Local Similarity
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      NCBI_TaxID=562;
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Q8Y106;
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01-MAR-2002 (
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
NCBI_TaxID=592;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Cox J.W., Edlezos S., Woolcock J.B.;
Virulence of Salmonella enteritidis in chickens correlates with colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; US3207; AAA98671.1;
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                                                                                                                                 53.1%; Score 411.5; DB 2; Length 150; 57.6%; Pred. No. 3.1e-26; ive 25; Mismatches 38; Indels 1
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Pred. No. 4.7e-17;
1; Mismatches 15; Indels
                                                                                            15112 MW; 5D8BB2D872DF15F3 CRC64;
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78.98;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
SEF17 fimbrin (Fragment).
                                                                                                                                                                                  87; Conservative
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                                                                                            150 AA;
                                                                                                                                                             Best Local Similarity
Matches 87; Conser
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Q54069;
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                        MEDLINE 999314153; PubMed=10386375; La Ragione R.W., Collighan R.J., Woodward M.J.; La Ragione R.W., Collighan R.J., Woodward M.J.; Mood Collighan R.J., Woodward M.J.; Lastination of Escherichia coli 078:K80 isolates associated with IS1 inserti on in csgB and reduced persistence in poultry infection."; FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1; -- 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res: 9:189-197(2002).
EMBL; APO05954; BAC50564.1; -.
Complete proteome.
SEQUENCE 130 AA; 12699 MW; ACFB2D66A48D260F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22484998, PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada I
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Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                        2; Length 29;
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                                                                                                                                                                                                                                E290DFC07ABBB243 CRC64;
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Last annotation update)
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26.5%; Pred. No. 0.085;
ive 28; Mismatches 55;
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Last sequence update)
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Pred. No. 0.0021;
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                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
TRANSPOSON=Insertion sequence IS1;
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Gaps

26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 SGRDNLIDLVQQGTANQGIVFQSGSDNS-AYVTQAGNDN----ISLVTQIGT----- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Deboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Genome sequence of the dissimilatory metal ion-reducing bacterium S. Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFR
                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 3552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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14.2%; Score 110; DB 16; Length 13
Best Local Similarity 28.3%; Pred. No. 0.13;
Matches 30; Conservative 19; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        52; Indels
                                                                                                                                                                                                                                                                                                                      3552 AA; 352934 MW; C5432AABE2CCF59C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA---
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R-2003 (TrEMBLrel. 23, Last sequence update)
R-2003 (TrEMBLrel. 23, Last annotation update)
curlin subunit CsgB, putative.
Nature 415:497-502(2002).

EMBL, AL646079; CAD17691.1; -. EMBL, AL646079; CAD17691.1; -. GO; GO:0004519; F:endonuclease activity; IEA. GO; GO:0003676; F:endonuclease activity; IEA. GO; GO:0003676; F:nucleic acid binding; IEA. InterPro; IPR008619; Fil haemagg.

7 InterPro; IPR008638; Haemagg. act.
                                                                                                                                                                                                                                                                                                                                                                     14.4%; Score 111.5; D
29.3%; Pred. No. 5.3;
:ive 20; Mismatches
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                                                                                                                                                                                                                  pfam; PF05594; Fil_haemagg; 20.
Pfam; PF05860; Haemagg act; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
Plasmid; Complete proteome.
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EMBL; AE015532; AAN53942.1; -.
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MEDLINE=22297686; PubMed=12368813;
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NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 29.3 (es 41; Conservative
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SEQUENCE 139 AA
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Nature 415:497-502(2002).
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MEDLINE-21661879; PubMed=11823852;
Salanoubat M., Genin S., Artiguenev F., Gouzy J., Mangenot S.,
Artiguenet M., Especier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3501;
                                                                                         Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 111.5; DB 16; Length 29.3%; Pred. No. 5.2; indels ive 20; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3501 AA; 348421 MW; 290B41C99018A107 CRC64;
                     01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Probable hemagglutinin-related protein. RSC0887 OR RS06116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable hemagglutinin-related protein.
RSP0540 OR RS06117.
Ralstonia solanacearum (Pseudomonas solanacearum).
Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 415:497-5021200.

EMBL, ALG46061, CAD14589.1; --
EMBL, ALG46061, CAD14589.1; --
GO:0004519; F:endonuclease activity; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR0016619; F:nhaemagg.
InterPro; IPR008619; F:nl haemagg act.
InterPro; IPR008619; F:nl haemagg act.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfan, PF05594; Fil haemagg; 20.
Pfam; PF05860; Haemagg act; 1.
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                    MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2542 DLGGNGYSGTVGVRSASSTL 2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 QYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burkholderiaceae; Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome
SEQUENCE 3501 A
                                                                                                                                                                        NCBI_TaxID=305;
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12

g ò g ò a

Matches

QBXSD6;

RESULT 10 Q8XSD6

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Gaps

RESULT 12 OBEFU3

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66 SETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAK---NSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               750 GLILITOGSHAAG-----IVAQSVGGGGGTGGTASSYSAGIGFTASVAVGGTGGNG 800
MEDLINE=21396508; PubMed=11481431;
Pinan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
A Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Pubhler A., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Pubhler B., Bender B., Esperander B., Esperander B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Bender B., Complete protecome.

Special B., Bender B., Bender B., Complete protecome.
Special B., Bender B., Complete protecome.
Special B., Bender B., Complete Brotecome.
Special B., Bender B., Complete Brotecome.
Special B., Bender B., Complete Brotecome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MR-1;
MEDIINE=2229686, PubMed=12368813;
MEDIINE=2229686, PubMed=12368813;
MEDIINE=2229686, PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Heidelberg J.F., Paulsen I.T., Meson K.D., Daugherty S., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Umayam L.A., Mnite O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Wuller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Genome, sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 106.5; DB 16; Length 502; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 107; DB 16; Length 2174; 26.2%; Pred. No. 6.8; ive 21; Mismatches 61; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 protein; Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBEIH4;
01-MAR-2003 (TYEMBLrel. 23, Created)
01-MAR-2003 (TYEMBLrel. 23, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801 GAGGEVSVSLTDSAIRTGQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein. S00865.
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24.2%;
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EMBL; AE015532; AAN53941.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 26.23
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shewanella oneidensis.
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Best Local Similarity
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SEQUENCE 50
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QBEIH4
                  d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1294 AAFAAFKIDGS-----VVTWGGWGDGNGGDSSAVAEQLISGVKAIYSTVSAFAAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 ARKSETTITQSGYGNGADYDQLVTRVV-----THEMAHAFRNNATIDQMNAKNSDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.
Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Melblyum T.W., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales,
Alteromonadaceae, Shewanella.
NCBI_TaxID=70863;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SMb21548.
R0989 OR SMB21540.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NIBI_TAXID=382;
                  --NNEVOLLQVGAQNKASITQIGNDNLVQLNQLGSGN 122
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                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Complete proteome.
SEQUENCE 1422 AA; 148253 MW: 840PRATO
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EMBL, AE015630, AAN54924.1; -.
TIGR; SO1872; -.
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01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  Lipoprotein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                          Shewanella oneidensis.
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SEQUENCE FROM N.A.
STRAIN=1021;
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Query Match Best Local

Matches

à 원 ò 1400

g à g Q920U8

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79 ADYD------QLVTRVVTHEMAHAFRNNATIDQW-------NAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYG- 119
                                                                                                               29 GGNHNGGGNSSGPDSTLSIYQYGSANAA-----LALQSDARKSETTITQSGYGNG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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      Gaps
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MEDLINE=22484998; PubMed=12597275;
Raneko T., Nakamura Y., Saro S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Indels 37; Gaps
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BNA Res. 9:189-197(2002).
BNBL; AP005954; BAC50565.1; -.
Complete proteome.
SEQUENCE 171 AA; 17448 MW; 995DB08C01498381 CRC64;
      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.8%; Score 99.5; DB 16; Length 171; Best Local Similarity 24.7%; Pred. No. 1.2; Matches 39; Conservative 26; Mismatches 56; Indels 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CsgA protein.
CsGA protein.
CsGA OR BLL5300.
Bradyrhizobium japonicum.
Bradyrhizobium japonicum.
Bradyrhizobiacee; Bradyrhizobium.
Bradyrhizobiacee; Bradyrhizobium.
      59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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## ALIGNMENTS

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use. of thin aggregative fimbriae (SE17/TAF) nucleation depended assembly system of strains of Salmonella. Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene are combinant gene back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the back into the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromesome of the chromosome of the chromosome of the chromosome of t Salmoneila; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen. AgfA::PT3#10 amino acid sequence SEQ ID NO:30. Kay WW; Disclosure; Page 139; 139pp; English. Collison SK, AAB36355 standard; protein; 151 AA. 05-APR-2000; 2000WO-CA000356. 99US-0127888P (first entry) Salmonella enteritidis. Escherichia coli. (UYVI-) UNIV VICTORIA. Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64631. WO200060102-A2 05-APR-1999; 26-FEB-2001 12-OCT-2000. White AP, Synthetic. AAB36355; RESULT 1 AAB36355 

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compy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein contraining a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and incompantation of the present invention
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N-PSDB; AAC64628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TAF) nucleation depended a seembly system of strains of Salmonella, Escherichia coli and addeding Entering recombinant of a recombinant gene into the chromosome of the homologue fimbria subunits, respectively; (2) directing recombinant on a recombinant gene into the chromosome of the homologus species; (3) directing recombinant on of a recombinant gene comprising separating a namino acid polymer comprising a recombinant gene comprising separating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or containing a naminal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sequence is given in munogens, which may be important for directing an immune response in an animal response in an animal response in an animal in conjunctine relevant to an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Pred. No. 6.8e-60;
0; Mismatches 0
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89.9%;
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(first entry)
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cc thin aggregative finbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella Escherichia coli and cc Enterobacteriacae for the production of finbriae comprising recombinant companies. The production of separating recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a comprising separating a namino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E coli or an introducing the carrier of introducing the correspondence or segments of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant protein possesses both the correspondencity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial submit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial submit proteins are usually strong immunogenicity which may be important for directing an immune response consequence is given in the exemplification of the present invention present sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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Pred. No. 4.7e-58;
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2; Mismatches
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90.7%;
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hes 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1994;
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29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTIITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                     Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                 immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfa gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                The Salmonella AgfA protein and DNA are used in vaccine and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            omal gene replacement; fimbrin; epitope; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 681; DB 2; I
Pred. No. 4.7e-58;
2; Mismatches 12;
                   Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNOTASDSSVMVRQVGFGNNATANQY
                Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36341 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                    7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a; agfA; chromosomal immune response; immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.7%;
90.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis.
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                                                                           WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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                                                                                                                                                                                                                                                                    Disclosure, Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                   Кау мм,
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09 9

Gaps

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AAB36351 standard; protein; 151
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milarity 81.9%;
Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITIQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA seguence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                               The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                              Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 676; DB 2;
Pred. No. 1.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response; immunogen.
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                                                                                                                                               2; Fig 7; 85pp; English
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90.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-672631/65.
                    WPI; 1997-309886/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 136; Conserv
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                                          N-PSDB; AAT74142
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36347;
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                                                                                                                                               Example
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and aggregative fimbriae (SEPI)/TAF) nucleation depended sesembly system of strains of Salmonella, Escherichia coli and addition of a recombinant coli and addition of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene comprising species, replacing the native back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign animal, conjunction of a selection which is useful for sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (T) is useful for the expression of recombinant host cell and introducing the cliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein ser usually strong immunogens, which may be important for directing an immune response in an animal conjunction are usually strong aminunogens, which may be important for directing an immune response in in animal in conjunction in the exemplification of the present invention in manner is given in the exemplification of the present invention response is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SVMVRQVGFGNNATANOY
protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 659; DB 3;
Pred. No. 6.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#6 amino acid sequence SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                            Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbried (SETHY)TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and strenchardereriaceae for the production of fimbriae comprising recombinant of directing recombination of a recombination of a recombinant gene (Enchoracions species, (3)) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or copy where into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant for an efficient live vaccine, the carrier fibbrial subunit protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the enrier fimbrial subunit for directing an immune response in an animal. The administrated are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be importent for directing an immunogens, and properties relevant for an efficient live immunofens, the inserted epitope, and properties relevant seasy and in the properties of an efficient live inserted epitope, and properties relevant seasy and intention in the properties are presented in seasy and intention in the properties are presented in seasy and intention in the properties are presented in seasons.
                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                 Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 137; 139pp; English.
                                                                                                                    Collison SK,
99US-0127888P
                                                        (UYVI-) UNIV VICTORIA
                                                                                                                    Doran JL,
                                                                                                                                                                             WPI: 2000-672631/65,
                                                                                                                                                                                                            N-PSDB; AAC64627.
05-APR-1999;
                                                                                                                       White AP,
   %X4X4X4X4X444444444444X
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Sequence 151 AA;

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SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
                                                                                                                                                                                                       61 SDARKSETTITQSGYGNGADVGQGADN-------YDQLVTRVVTHEMAHADQ 105
                                                                                  1. MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                           Gaps
                                           30;
85.5%; Score 657; DB 3; Length 151;
81.9%; Pred. No. 1e-55;
ive 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                  ------GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                        AAB36354 standard; protein; 151 AA
                                           Matches 136; Conservative
                       Local Similarity
                                                                                                                                                                    61
                                                                                                                                                                                                                                                  119
    Query Match
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99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151

RESULT

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Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen. AgfA::PT3#9 amino acid sequence SEQ ID NO:28, 

(first entry)

26-FEB-2001

AAB36354;

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP1/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and considerate and sequences for the production of fimbriae comprising recombinant of a recombination of a recombinant gene into the chromosome of the compositions of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a namino acid polymer comprising a replacement segment or segments of foreign amino comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or cuseful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein minemer response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response consequence is given in exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------YDQLVTRVVTHEMAHAFR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 613, DB 3; Length 151;
Pred. No. 1.9e-51;
0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                    Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SDARKSETTITQSGYGNGAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                      Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.8%;
                                                                                                                                                                                           05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 129; Conservative
                    Salmonella enteritidis.
                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                      White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAC64630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                        WO200060102-A2.
                                                                                                                                                                                                                                    05-APR-1999;
                                                                                                                                                  12-OCT-2000.
                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
염
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SDARKSETTITOSGYGNGADVGOGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120

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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 603; DB 3;
Pred. No. 1.7e-50;
6; Mismatches 23;
                                                        AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                    Kay WW;
                                                                                                                                                                                                                                                                                            Disclosure; Page 135; 139pp; English.
                                                                                   vaccine; immune response; immunogen.
       AAB36346 standard; protein; 151 AA.
                                                                                                                                                                                                                   Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.5%;
                                                                                                                                                                  05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                  99US-0127888P.
                                        (first entry)
                                                                                                 Salmonella enteritidis.
                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                   Doran JL,
                                                                                                                                                                                                                                    2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 122; Conserv
                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                           N-PSDB; AAC64622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                  WO200060102-A2.
                                                                                                                                                                                   05-APR-1999;
                                        26-FEB-2001
                                                                                                                                                  12-OCT-2000
                                                                                                                  Synthetic.
                                                                                                                                                                                                                    White AP,
                        AAB36346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
AAB36346
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEPI7/TAP) mucleation depended assembly system of strains of Salmonella Escherichia coli and CE netwobacteriaceae for the production of fimbriae comprising recombinant CC directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an ammon acid polymer response in an animal, compy of that gene; and (4) eliciting an immune response in an animal, protein containing a replacement segment or segments of foreign amino acid polymer comprising separating an amino acid polymer comprising asparating an amino acid polymer comprising asparating an inconjunction with a carrier of foreign amino acid polymer comprising are passented or sequences grown on a Salmonella, E. coli or Enterobacterizaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbria protein proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Gaps

· 0

23; Indels

Conservative

Matches

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9 9

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coll and assembly system of strains of Salmonella, Escherichia coll and directing recombination of Imbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant of a recombinant gene copy of that gene, and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino comprising separating an amino acid polywer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino cut sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is cusful for the expression of recombinant AgfA protein much expression of recombinant portein or system the heterologous antigens are presented in high numbers (up to coli of munume response in an animal. In a finibrial presentation system the carrier finbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong capinope, which may be important for directing an immune response capinope, and hybrid finbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                    Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                                                                           121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay WW;
                                                  121 NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                    AAB36353 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888P
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           )5-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coll and Bnterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue finbrin submits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coll or
                                                                                                                                                                                                     120
                                                                                                                                                                                                                             61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                     9
                                                                                                                                                                   9
                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene replacement; fimbrin; epitope;
                                                                                                    6
                                                                    Length 151,
                                                                                                  Indels
                                                                                                    24;
                                                                  Score 600; DB 3;
Pred. No. 3.4e-50;
4; Mismatches 24
 of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1mmnnogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                     AAB36349 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0127888P
                                                                  Match 78.1%;
Local Similarity 81.5%;
es 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doran JL,
the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteri
Escherichia coli.
                                   Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         White AP,
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                                                                    Query Match
                                                                                                                                                                                                                                                                    121
                                                                                      Best Loca
Matches
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AAB36349
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to $500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 599; DB 3;
Pred. No. 4.2e-50;
5; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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ilarity 81.5%;
Conservative 5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123;
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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of fimbriae comprising recombinant of directing recombination of a recombinant gene comprising species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising species, (3) directing an immune response in an animal, back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the racriter fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response immunogens the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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Pred. No. 6.6e-50;
5; Mismatches 23;
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Best Local Similarity 81.5%;
Matches 123; Conservative
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment with the encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbries (BER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and directing recombination of fimbries comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal; comprising sperarating an amino acid polymer comprising a replacement segment comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or collymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion preperties relevant for a efficient live in the contraction of the contraction and efficient live formation and efficient live in an efficient live.
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                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Pred. No. 6.7e-47;
5; Mismatches 24
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80.8%;
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Best Local Similarity
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATYDOLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
Plasma protein; immune response; antibacterial; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 512; DB 7;
; Pred. No. 1.2e-41;
17; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                              Herwald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GNGAAVDOTAŚNSSVNVTOVGFGNNATAHOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2, 2004, 14:48:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                 Σ
                                                                                                                                                                                                                                                                                                                                                                 Wikstroem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7%;
                                                                                                                                                                                                       30-JAN-2003; 2003WO-EP000943.
                                                                                                                                                                                                                                                           31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                                                                                             (HANS-) HANSA MEDICAL RES AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104; Conservative
                                                                                                                                                                                                                                                                                                                                                              Olsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            completed: August
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-646136/61.
N-PSDB; ACF36153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
                                                                                                     WO2003064446-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: Au
Job time : 44.9 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 kDa protein
                                                                                                                                                      07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                 Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(I) use of thin aggregative fimbrise (SETI/TAR) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of fimbrise comprising recombinant of Agra, CspA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are amino acid polymer comprising are mino acid polymer comprising an amino acid polymer comprising an amino acid polymer comprising an amino acid polymer comprising an amino acid polymer comprising amino acid colymer coll and inroducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the animal in conjunction with a carrier or diluent. (I) is useful for the animal in an animal. In a finhalfal presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MK1LKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogencity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 517; DB 3;
69.5%; Pred. No. 3.8e-42;
iive 17; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                         English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. coli CsgA subunit 15 kDa protein
                                                                                                                                                         Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR82651 standard; protein; 151 AA
  05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 135; 139pp;
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                                                                                                     (UYVI-) UNIV VICTORIA
                                                                                                                                                         White AP, Doran JL,
                                                                                                                                                                                                             2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                   N-PSDB; AAC64619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR82651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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Length 151; 30; Indels

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5434, Appli 9, Appli 9, Appli 8, Appli 6, Appli 2, Appli 10, Appli

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Sequence 2, Appli
Sequence 10, Appl
Sequence 3827, Ap
Sequence 91, Appl
Sequence 42, Appl
Sequence 10, Appl
Sequence 28148, A
Sequence 28148, A
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                              Sequence 39,
Sequence 3, A
                                                                             Sequence 54
Sequence 7,
Sequence 9,
Sequence 9,
Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59 Application US/08233788A

Sequence 59 Application US/08233788A

Patent No. 5635617

GENERAL INFORMATION:

APPLICANT: Doran, James L.

APPLICANT: Collinson, Karen S.

APPLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION ITTLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61

CORRESPONDENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREE; Saattle

CITY: Seattle

STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

88.0%; Score 676; DB 1; Length 151;
Best Local Similarity 90.1%; Pred. No. 2.7e-61;
Matches 136; Conservative 2; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FOLDPY disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PG-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT! APPLICATION DATA:
APPLICATION NUMBER: US/08/23,788A
FILING DATE: 26-APR-1994
CLASSIFTATION NUMBER: 994
ATTORNEY/AGENT INFORMATION:
NAME: King, JOSHUM
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: 708-3836 SEEDABBERRY
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
FURGURANT OF SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
US-09-252-991A-26658

US-09-595-684B-39

US-08-604-227C-3

US-09-543-681A-5434

US-09-336-447A-9

US-08-336-447A-9

US-08-346-47A-9

US-08-94-818B-8

US-08-9445-472-6

US-08-9445-472-6

US-08-9445-472-6

US-08-95A-12

US-09-540-8887-10

US-09-177-650-91

US-09-495-880A-12

US-09-495-880A-12

US-09-495-891A-322

US-09-489-847-322

US-09-489-847-322

US-09-489-847-322

US-09-403-089A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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ZIP: 98104-7092
     RESULT 1
US-08-233-788A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 7849, Ap
Sequence 7849, Ap
Sequence 2676, Ap
Sequence 2676, Ap
Sequence 2676, Ap
Sequence 22266, Ap
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
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11518, A
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Sequence 4764, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 59, Appl
Seguence 57, Appl
Seguence 3, Appli
                                                                                                                                                                 August 2, 2004, 14:40:48; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                   US-09-543-407-30
768
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-233-788A-59

US-08-824-834-57

US-08-824-835-8

US-09-196-387-8

US-09-196-387-12

US-09-841-835-10

US-09-841-835-10

US-09-841-835-10

US-09-841-835-10

US-09-336-115A-8

US-09-336-115A-8

US-09-336-115A-8

US-09-336-115A-8

US-09-336-115A-8

US-09-336-144-144-1

US-09-356-266-1

US-09-36-3401

US-09-356-366-1

US-09-356-3401

US-09-356-3401

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US-09-368-3601

US-09-368-360
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                                                                                                                                                                                                                                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
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Match Length
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1327
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1327
2736
1216
589
867
867
878
878
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Perfect score:
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78.5
77.5
77.5
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92.59
91.55
91.55
91.56
91.56
91.56
91.56
91.56
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Maximum DB
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                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                SDARKSETTIITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen C.
APPLICANT: Collinson, Karen C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 496; DB 1; Length 120;
Pred. No. 4e-43;
2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: 8300 COLUMDIA CENTER; 701 FILLI AVENUE
CTTY: Seattle
CONTRY: U.S.A.
ZIP: 88104-7092
ZIP: 88104-7092
COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: BM PC COMpatible
COMPUTER: BM PC COMpatible
COMPUTER: BM PC COMPatible
COMPUTER: BM PC COMPatible
COMPUTER: BM PC COMPatible
COMPUTER: BM PC COMPatible
COMPUTER: BM PC COMPatible
COMPUTER: BM PC COMPatible
CURRENT MARE: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: 35,570
REPERBUCE/COCKET NUMBER: 35,570
REPERBUCE/COCKET NUMBER: 35,570
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (206) 622-4900
TELERAX: (206) 622-4900
TELERAX: (206) 622-4900
TELERAX: 1709 682-6031
TELEX: 3723846 SEEDANBERX
SEQUENCE CHARACTERISTICS:
TENDERATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   121 NNPALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-08-864-038A-3
Sequence 3, Application US/08864038A
Patent No. 6001592
GENERAL INFORMATION:
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87.5%;
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amino acid
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Best Local Similarity
Matches 98; Conserv
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TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THERBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 ----AALAAAGAGGGGGGGGGGALAAALAAAG-AGGGGFGGL-----GGLGGLGGG
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Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                    ZIF: 3.14.~..
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
APPROACHING SYSTEM: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.0%; Score 92.5; DB 3;
Best Local Similarity 27.7%; Pred. No. 0.46;
Matches 43; Conservative 12; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (by experiment)
                                                                                                                                                                                                                                                                                                                                                                                 MEDLUM
COMPUTE: IBM Compatible
COMPUTE: IBM Compatible
COMPATE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 8-184459
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/POCKET NUMBER: E-5610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                   Aub...
STREET: 155...
CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
7TP: 514-01
                                                                                                                                                                                                 812-5 Hirano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AALVNQTASDSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TYPE:
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65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VAAFAAI-VVSGSALAGVVPOWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALALQSDAR 64
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US-09-196-387-10

Sequence 10. Application US/09196387

Patent NO. 6277613

PAPPLICANT: de Lange, Titia

APPLICANT: Gmith, Susan

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STREET: New Jersey

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 673;
OFFWARE: PATEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 ADM: ADM: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.4%; Pred. No. 0.51;
Matches 42; Conservative 17; Mismatches 65;
                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-230 CIP1

TELEFONMUNICATION INFORMATION:

TELEFOX: 201-487-5800

TELEFOX: 201-343-1684

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
                                                                                       APPLICATION NUMBER: US/09/841,835 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 VNAK - - DMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: "07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 673 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65; Indels 19; Gaps
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Patent No. 6506587
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 673;
                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.9%; Score 91.5; DB Best Local Similarity 29.4%; Pred. No. 0.51; Matches 42; Conservative 17; Mismatches
            NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSBE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 600-1-230 CIP1
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998.
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-23
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR ESQ. ID NO: 8:
SEQUENCE CHARATIERISTICS:
LENGTH: 673 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-196-387-8
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: USA
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STREET: 411 Hacke
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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600-1-230 CIP1
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                   Conservative
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, MOLECULE TYPE: protein US-09-841-835-10
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STRANDEDNESS: si
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                                                                           Best Local Similarity
Matches 42; Conserv
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MOLECULE TYPE:
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                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                 19;
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Sequence 10, Application US/09841835
Factor to 0. Application US/09841835
Factor to 0. Application US/09841835
Factor to 0. Application US/09841835
FAPLICANT: Saith, Susan
APPLICANT: Saith, Susan
FITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
FITLE OF INVENTION: OF USE THEREOF
FORESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                   ch 11.9%; Score 91.5; DB 3; Length 949; 1 Similarity 29.4%; Pred. No. 0.8; 42; Conservative 17; Mismatches 65; Indels 19
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APPLICATION NUMBER: US/09/841,835
FILING DATE:
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-196-387-10
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STATE: New Jersey
COUNTRY: USA
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                    99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                             6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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11.9%; Score 91.5; DB 3; Length 1327;
Best Local Similarity 29.4%; Pred. No. 1.3;
Matches 42; Conservative 17; Mismatches 65; Indels 19; Gaps
                                                        Gaps
                                                        19;
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Patent No. 6277613

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSED: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
     DB 4; Length 949;
                                                        65; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
11.9%; Score 91.5; DE
29.4%; Pred. No. 0.8;
tive 17; Mismatches
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LENGTH:
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                                                                       158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD-----VSRV--KRLVDAAN 206
99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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US-09-841-835-2
US-09-841-835-2
Sequence 2, Application US/09841835
Fatent No. 6506897
GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
ADDRESSEE: Albuber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: Lange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
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11.9%; Score 91.5; DE
Best Local Similarity 29.4%; Pred. No. 1.3;
Matches 42; Conservative 17; Mismatches
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                                                                                                               121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                  207 VNAK--DMAGRKSSPLHFAAGFG 227
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APPLICATION NUMBER: US/09/841,83
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1327 amino acids
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT GUY, Bruno
TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-19
PRIOR PILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                  APPLICANT Greeg, Morin B.
APPLICANT Walter, Funk D.
APPLICANT Walter, Funk D.
APPLICANT Wile Cayslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Xaa = Any Amino Acid US-09-336-115C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 VNAK--DMAGRKSSPLHFAAGFG 227
                     Sequence 8 Application US/09972115A Patent No. 6599728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-336-115C-6
; Sequence 6; Application US/09336115C
; Patent No.; 6576244
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                : PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.4%;
Matches 42; Conservative 1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Weltzin, Richard A. APPLICANT: Guy, Bruno
                                                                                                APPLICANT Geron Corporation
APPLICANT Gregg, Morin B.
APPLICANT Walter, Funk D.
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1327
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SIGNAL LOCATION: (1)...(20)
                                                                          GENERAL INFORMATION;
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US-09-972-115A-8
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RESULT 15
US-09-540-236-2676
US-09-540-236-2676
Sequence 2675, Application US/09540236
Patent No. 6672910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAF;
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 100-2005-001
TITLE OF INVENTION: 100-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7549, Application US/09489039A
Sequence 7649, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
PAPPLICANT GALY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PELING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7849
LENGTH: 589
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                                                                                                                                                                                                                                          181 VTGNTSLVVNDSGGRIASI---YGGGYGTNATNTANVTGNVSTKVAITNAATGFQLSTYY
                                                                                                                                                                                                                                                                                                                                          238 GGVQYGNIG------GKVTNDISGYGRWYTAGQRFIGGSSRGDIGTNRATDGITT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 --DVGQ--GADNSTIELTQNG----FRNNATYDQLVTRVVTHEMAHAGGN---NAALVNQ
                                                                                                                                                                                                                                                                                            --GADNSTIELTQ
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                                                                                             Query Match 10.8%; Score 83; DB 4; Length 1216; Best Local Similarity 24.4%; Pred. No. 8.2; Matches 49; Conservative 19; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                            -----GFRNNATYDQLVTRVVTHEMAHAG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                            49 ---QYGSANAALALQSDARKSETTITQSGYGNGADVGQ-----
                                                                                                                                                                                              6 VAAFAAIVV -- SGSALAGVVPOWGG -- GGNHNGGGNSSGPDST-
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llarity 24.5%; Pred. No. 4.5;
Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 TASDSSVMVRQVGFGNNATANQY 151
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|-----QIGASNEALYDAY
TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Klebsiella pneumoniae
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Matches 35; Conserv
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US-09-489-039A-7849
                                                    US-09-134-000C-5130
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US-00-252-91A-30227

US-00-252-91A-30227

Sequence 30227, Application US/0925291A

Parent No. 6551795

GENERAL INFORMATION:

APPLICANT MARC J. Rubenfield et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

PRIOR APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30227
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; Sequence 5130, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: DATE DOUCETTON: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT APPLICATION NUMBER: US 60/055,778
FRIOR APPLICATION NUMBER: US 60/055,778
FRIOR APPLICATION NUMBER: US 60/055,778
FRIOR FILING DATE: 1997-08-15
SEQ ID NOS: 6812
; SEQ ID NOS: 6812
; SEQ ID NO 5130
; LENGTH: 1216
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                                                                                                                                                    102 ÁYQÁVFLAINÁAVGL---WNTIGYAVMCGNĠNGTESĞÞGSVIFNDQÞGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                    159 STGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKV---SVNYNYECRQTAD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 GQA------EAGASVGIDTNGDGKPDLİVIADANGNFTAPLNPPLİNGQTVİV 252
                                                                                                                                                                                                   SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
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                                                      Gaps
                                                                                                                                                                                                                                                                                                 98 RNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                     215 INGGVYQFCKAKNGSSSSNGGNGSSTQTTATTQDGVTITTTYNNNKAT 264
                                                    37;
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     DB 4; Length 745;
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10.9%; Score 84; DB 4; Length 2736;
Best Local Similarity 29.7%; Pred. No. 19;
Matches 43; Conservative 17; Mismatches 49; Indels
                                                      Indels
     Query Match 11.3%; Score 86.5; DB 4; I
Best Local Similarity 20.0%; Pred. No. 1.9;
Matches 34; Conservative 27; Mismatches 72;
                                                                                                        -GGGGNHNGGGN
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                                                                                                        AFAAI VVSGSALAGVVPQW-----
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-30227
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US-09-134-000C-5130
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us-09-543-407-30.rai
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Query Match
Best Local Similarity 26.8%; Pred. No. 11;
Matches 49; Conservative 23; Mismatches 65; Indels 46; Gaps 10;
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                                                                                                                                                                                                                                                                                                                               98 R-NNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMV-----RQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                     4 LKVAAFAAIVVSGSALAG--VVPQWGG-----GGNHN------GGG---NSSGPDS 43
                                                                                                                                                                                                              44 TLSIYQYGSANAALALQSDARKSETTITQSGY----GNGADVGQGADNST--IELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: August 2, 2004, 14:58:37 Job time : 13 secs
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2676
; LENGTH: 867
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2676
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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| cgn2_6/ptodata/2/pubpaa/PCT NEW PUB. pep:*
| cgn2_6/ptodata/2/pubpaa/PCT NEW PUB. pep:*
| cgn2_6/ptodata/2/pubpaa/PCT NEW PUB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCG NEW PUB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCGO NEW PUB. pep:*
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| cgn2_6/ptodata/2/pubpaa/NCGO NEW PUB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCGO PUBCOMB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCGO PUBCOMB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCGO PUBCOMB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCGO NEW PUB. pep:*
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| cgn2_6/ptodata/2/pubpaa/NCGO PUBCOMB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCGO PUBCOMB. pep:*
| cgn2_6/ptodata/2/pubpaa/NCGO PUBCOMB. pep:*
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| cgn2_6/ptodata/2/pubpaa/NCGO PUBCOMB. pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 20638, A Sequence 211, Appl Sequence 11, Appl Sequence 196154, A Sequence 64364, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 62548, A Sequence 2, Appli Sequence 2, Appli Description 2 US-09-741-873B-4 2 US-09-741-873B-4 2 US-09-741-873B-2 2 US-09-741-873B-2 3 US-10-369-493-20638 5 US-10-369-493-20638 6 US-00-437-9633-141342 0 US-09-833-141342 0 US-09-833-141342 0 US-09-833-141 0 US-09-833-141 0 US-10-282-122A-64364 2 US-10-282-122A-64364 2 US-10-282-122A-64364 0 US-09-841-835-10 0 US-09-841-835-10 0 US-09-841-835-10 0 US-09-841-835-2 SUMMARIES Query Match Length DB Result No.

Seguence 4, Appli	Sequence 53269, A	Sequence 173860,	Sequence 108981,	Sequence 48048, A	Sequence 147748,	Sequence 2, Appli	Sequence 49757, A	ednence	Sequence 56041, A	equence	Sequence 57763, A	Sequence 146, App	Sequence 67750, A	Seguence 6, Appli	ednence	Sequence 68152, A	ednence	equence	equence	equence	ednence	equence	equence	Sequence 749, App	Sequence 24, Appl		Sequence 16, Appl	ednence	
US-10-199-937-4	282-122A-5326	424-599-17386	437-963-1	282-122A-4804	437-963-14774	311-40	282-122A-	437-963-1	425-114-5	424-599-2	425-114-5	93-306	US-10-425-114-67750	34-666A-6	282-122A-586	425-114-68	437-963-1	282-122A-	412-699B-	374-780A-5	437-963-1	659-869-2	021-811-2	10-238-075-7	9-905-176-24	-282	9-996-194-16	10-164-9	US-10-437-963-115033
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## ALIGNMENTS

US-09-741-14154-4

Sequence 4: Application US/09741873B

Publication No. US20020081722A1

SEGNERAL INFORMATION:
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT FILING DATE: 1998-06-06

PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: US 08/378,876

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-05

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.0 ö Gaps ó Length 151; Indels Query Match 66.9%; Score 514; DB 12; Best Local Similarity 68.9%; Pred. No. 1.4e-43; Matches 104; Conservative 18; Mismatches 29; ORGANISM: Escherichia coli RESULT 1 US-09-741-873B-4 US-09-741-873B-4 SEQ ID NO 4

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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US-09-741-873B-2
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GENERALL INFORMATION:

APPLICANT: Olsen, Arne

1 TITE OF INVENTON: Fibronectin Binding Protein As Well As Its Preparation

FITE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT FILING DATE: 1998-06-06

FRIOR APPLICATION NUMBER: US 08/978,878

FRIOR APPLICATION NUMBER: US 08/978,878

FRIOR APPLICATION NUMBER: US 07/397,1189

FRIOR FILING DATE: 1999-05-04

FRIOR FILING DATE: 1991-11-06

FRIOR PELICATION NUMBER: US 07/789,437

FRIOR APPLICATION NUMBER: US 07/789,437

FRIOR APPLICATION NUMBER: US 07/99,865

FRIOR APPLICATION NUMBER: US 08/187,865

FRIOR APPLICATION NUMBER: US 08/187,865

FRIOR APPLICATION NUMBER: US 08/187,865

FRIOR APPLICATION NUMBER: US 08/187,865

FRIOR PELING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SCOFTWARE: PARCENTIN VARIETY US 08/318,519
                                                                                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
1 MKLIKVAAIAAIVFSGSAVAGVVPQYGGGGNHGGGGNNSGFNSELNIYQYGGGGNSALALQ 60
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APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION UMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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66.9%; Score 514; DB 12; Length 15
Best Local Similarity 68.9%; Pred. No. 1.4e-43;
Matches 104; Conservative 18; Mismatches 29; Indels
                                                                                                                                                                    121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                     121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09741873B Publication No. US20040096965A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09741873B Publication No. US20020081722A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CRGANISM: Escherichia coli US-09-741-873B-4
                                                                                                                                                                                                                                                                                                                 -09-741-873B-4
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JUDICARIATION NO. USZUGUGUSESENSY

JUDICARIATION NO. USZUGUGUSESENSY

APPLICANT: NORMATION:
APPLICANT: NORMATION:
APPLICANT: NORMATION:
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT FAPLICATION NUMBER: US/09/741,878
PRIOR PELING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-03
PRIOR PILING DATE: 1991-11-03
PRIOR PILING DATE: 1991-11-03
PRIOR PELING DATE: 1994-00-05
PRIOR PELING DATE: 1994-00-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VGQGSDDSSIDLIQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1981-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1994-11-03
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 2
LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09741873B Publication No. US20040096965A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Escherichia coli
US-09-741-873B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86; Conservative
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ORGANISM: Escherichia coli
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Best Local Similarity
Matches 86; Conserv
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DB 12; Length 131;

56.8%; Score 436;

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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 141342
LENGTH: 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 GNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG-----GNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 GNAGDVNTGLGNSG-NINTGGF-NPGTLNTGFFSAMTQAGPNSGFFNAGTGNSGFGHNDP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                               400 EPAGTLP-----QMSATALLQXAAQMGATTSSYNAGGAGGASSLLRGASSHGISVGEGPA 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 GPDSTLSIYQYGSANAALALQSDARKSETTITQS--GYGNGADVGQGADNSTIELTQNGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NERSSYONL----IMGSMA-SGGGGAGFAGSFSGAS-----GFG 488
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                                                                                                                                                                                                                                                           ; CTHER INFORMATION: Clone ID: PAT_MRT4530_42455C.1.pep
US-10-437-963-141342
                                                                                                                                                                                                                                                                                                                                 12.3%; Score 94.5; DB 16; 27.1%; Pred. No. 0.71;
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Pred. No. 0.47;
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CTHER INFORMATION: PPE
NAME/KEY: misc feature
CTHER INFORMATION: gi|1781260
US-09-820-843A-21
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l.Similarity 25.0%;
35; Conservative 16
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Best Local Similarity 27.1%
Matches 45; Conservative
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                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20638, Application US/10369493
; Sequence 20638, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Gladman, Barry S.
APPLICANT: Glodman, Barry S.
; APPLICANT: Glodman, Barry S.
; APPLICANT: Glodman, PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE OF INVENTION: DAMPS: US/10/369, 493
; CURRENT APPLICATION NUMBER: US/10/369, 493
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 GNSNSV-----GRDIQGKQSGAGNSAAIPQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                                                    81 VGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                          19 AAFAADSNIVYINQIGNDQQANIIQSGNGNSVGAFNGNSGFLQENGILSGA-NLLIVKQS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY 50
                                                                                                           21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 13.4%; Score 103; DB 15; Length 445; l Similarity 26.3%; Pred. No. 0.079; 44; Conservative 27; Mismatches 62; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPGVFNKITQD-SSSNGSKVSVI-QDGKNNVFSIKQGNTGNSTSVNQ 174
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                      Best Local Similarity 65.6%; Pred. No. 7.7e-36;
Matches 86; Conservative 17; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
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publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Wu, Nei
APPLICANT: Wu, Nei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                           GFGNNATANOY 151
                                                                                                                                                                                                                                                                                        GFGNNATAHQY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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Matches
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Sequence 49960, Application US/10425114

Sequence 49960, Application No. US2004034888A1

Sequence 49960, Application No. US2004034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: APPLICANT: And Uses Thereof for Plant Improvement

FILE REPRENCE: 38-21 (53131) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 NAALALQSDARKSETTITQSGYGNGADVGQGADN-----STIELTQNGFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YGNGA--DVGQGADNSTIEL--TQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
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PRIOR APPLICATION NUMBER: 60/253,025

PRIOR PILING DATE: 2000-11-27

PRIOR PELICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-25

PRIOR FILING DATE: 2000-12-26

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

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PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           840 AAITVGGPTTSIGITASAGIGSITIPIIDIPATSGFGN----STTSPSSGFFNSGAGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 YDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVM---VRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                949 RDGMGTMTLNLGLANLGSNNAGFGNTGIFDVGVANLGNYNIGFGN 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%; Score 93.5; DB 12; 26.1%; Pred. No. 5.1; tive 18; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Clone ID: 700071884_FLI.pep
US-10-425-114-49960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis US-10-282-122A-64364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 26.1%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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ORGANISM: Zea mays
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US-10-425-114-49960
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Best Local S:
Matches 33
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                                                                Sequence 196154, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About Withua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 498
LENGTH: 498
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
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PRIOR FILING DATE: 2000-09-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 GSSNSDNNASOSDTSSEQNNKEGSSNSDNS--NDANONGSNSNENANDNGNASHEAONNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GNHNGGGNSSGPD-STLSIYQYGSANAALALQSDARKSETTIIQSGYGNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.2%; Score 94; DB 12; Length 498; 28.1%; Pred. No. 0.72; ive 24; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_19152C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 64364, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.1%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carr, Grant
Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                                              US-10-424-599-196154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-196154
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US-10-282-122A-64364
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANI: AU, H.

TITLE OF INVERTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR PILING DATE: 2001-02-09
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PRIOR PILING DATE: 2001-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 1721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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29.5%; Pred. No. 4.8;
Live 18; Mismatches
                                                                                                                                                          Sequence 62848, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1030 -NEGLANHGNEN 1040
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Best Local Similarity 29.5<sup>3</sup>
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 ROVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wall, Daniel
SGA 190
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RESULT 12 US-09-841-835-8 ; Sequence 8, Application US/09841835

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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 KSETIII----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THAT BINDS TO TRF1 AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: General Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                         ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26,742
R: 600-1-230 CIP1
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Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNOTASDSSVMVROVGFG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.4%;
                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-09-841-835-8
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                               CITY: Hackens.
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hackensack
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US-09-841-835-10
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Indels
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APPLICANT: Gregg, Morin B.
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Wideryslaw, Platyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REPERBURCE: 080/003C
CURRENT FILING DATE: 2001-10-05
PRIOR PILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%; Score 91.5; DB
29.4%; Pred. No. 4.3;
Live 17; Mismatches
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                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09972115A Publication No. US20030032769A1 GENERAL INFORMATION:
                                                          FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECHMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                              TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 29.4
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
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CRGANISM: Homo sapiens
US-09-972-115A-8
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.9%; Score 91.5; DB 9; Length 949;
Best Local Similarity 29.4%; Pred. No. 2.9;
Matches 42; Conservative 17; Mismatches 65; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835 FILING DATE:
                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEFHOR: 201-343-1684
TELEFA: 133521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 VNAK--DMAGRKSSPLHFAAGFG 227
                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                 COMPUTER READABLE FORM:
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                    07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-841-835-10
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US-09-841-835-2
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Db 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD-----VSRV--KRLVDAAN 206
Qy 121 NNAALVNQTASDSSVMVRQVGFG 143
Db 207 VNAK--DWAGRKSSPLHFAAGFG 227
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Search completed: August 2, 2004, 15:36:14 Job time : 37.8 secs

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protein search, using sw model

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sequence 18, Appl
Sequence 20, Appl
Sequence 1, Appl
Sequence 4, Appli
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Sequence 2, Appli
Sequence 25, Appli
Sequence 55, Appli
Sequence 5834, Ap
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Sequence 34, Appli
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Sequence 8854, Appli
Sequence 8854, Appli
Sequence 202355, Appli
                               Sequence 5, Ap
Sequence 57, Ap
Sequence 14, A
Sequence 22, A
Sequence 28, A
  Sequence 30,
Sequence 24,
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APPLICANT White, Aaron P.
APPLICANT Doran, James L.
APPLICANT Collinson, S. Kazen
APPLICANT Xay, William K.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
SOPTWARE: PSECIET WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Sequence
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Sequence
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
9 US-09-543-407-30

10 US-09-543-407-24

10 US-09-5543-407-25

10 US-09-543-407-12

10 US-09-543-407-12

10 US-09-543-407-22

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US-09-543-40,-30
Sequence 30, Application US/09543407
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 30
LENGTH: 151
TYBE: PRT
ORGANISM: Artificial Sequence
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3331
3330
3331
3330
3331
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3331
     103
101.5
99.5
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217.5
1114.5
114.5
114.5
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                                                                                                                              August 2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                6019581
                     5.1.6
Compugen Ltd.
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hits satisfying chosen parameters: 6019581 segs, 976053577 residues

Total number of

Searched:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

US-09-543-407-30 768

Perfect score:

Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

score greater than or equal to and is derived by analysis of

Pred. No.

£

Query Match Length DB

Score

Result š.

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TELEPANONE: (206) 622-4900
TELERAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 amino acids
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APPLICATION NUMBER: US,
FILING DATE: 26-APR-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-233-642A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                              61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-543-407-5
Sequence 5, Application US/09543407
Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Ray, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES;
FILE REPERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                          100.0%; Score 768; DB 19; Length 151; 100.0%; Pred. No. 7e-73; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 HEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-24
; Sequence 24, Application US/09543407
; GENERAL INFORMATION:
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                                          Query Match
Best Local Similarity 100.
Matches 151; Conservative
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Best Local Similarity
US-09-543-407-30
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APPLICANT: Calinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                              Query Match

88.7%; Score 681; DB 19; Length 151;
Best Local Similarity 90.7%; Pred. No. 1.2e-63;
Matches 137; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATIS: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

88.0%; Score 676; DB 6;
Best Local Similarity 90.1%; Pred. No. 4.2e-63;
Bact Local Similarity 20: Mismatches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
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26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 57, Application US/08233642A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
                                                                                                                               ; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-5
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYBQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                               61 SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Mitte, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SOUGHOUS

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SEQ ID NO 22

LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-543-407-14

SQUEAL INFORMATION:
SEQUEAL INFORMATION:
SEPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Ky, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE DETAING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

85.8%; Score 659; DB 19; Length 151;
Best Local Similarity 81.9%; Pred. No. 2.7e-61;
Matches 136; Conservative 0; Mismatches 0; Indels 30
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                                                                                                                                                                                                                                                                                                                    121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                        121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADN------YDQLVTRVVTHEMAHADQ 105
                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                    0; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 44; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
                                                      OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA porter information: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-22
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                                                                                                                                                                                                     85.5%; Score 657; DB 19; Length 151;
81.9%; Pred. No. 4.3e-61;
tive 0; Mismatches 0; Indels 3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.8%; Score 613; DB 19; Length 151; 74.6%; Pred. No. 2e-56; ative 0; Mismatches 0; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 WNAKWSDITVGOYGGNNAALVNOTASDSSVMVROVGFGNNATANOY 151
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CURRENT APPLICATION NUMBER: U5/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRACESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 28, Application US/09543407; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                        Query Match
Best Local Similarity 81.94
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 129; Conservative
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Best Local.Similarity
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LENGTH: 151
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DB 19; Length 151;

77.7%; Score 597;

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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US-09-543-407-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTERQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.5%; Score 603; DB 19; Length 151; 80.8%; Pred. No. 2.4e-55; tive 6; Mismatches 23; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
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78.1%; Score 600; DB 19;
Best Local Similarity 81.5%; Pred. No. 4.9e-55;
Matches 123; Conservative 4; Mismatches 24;
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.8
Matches 122; Conservative
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US-09-543-407-26
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US-09-543-407-26
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LENGTH: 151
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SEQ ID NO 26
LENGTH: 151
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

CURRENT PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARES FRESENCE: 2000-04-05

SOFTWARES FRESENCE: Mindows Version 4.0

LENGTH: 151
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                                                                                                                                                                                                                                                  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.40
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA, OTHER INFORMATION: sequence containing the replacement fragment, OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 78.0%; Score 599; DB 19; 1
Best Local Similarity 81.5%; Pred. No. 6.3e-55;
Matches 123; Conservative 5; Mismatches 23;
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                       ; Sequence 18, Application US/09543407; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: NORMARK, Staffan
TITLE OB. INVANTION: FIRSONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
TITLE OF INVANTION FIRSONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT PAPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT Doran, James L.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BACTERIAL FINERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 220043.406
CURRENT APPLICATION NUMBER: US/09/543.407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRESEQ for Mindows Version 4.0
                                         sequence containing the replacement fragmer encoding PT3 from GP63 of Leishmania major.
                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                           Query Match 73.7%; Score 566; DB 19; Length 19
Best Local Similarity 80.8%; Pred. No. 2e-51;
Matches 122; Conservative 5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
67.3%; Score 517; DB 19;
Best Local Similarity 69.5%; Pred. No. 3.2e-46;
Matches 105; Conservative 17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GNGAAVDOTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 Application US/09543407; GENERAL INFORMATION: APPLICANT White, Aaron P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Escherichia coli
US-09-543-407-7
                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                      US-09-543-407-16
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US-09-543-407-7
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US-08-978-878-4
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                                                                                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                           9
                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                    Gaps
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERTAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESURATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043:406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASLEGO for Windows Version 4.0
LENGTH: 151
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                    Indels
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81.5%; Pred. No. 1e-54;
tive 5; Mismatches 23;
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Pred. No. 1.8e-54;
2; Mismatches 12;
                                                                                                                                                                                                                                        121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-16
Sequence 16, Application US/09543407
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.3%;
Matches 117; Conservative 2
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ORGANISM: Artificial Sequence
Best Local Similarity 81.5
Matches 123; Conservative
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US-09-543-407-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.9%; Score 514; DB 13; Length 151;
Best Local Similarity 68.9%; Pred. No. 6.7e-46;
Matches 104; Conservative 18; Mismatches 29; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-06
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER PELING DATE: 1994-01-08
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER PELING DATE: 1994-01-05
EARLIER PELING DATE: 1995-06-28
EARLIER FILING DATE: 1995-06-28
NUMBER: OF SEQ ID NOS: 10
SOFTWARE: PATENTIN NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
NUMBER: OF SEQ ID NOS: 10
SEQ ID NO 4
LENGTH: 151
TYPE: PRT
TYPE: PRT
CREANISM: Escherichia coli
US-08-978-878-4
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Search completed: August 2, 2004, 15:26:47 Job time : 168.9 secs

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Sequence 4, Application US/09741873C

GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olean, Arne
FILE REFERENCE: 012889-084
CURRENT FAILNG DATE: 2000-12-22
PRIOR PAPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1998-05-06
PRIOR PLINGATION NUMBER: US 08/978,878
PRIOR PELING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-26
PRIOR PELING DATE: 1997-11-06
PRIOR PLING DATE: 1997-11-06
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PRIOR PELING DATE: 1997-11-06
PRIOR PELING DATE: 1997-11
Sequence 9194, Ap Sequence 27, Appli Sequence 27, Appli Sequence 9810, Ap Sequence 343835, Sequence 11, Appl Sequence 285216, Sequence 385214, Sequence 34256, Sequence 511, App Sequence 511, App Sequence 9806, Ap
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Sequence 9807, Ap
Sequence 2, Appli
Sequence 351875,
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US-60-579-062-9194

US-10-491-733-2

US-09-248-733-2

US-06-581-351-9810

US-10-10-688-7608

US-10-10-688-7608

US-10-778-804-11

US-10-425-115-285216

US-10-425-115-285216

US-10-425-115-382216

US-10-425-115-38226

US-10-425-115-38226

US-10-854-439-511

US-10-854-351-190187

US-10-861-351-9807

US-60-581-351-9807

US-10-861-351-9807

US-10-861-115-826

US-10-861-115-10187

US-10-861-115-10187

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US-10-861-115-10187
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; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-741-873C-4
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Best Local Similarity 68.99
Matches 104; Conservative
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24.6%; Pred. No. 0.68;
tive 25; Mismatches
                                                                                                                                                                                                                                                                             457 --VISNIFSGVSSSAGSY 472
                                                                                                                                                                                                                                                 134 SVMVRQVGFGNNATANQY 151
                            34; Conservative
Best Local Similarity
Matches 34; Conserv
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US-10-425-115-300390
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                              Sequence 2, Application US/09741873C

Sequence 2, Application US/09741873C

GENERAL INPORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE CF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTION SIDERS 102889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-04
PRIOR PRILING DATE: 1999-11-26
PRIOR PRILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1994-01-28
PRIOR PRILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
SPRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
LENGTH: 131
LENGTH: 131
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Sequence 21, Application US/10479638

Sequence 21, Application US/10479638

GENERAL INFORMATION:

APPLICANT: Randolph V. Lewis

APPLICANT: Randolph V. Lewis

APPLICANT: Randolph V. Lewis

TILLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants

TILLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants

CURRENT APPLICATION NUMBER: US/10/479,638

CURRENT FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: PCT/US02/18256

PRIOR PLILNG DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 54

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FasteEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: 520

TYPE: PRT

CORGANISM: Argiope trifasciata

US-10-479-638-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 VGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.8%; Score 436; DB 5; Length 13
Best Local Similarity 65.6%; Pred. No. 1.7e-30;
Matches 86; Conservative 17; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 GFGNNATANOY 151
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwa J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 301334
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 300390.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ATGGG 182
                                                                                                                                                                                                                                                                                                                          74 GYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDS 133
                                                                                                      15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA----RKSETTITQ
                                                                                                                                                                                 347 AGAGAAAASAGAGAGGYGGGYGGGYGGGSS----18YGAISSSAISSSIASSSRGIVISG
     13; Gaps
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Best Local Similarity 25.2%; Pred. No. 1.5;
Matches 38; Conservative 15; Mismatches 51; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 GGMGGGADGAYGSGAGGGVGKGQGESGVALAPSSDGYYNGGAAD----
     Indels
99
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US-10-425-115-301334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GGHGGGAGAPSY 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-10-425-115-301334
Sequence 301334, Application US/10425115
GENERAL INFORMATION:
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ORGANISM: Zea mays
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APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT PILING DATE: 2002-06-13
WUMBER OF SEQ ID NOS: 40112
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                         TQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVN-QT 129
                                                                                                                                                                                                                                                                                                                                                                                                          ----EAAGAENAAAGNGQA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                              19 LAGVVPQWGGGG------NHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI
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                                                                                                                                                                                              Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65; Indels
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%; Score 91.5; DB 6; 29.4%; Pred. No. 2.6; iive 17; Mismatches 65;
                                                                                                                              OTHER INFORMATION: Clone ID: MRT4577_78839C.1.pep
                                                                                                                                                                                            11.9%; Score 91.5; DB 27.7%; Pred. No. 1.5; iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35751, Application US/10170205E GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 VNAK -- DMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 741, Application US/10170205E; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                130 ASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 QIEGEDEQAQGNAGNENAAEE 176
        NUMBER OF SEQ ID, NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.4%
Best Local Similarity 29.4%
                                                                                                                                                                                                                Best Local Similarity 27.73
Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                  TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                    US-10-425-115-346132
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US-10-170-205E-35751
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                          SEQ ID NO 346132
LENGTH: 179
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US-10-170-205E-741
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                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SIGO ID NOS: 369326
SEQ ID NO 312468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Expansion, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REPRENCES: 38-21(5322.2)
CURRENT APPLICATION TOWNER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                          -----YGNGA--DVGQGADNSTIEL--TQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                  133 GGMGGGANGAYGSGAGGGVGKGEGVSGVALAPSSNGYYNGGAAD-----ATGGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 YGGGGYSSGGGYSSG-GYAANGYGVGSGSGNYSNASGGGYSGS----DGYGNGAASGGYA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA 85
                                                                                                                                                                                                                                                                                17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNN-----AALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                    12.1%; Score 93; DB 6; Length 258; 26.8%; Pred. No. 1.7; tive 16; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.0%; Score 92; DB 6; Length 295; 30.2%; Pred. No. 2.4; rive 13; Mismatches 46; Indels
                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_37025C.1.pep
US-10-425-115-300390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
US-10-425-115-312468
                          LOCATION: (1)..(258)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 312468, Application US/10425115 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-425-115-346132
; Sequence 346132, Application US/10425115
; GENERAL INFORMATION:
                                                                                                                                                             Query Match
Best Local Similarity 26.84
Matches 33, Conservative
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Best Local Similarity 30.28
Matches 35; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                       121 NNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGA 184
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(;
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Gaps

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Sequence 17306, Application US/09248796A

Sequence 17306, Application US/09248796A

Sequence 17306, Application US/09248796A

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: WOUTEEC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

LENGTH: 388
                                                     TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
LENGTH: 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 GLAKGTAPASTSATY-GESPSADYSKSGATGVVPATYLNTSGAPTGSLN----TAGVVG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 QSGYGNGADVGQ--GADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVN-Q 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 -GGTGGGGAGGAMNSNAQGSGSGTGSGSSYANRYWYGSNEAGASANGNGGGTGNSQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLS---IYQYGSANAALALQSDARKSETTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 88.5; DB 6; Length 197; 27.3%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 GNHNGGGNSSGPDSTLSIYOYGSANAALALQSDARKSETTITQSGYG
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                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_40676C.1.pep
US-10-425-115-304391
                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(197)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 TASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 NGGGGGGGGGAGSGYGNAXTPSFY 196
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Candida albicans
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Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
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                              APPLICANT:
APPLICANT:
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APPLICANT: EXELIXIS,
TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF
TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF
TITLE OF INVENTION: USE
THILE PERFERNES: EXO4-003C-PC
CURRENT PILLING DATE: 2004-01-28
CURRENT PILLING DATE: 2003-01-29
PRIOR FILLING DATE: 2003-01-29
PRIOR FILLING DATE: 2003-02-11
PRIOR FILLING DATE: 2003-04-10
PRIOR FILLING DATE: 2003-04-10
PRIOR FILLING DATE: 2003-04-10
PRIOR FILLING DATE: 2003-06-19
PRIOR FILLING DATE: 2003-06-19
PRIOR FILLING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 54
SURVEY FILLING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 54
SURVEY FILLING DATE: 2003-06-19
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                                                                                                                                                                                                                                                                         99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                        65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 VAAAPVVPAVSTSSAAGVAPNPAGGGSNNSPSSSSSPTSS-SSSPSSPGSPLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                      -----VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                             6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                  Length 1203;
                                                                                                                                             11.9%; Score 91.5; DB 6; Length 1 llarity 29.4%; Pred. No. 13; Conservative 17; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                      158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD---
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 VNAK -- DMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFG 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application PC/TUS0402338 GENERAL INFORMATION:
  ; SEQ ID NO 741
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-741
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                                                                                                                                                  Query Match
Best Local Similarity
Matches 42; Conserv
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US-10-425-115-304391
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PCT-US04-02338-49
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LENGTH: 1327
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81 VGQGADN-STIELTQN------GFRNNATYDQLVTRVVTHEMAHAGGNNA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GGGASQNGGSGYGSGSGSGSGTYSQGGYYSGYGESSNA------GGTGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 --GADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQT-----ASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AGYWNSNAQGSGSGTGSGSSYANRYWDGSSEGGANANGNGGMGNSQNGGGGGGGGGGGT 186
                                                                                                                                             241 GNENGTGAENNANADAQTDVAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD
                                                                            30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 GGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Indels
              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: MRT4577_163446C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.3%; Score 86.5; DB 6;
Best Local Similarity 26.9%; Pred. No. 4.3;
Matches 35; Conservative 15; Mismatches 53;
              16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: August 2, 2004, 15:29:56 Job time : 18.8 secs
              34; Conservative
                                                                                                                                                                                                                                                                                                                                                     124 ALVNOTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                      360 AAENNGNADAA 370
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              Matches
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APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Barow, James A
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, James K.
APPLICANT: Win, Wei
APPLICANT: Win Wei
APPLICANT: Roberts, James K.
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APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Baum, James J
APPLICANT: Lu, Maclong
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Moberts, James K
APPLICANT: APPLICANT: Why Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Compositions thereof
FILE REPERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT APPLICATION NUMBER: 1204-06-11
NUMBER OF SEQ ID NOS: 414445
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GNENGTGAENNANADAQTDVAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 VGQGADN-STIELTQN-----GPRNNATYDQLVTRVVTHEMAHAGGNNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 AAQGTDNGAAAENTGNADPAQGNDNGAAAENSGNENGTAAENNANADVQNDAAQVNDNGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKSETTITQSGYGNGAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
11.4%; Score 87.5; DB
Best Local Similarity 26.0%; Pred. No. 12;
Matches 34; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 87.5;
Pred. No. 12;
                                                                                                                                                               Sequence 7907, Application US/60565632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7907, Application US/60579062
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Diabrotica virgifera US-60-565-632-7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Diabrotica virgifera
US-60-579-062-7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%;
26.0%;
   240 GAGFGDNSNTSSY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 AAENNGNADAA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ALVNOTASDSS 134
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Best Local Similarity
                                                                                                  RESULT 13
US-60-565-632-7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-60-579-062-7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 7907
LENGTH: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 7907
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec Run on:

US-09-543-407-30 768 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

283366

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	fimbrin protein ad	5	curlin protein csg	curlin major subun	hypothetical prote	curlin nucleator p		curlin minor chain	cnjB protein - Tet	fimbrin protein ad	nucleation compone	hypothetical glyci	5	hypothetical prote	probable PPE prote	prot	ò	prot		probable PPE prote	DNA-binding protei	ovo protein - frui	protein kinase sgg	hypothetical prote	.21 pro	probable adhesin h	surface anti	probable disease r	e PPE prot
SUMMARIES	ID	JC6039	AI0635	S70788	D90806	H85665	S70787	90806	G85665	. S42136	JC6040	AH0635	E95965	AD3143	7	32	77	B70663	33	37	22	33	ຕ	22	34	9	F03	9785	468	7052
	DB	0	N	Ŋ	7	7	~	ď	Ŋ	∾	C)	(7	N	~	Ŋ	C)	C)	C1	~	~1	N	7	7	N	(7	~	N	7	0	7
	Length	15	15	15	15	15	15	г	15	174	15	15	217	14	14	64	31	32	65	25	220	102	121	57	40	57	191	65	44	96
æ	Query	88.7	œ	7	S	S	3	13.6	3	3	3	3	3	2	2	3	N	N	N	a	O	N	N	2	н	н	н	-1	-1	н
	Score		681	Ŋ	02	02	04	104.5	9	ч	σ	99.5	σ	8 8		97.5	9	94		93.5	m	N	S		Н	91.5	н	16	90.5	on .
	Result No.	1	7	m	4	Ŋ	9	7	∞	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	23	29

	probable exported	hypothetical prote		hypothetical prote	sericin1B - silkwo	hypothetical prote	hypothetical prote	probable nucleopor	probable PPE prote		large repetitive p	tail fiber protein	leishmanolysin (EC	outer membrane pro	probable PPE prote	
	AH0038	T05221	B44402	866852	S52714	T21956	T26667	T50074	B70987	E70946	AD0835	800275	A45621	E64559	F70675	C42049
									2			2	0			0,
	1238	34	956	196	121	407	586	1778	1053	59(	3624	262	59	745	583	638
	11.7	11.6	11.6	11.5	11.5	11.5	11.5	11.5	11.4	11.3	11.3	11.3	11.3	11.3	11.2	11.2
-71	89	89	8	88.5	ത	88	88	88	87:5	87	87	w	9	86:5	88	ю ю.
		31					36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1	
JC6039 fimbrin p	JC6039 fimbrin protein agfA precursor - Salmonella enteritidis
C.Species	C:Species: Salmonella enteritidis C:Date: 31-Dec-1994 #semience revision 31-Dec-1994 #text change 08-Oct-1999
C, Accessi	citatige of occ-199
R;Collins	on, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
A; Title:	u. Bacceilul. 178, 882-887, 1998 A,Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A;Referen	
A; Molecul	A Molecular type: DNA
A;Cross-ru	A; Gestudes: 1-151 < COL> A; Cross-references: GB: U43280; NID: g1184712; PIDN: AAC43599.1; PID: g1184714
A; Accession	
A;Residue	A;Modecule (Type: procein A;Residues: 21-52 <cc2></cc2>
A; Experim	strain 27655-3b
A; Note: t.	le authors translated the codon ACG for residue 44 as Ile no 8 k · Bmody 1. · Moller k u · Trost u u
J. Bacter	ol, 173, 4773-4781, 1991
A, Title:	urification and characterization of thin, aggregative fimbriae from Salmonell
A; Reteren	e number: A44898; MUID:91310586; PMID:1677357 : 27656
A: Accessic	. 2.00 101: 244898
A;Status:	A; Status: preliminary
A, Molecul	: type: protein
A; Kesidues: ZI-33	1881 11-3 CCU3A CCU3A From MOT brailbon (MOTTH 1603C)
C:Genetics	saciacced iiom nobi bacabone (nobir:4333
A;Gene: agf/	agf.A.
C; Function:	
A; Descript	Albescription: major component of thin aggregative fimbriae Albore: fimbrise bind to fibronectin, plasminomen, tissue plasminomen activator
C; Keywords	rasminosen,
F;1-20/Dor F;21-151/E	F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <wat></wat></sig>
Query Ma Best Loc	, ,
Maccines	delive Z; Mismacches 1Z;
λ	MIKLIKVAAFRAIVVSGSALAGVVPQWGGGGNBNGGGNSSGPDSTLSIYQYGSANAALALQ 60
Db	1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
٥٧	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
ΩÞ	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
δλ	121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

csgA

g

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Curlin major subunit CagA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C.Species: Escherichia coli (C.Species: Escherichia coli (C.Species: Bs.Jul-2001 #sequence_revision 18-Jul-2001 #sequence_revision 18-Jul-2001 #sequence_revision 18-Jul-2001 #sequence_revision 18-Jul-2001 #sequence_revision 18-Jul-2001 #sepaswara, K.; Ishii, K.; Yokoyama, K.; Han, C.G. R.; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. A.; Ress 8, 11-22, 2001 #sequence of enterchemorrhagic Escherichia coli O157:H7 and gency A.; Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Description: major component of wild-type curli, interaction between CsgA and CsgB tri
A,Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A;Reference number: S31202; MUD:93211294; PMID:8459772
A;Accession: S31202
A;Molecule type: DNA
A;Reducts: 1-6, 'V', 8-151 < OLS1>
A;Cross-references: EMB::L04979
A;Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLIKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-133, 'RQRDSGWLW' <0LS3>
A;Cross-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 517; DB 2; Length 15; Pred. No. 1e-35; 17; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.4%; Score 502.5; DB 2;
llarity 68.4%; Pred. No. 1.6e-34;
Conservative 18; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                       A, Molecule type: protein
A, Residues: 21-42;44-50 < 0LS2>
R;Olsen, A.N.; Armqvist, A.M.
Submitted to the EMBL Data Library, October 1992
A, Reference number: S34559
A, Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.58
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: csgA
A,Map position: 23.15
C,Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
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NyAlternate names: cagA protein; major curlin protein

C;Species: Escherichia coli

C;Species: Bscherichia coli

C;Species: 12-Peb-1998 #text_change 01-Mar-2002

C;Accession: 570788, G4846; S31302; S34569; S34559

R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.

Mol. Mcrobiol. 18; 661-670, 1995

R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.

Mylitle: Expression of two csg operons is required for production of fibronectin- and CA

A;Reference number: 570783; MUID:96414468; PMID:8817489

A;Reference number: 570783; MUID:96414468; PMID:8817489

A;Reference number: 570783; MUID:96414468; PMID:8817489

A;Reference number: ENEL: 151 < AAM>
A;Reference references: ENEL: 570784

A;Reference references: ENEL: 570784

A;Reference references: ENEL: 570784

A;Reference references: ENEL: 570784

A;Reference number: Ref. 1995

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Typis Species: Salmonella enterica subsp. enterica serovar Typis Species: Salmonella enterica subsp. enterica serovar Typis Species: Salmonella enterica subsp. enterica serovar Typis C;Species: Salmonella enterica subsp. enterica serovar Typis C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: A10635 R;Parkhill; J; Dougen, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-882, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Returus: preliminary A;Ancession: A1063 A;Status: preliminary A;Ancession: A1063 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-151 < PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
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R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mol. Microbiol. 7, 523-536, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITŲSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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Pred. No. 3.3e-49;
2; Mismatches 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.7%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: STY1181
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A,Description: minor component of wild-type curli, interaction between CsgA and CsgB tr A,Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kintingeni, in the absence of CsgA, CsgB can self-assemble into polymers
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession. G85665
R;Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-151 <STO>
A;Cross-references: G8:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, si CiSpecies: Escherichia coli CiSpecies: Escherichia coli CiSpecies: Escherichia coli CiSpecies: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 R;Hayashi, T;Makino, K;Ohnishi, M;Kurokawa, K;Ishii, K:;Yokoyama, K;Han, Gasawara, N;Yakawara, N;Yakunaga, T;Kuhara, S;Shiba, T;Hattori, M;Shinagawa, H. A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Accession: C90806 A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 RNNATYDQLVTRVVTHEMAH -- - AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAĞTNNSAQIRQĞGSKLLAVVAQEĞS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNNATYDQLVTRVVTHEMAH - - - AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                          ; Score 104.5; DB 2; Length
; Pred. No. 0.087;
15; Mismatches 57; Indels
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13.6%; Score 104.5; DB 2;
Best Local Similarity 29.1%; Pred. No. 0.087;
Matches 34; Conservative 15; Mismatches 57;
                source: strain K-12, substrain MG1655
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29.1%;
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                                                                                                        23.15
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A;Residues: 1-151 <H
      A,Experimental so
C,Genetics:
A,Gene: csgB
A,Map position: 2
C,Function:
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Nalternate names: csgB protein; curlin nucleation component; minor curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accesion: 370789; F64846
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production of fibronectin- and Cc
A;Reference number: 370783; MUD:96414468; PMID:8817489
A;Reference number: 370783; MUD:96414468; PMID:8817489
A;Ression: 570783; MUD:96414468; PMID:8817489
A;Ression: S70783; MUD:96414468; PMID:8817489
A;Ression: S70783; MUD:91414558; PIDN:CAA62281.1; PID:g1147563
A;Residues: 1-151 cHAM
A;Residues: 1-151 cHAM
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A;Residues: 1-151 cHAM
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A,Residues: 1-151 <BLAT>
A,Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278.
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Gaps
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68.4%; Pred. No. 1.6e-34;
live 18; Mismatches 29;
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                                                                                                                                          GGGGAAVDQTASNSTVNVTQVGFGNNATAHQY
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                                                                                                 GNNAALVNQTASDSSVMVRQVGFGNNATANQY
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Best Local Similarity 68.4%
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skelton, J.; Stevens, K. Salmonella enterica sero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.; Wain, J.; Churcher
L.; White, N.; Farrar
                                                                                                                                                                                                                                                               aggregative fimbriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleation component of curlin monomers [imported] - Salmonella enterica subsp. C.Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: minor component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AL513382; PIDN: CAD08267.1; PID: g16502314; GSPDB: GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                            fimbrin protein agfB precursor - Salmonella enteritidis
C,Species: Salmonella enteritidis
C,Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 NGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 NGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 EGGNNRAKVDQAGNYNFAY-IEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                               Cyaccession: JC6040

R/Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996

A,Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fila, Reference number: JC6039, MuID: 96146512; PMID: 8550497

A,Accession: JC6040

A,Residues: 1-151 < COL

A,Residues: 1-151 < COL

A,Cross-references: GB: U43280; NID: g1184712; PIDN: AAC43598.1; PID: g1184713

A,Experimental source: strain 276755-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.; Wain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cjaces on H40635
R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D th, T; Connerton, P; Connerton, P; Davis, P; Davies, R.M.; Dowd, J.S.; Moule, S.: O'Gara, Conin, A.; Davis, P; Davies, R.M.; Dowd, J.S.; Moule, S.: O'Gara, Dowd, J.S.; Moule, S.: O'Gara, Dowd, J.Y.; Simmonds, M.; Skej A; A; Hitle: Complete genome sequence of a multiple drug resistant Sala A; Reference number: ABO502; MUID:21534947; PMID:11677608
A; Accession: AH0635
A; Statutus: preliminary
A; Molecule type: DNA
A; Residues; 1-151 PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 99.5; DB 2; Length 151; 28.2%; Pred. No. 0.22; rive 16; Mismatches 51; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fil 21/Domain: signal sequence #status predicted <SIG>
F;22-151/Product: fimbrin protein agfB #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-
                                                                                                                                          Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Conservative
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                          :|:| |:
1723 WGSNNQAS 1730
142 FGNNATAN 149
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Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 GOGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                       38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                        21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWGGGGNHNGG----GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                            CijB protein - Tetrahymena thermophila
CjSpecies: Tetrahymena thermophila
CjSpecies: Tetrahymena thermophila
CjSpecies: Tetrahymena thermophila
CjAccesion: 842136; Sal356
RjTaylor, F.M.; Martindale, D.W.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
                                                                                                                                                                                                                                                                                RNNATYDOLVTRVVTHEMAH --- AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1640 ÓFGGGGNSNGGOSWGTSSGSDWN-------CQSNVQES-TTTSSGGWGS---
                                                                                                                               Gaps
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                                                                                                                               11;
                                                                                       Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Indels
                                                                                                                             Indels
      strain O157:H7, substrain EDL933
                                                                                   13.6%; Score 104.5; DB 2; 29.1%; Pred. No. 0.087; iive 15; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.2%; Score 101; DB 2; Best Local Similarity 29.7%; Pred. No. 2.6; Matches 38; Conservative 18; Mismatches 32.
                                                                                                                                 Conservative
                                                                                       Query Match
Best Local Similarity
Matches 34; Conserva
      A;Experimental s
C;Genetics:
A;Gene: csgB
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Dypothetical protein AGR L 228 [imported] - Agrobacterium tumefaciens (strain C58, Cere. C) Species: Agrobacterium tumefaciens C) Species: Agrobacterium tumefaciens C) Species: Agrobacterium tumefaciens C) Species: Agrobacterium tumefaciens C) Agrobacterium tumefaciens C) Agrobacterium tumefaciens C) Agrobacterium (S) Agrobacterium (S) Agricus C) Agricus C) Agricus C) Agricus C) Agricus C) Agricus C) Agricus C) Agricus C) Agricus C) Agricus C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacterium tumer C) Agrobacteri
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A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DM
A/Residues: 1-645 cOD.>
A/Cross-references: GB:AL021958; GB:AL123456; NID:g3261536; PIDN:CAA17522.1; PID:e12532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: F70825
R;Cole, S.T.; Erosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, C; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-145 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88682.1; PID:g15158413; GSPDB:GN00170
C;Genetics:
A;Gene: AGR L 228
A;Gene: AGR L 228
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                              104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IVGHQYGRHNLS-AVGQEGHDNYGSTTQNGNRNVAGIGQFGSNHTTILTQDGNGNIAAGV 119
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                                                                                                                                                                                                                                                                                                                                                      45 LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYD
                                                                                                                                                                                                                                                 20;
                                                                                                                                20;
                                                        Length 145;
                                                                                                                                                                                                 3 LLKVAAFAAIVVSGSALAGVVP-----QWG----GGGNHNGGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 145,
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                                                                                                                            Indels
                                                                                                                            57;
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12.8%; Score 98; DB 2;
Best Local Similarity 27.1%; Pred. No. 0.29;
Matches 38; Conservative 25; Mismatches 57
                                                12.8%; Score 98; DB 2; 27.1%; Pred. No. 0.29; iive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLKVAAFAAIVVSGSALAGVVP-----
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Q-VGRGCSANVSQGGNDNVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLVTRVVTHEMAHAGGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : :: | :| Q-VGRGCSANVSQGGNDNVA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OLVTRVVTHEMAHAGGNNAA 124
                                                                                                                        Conservative
                                    Query Match
Best Local;Similarity
Matches 38; Conserv
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A;Experimental source: strain CS8 (Dupont)
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13.0%; Score 99.5; DE
Best Local Similarity 23.0%; Pred. No. 4.3;
Matches 32; Conservative 14; Mismatches
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A;Map position: linear chromosome
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C;Genetics:
A;Gene: SMb21548
A;Genome: plasmid
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                                                                 Query Match
Best Local Similarity 25.9%; Pred. No. 1.6;
Matches 43; Conservative 15; Mismatches 59; Indels 49; Gaps
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A, Experimental source: strain H37Rv C, Genetics:
A, Gene: PPE
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:*

Database :

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SPECIESS.senertidis; STRAIN=27655-3B;
MEDLINE=91310596; PubMed=1677357;
Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
Collinson S.K., Emcedy I., Mueller K.-M., Trust T.J., Kay W.W.;
Salmonella enteritidis.",
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLII IS THE STRUCTURAL SUBGNIT OF THE CURLI. CURLI ARE
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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                                                                                                                                                                                                                                                                  SPECIES-S.enteritidis: STRAIN-27655-3B;
MEDLINE-9401373; PubMed=8104955;
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd B.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA,
the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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SVMVRQVGFGNNATANQY -> DSYTQVAS (IN
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151 AA; 15305 MW; B7DACOD16B621359 CRC64;
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90.7%; Pred. No. 1.8e-50;
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SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
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PIR, UC6039; UC6039.
StyGene; SG10608; csgA.
Fimbria; Signal; Complete proteome.
                                                   Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                                                              Bacteriol. 178:662-667(1996)
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Salmonella enteritidis.",
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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MEDIATDE=91310586; PubMed=1677357;
COllinson S.K., Emcedy L., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Minura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Moromura X., Nakamura Y., Nashimoto H., Nishio Y., Sanjeo I., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.,
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                          Eschericia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.;

Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.;

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"Intronectin binding in Escherichia coli HBIOL.";

Mol. Microbiol. 6:2443-2452(1992).
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Yang May 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
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SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A.;
The RpoS sigma factor relieves H-NS-mediated transcriptional
"The RpoS sigma factor relieves H-NS-mediated transcriptional
"repression of csgA, the subunit gene of fibronectin-binding or
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                                                                  01-DEC-1992 (Rel. 24, Created)
01-07-1996 (Rel. 34, Last sequence update)
8-EB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
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MEDLINE=97061202; PubMed=8905232;
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Mol. Microbiol. 7:523-536(1993).
                                 STANDARD;
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STRAIN=K12 / MG1655;
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
MEDLINE=96414468; PubMed=8817489;
MEDLINE=96500 Armqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
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Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MAJOR CURLIN SUBUNIT.
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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CSGB OR B1041 OR Z1675 OR ECS1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 68.4 Matches 104; Conservative
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152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 AA;
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MICHOR-21218556; PubMed=11319125;
Which G.A., Keen J.E., Elder R.O.;
Which G.A., Keen J.E., Elder R.O.;
Which G.A., Keen J.E., Elder R.O.;
Which G.A., Keen J.E., Elder R.O.;

Expression in certain strains of Escherichia coli 0157:H7.";

Percentary of Escherichia coli 0157:H7.";

Percentary of Escherichia coli 0157:H7.";

Percentary of Escherichia coli 0157:H7.";

Percentary of Escherichia coli 0157:H7.";

Percentary of Escherichia coli 0157:H7.";

Percentary of Escherichia coli 0157:H7.";

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Percentary of Escherichia coli 0157:H7.";
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28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
CSGA OR 21676 OR ECS1420.
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriais.
Enterobacteriaceae; Escherichia.
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C003470D208D395F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%; Score 517; DB 1; Le
69.5%; Pred. No. 9.7e-37;
iive 17; Mismatches 29;
        SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, L04979; AAA23616.1; --
EMBL, X89754; CAA2282.1; --
EMBL, AB000205; AAC74126.1; --
EMBL; D90741; BAA35832.1; --
EMBL; D90742; BAA35840.1; --
PIR; S70788; S70788.
EccGene; EG11489; csgA.
Finbria; Signal; complete proteome.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 105; Conservative
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[1]
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EMBL; X90754; CAA62281.1; -.

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"Sigma S-dependent growth-phase induction of the csgBA promoter in

"Sigma S-dependent growth-phase induction of the csgBA promoter in

Escherichia corli can be achieved in vivo by sigma 70 in the absence

of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).

-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE

COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERRITALLY AT GROWTH

TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO

FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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STRAIR-015-71+7 / RIMD 0509952;
MEDLINE=21156231; PubNed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurata T., Tanaka M., Tobe T., Iida T., Taraka M., Tobe T., Kuhara S., Shiba T., Hartori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitegawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                          STRAIN=KI2 / W01655;
MEDLINE=9742661; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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MEDLINE=21074995; PubMed=1120551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkparrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grobbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yano M., Horiuchi T., "A 718-kb DNa sequence of the Escherichia coli K-12 genome "A 718-kb DNa sequence of the Escherichia coli sequence 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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MEDLINE=95157246; PubMed=7854117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
                                      Mol. Microbiol. 18:661-670(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimura S., Kitagawa M.
Mori H., Motomura K.,
Sampei G., Seki Y., Ta
Yano M., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURLIN MONOMERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 RNNATYDQLVTRVVTHEMAH----AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                            B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%; Score 104.5; DB 29.1%; Pred. No. 0.033;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
EMBL; AE000205; AAC74125.1; -... EMBL; D90741; BAA3831.1; -... EMBL; AE005315; AAG55787.1; -... EMBL; AP002554; BAB34842.1; -... EMBL; C90806; C90806. PTR; G90806; C90806. PTR; G85665; G85665. PTR; S70787; S70787. ECOGene; Ed12621; csgBL. Finbria; Signal; csgBL. Finbria; Signal.
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MEDLINE=22531367; PubMed=12644504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 15882 MW;
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Best Local Similarity 29.1%
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                      -----IELTQ 94
                                                                                                                                                                                                                                                                                                         14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                                                                                                                                                                                                                                                                                                                      74 EĞENNRAKVDQAGNYNFAY-IEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 NGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-S. Typhimurium, STRAIN-LTZ / SGSC1412 / ATCC 700720; MEDLINE-1554948; Pubmdc=1167609; MEDLINE-2154948; Pubmdc=1167609; MCCIclland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=S enteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W. "Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGRB OR STM143.
Salmonella typhimurium, and
Salmonella enteritidis.
                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                   51; Indels
                                                                                                                                                                                                                                                                                  51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST---
                                                        Or Sein ...

EMBL; AL677269; CAD08267.1; -.

EMBL; AE016840; AA069400.1; -.

EMBL; AE016840; Complete proteome.

Fimbria; Signal; Complete proteome.

SIGNAL 21 POTENTIAL.

22 151 MINOR CURLIN SUBUNIT.

16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                               13.0%; Score 99.5; DB 1
28.2%; Pred. No. 0.088;
ative 16; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AA
                                                                                                                                                                                                                                                 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD:
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                                                                                                                                                                                                                                  Similarity
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ID _CSGB_SAL1
AC P55226;
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XM MEDLINE=91293102; PubMed=1712294;

MEDLINE=91293102; PubMed=1712294;

MEDLINE=91293102; PubMed=1712294;

IT he ovo gane of Drosophila encodes a zinc finger protein required for female germ line development.";

EMBO J. 10:2259-2266(1991).

LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-! FUNGTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE SEX DETERMINATION.

-! SUBGELLULAR LOCATION: Nuclear (Potential).

-! SUBGELLULAR LOCATION: Nuclear (Potential).

-! SUBGELLULAR LOCATION: Nuclear (Potential).

-! DEVELOPMENTAL STAGE: FIRST APPRARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OCCENESTS. STORED IN THE EGG, BUT IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           .----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGOVGTDNSARVRQEGSKLLSVISO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.,
"Multiple products from the shavenbaby-ovo gene region of Drosophila
melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila, NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST---
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Fimbria; Signal; Complete proteome.
SIGNAL:
CHAIN 22 151 MINOR CURLIN SUBUNIT.
1 22 151 MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                           13.0%; Score 99.5; DB 1; 28.2%; Pred, No. 0.088; cive 16; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSI521; 09xZU4;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1028 AA
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                                                                                                                                                                   EMBL, AG002301, CAA05316.1,
EMBL, AG008749; AAL20073.1; -
BMBL, U43280, AAC43598.1, -
PIK, JC6040, JC6040.
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        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 59 LONAAAAYIMSAGSG-----GGGCTGNGGGGASGPGGGPSANSGGGGGGG---- 104
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                                                    EMBL; X59772; CAB369210.1; ALT_SEQ.
EMBL; X59772; CAB36921.1; ALT_SEQ.
HSSP; P07248; 256038.
HSSP; P07248; 256038.
TRANSFAC; T00669; ...
TRANSFAC; T00669; ...
TRANSFAC; T00669; ...
TRANSFAC; T00669; ...
Flybace; Fegno003028; ovo.
Interpro; JR007087; Znf C2H2.
Flybace; JR007087; Znf C2H2.
SMART; SM00355; ZnF C2H2; 3.
SMART; SM00355; ZnF C2H2; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS00157; ZNC_FINGER_C2H2_2; 3.
Zinc-finger; Metal_binding; DNA-binding; Repeat; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                     12.0%; Score 92.5; DB 1; Length 1028;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              2.9;
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15; Mismatches
                                                                                                                                                    POLY-ALA.
POLY-GLY.
POLY-GLY.
POLY-GLY.
POLY-HIS.
POLY-HIS.
POLY-AIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AALVNQTASDSSVMVRQVGFGNNATA 148
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1028 AA;
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095271; 095272;
28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                                Transcription
                                                                                                                                                                                                                                                                                                                                                                                                     38;
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SEQUENCE
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Best Local
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-.. CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl} (N) -acceptor = nicotinamide + {ADP-D-ribosyl} (N) -acceptor = nicotinamide + {ADP-D-ribosyl} (N) -acceptor = nicotinamide + {ADP-D-ribosyl} (N) -acceptor = nicotinamide of telomeric TRF2. Interacts with the cytoplasmic domain of LNPEP/Otase with TYMS2. Interacts with the cytoplasmic domain of telomeric TRF1 via the ANK repeats.

-.. SUBCEDIULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriclar matrix of mitotic centromeres. During interphase, a small fraction of TNNS is found in the nucleus, associated with TRF1.
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Note=No experimental confirmation available;
ISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
PTM: Upon insulin-stimulation; phosphorylated on serine residues by MARK kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-59454782; PubMed-10523501;
Smith S., de Lange T.;
"Cell cycle dependent localization of the telomeric PARP, tankyrase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21602874; PubMed=11739745;
Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99040105; PubMed=9822378; Smith S., Giriat I., Schmitt A., de Lange T.; "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres."; Science 282:1484-1487(1998).
(TNKS-1) (TRF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by MAPK kinases.
--- PTM: ADP-ribosylated (-auto).
--- SIMILARITY: Belongs to the PARP family.
--- SIMILARITY: Contains 15 ANK repeats.
--- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                         interacting ankyrin-related ADP-ribose polymerase).
TNKS OR TNKS1 OR TIN1 OR TINF1 OR PARPL.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
    lankyrase 1 (EC 2.4.2.30) (Tankyrase I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nuclear pore complexes and centrosomes."; cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=095271-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. 22:332-342(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at human telomeres."; Mol. Cell. Biol. 22:33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION
                                                                                                                                                                                                          Mammalia; Euther
NCBI TaxID=9606;
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1656 AA

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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last sequence update)
416-OCT-2001 (Rel. 40, Last annotation update)
60uter membrane protein B precursor (168 kDa surface-layer protein)
610-MAY-2000 (Scas) (Tomps)
610-MAY-2000 (Scas) (Tomps)
610-MAY-2000 (Surface protein)
610-MAY-2000 (Surface protein)
610-MAY-2000 (Surface protein)
610-MAY-2000 (Surface protein)
610-MAY-2000 (Surface protein)
610-MAY-2000 (Surface protein)
610-MAY-2000 (Surface protein)
                                                                                                                                                                                 Uchiyama T.;
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
                                                                                                                                                                                                    japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDa SURFACE-EXFOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                        Rickettšia japonica.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Conservative
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1656
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1656 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=35790;
                                                                                                                                                                                                                                                        similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD-------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST -> GHS (in isoform 2).

/FTId='VSP 004538.

Missing (in isoform 2).
/FTId='VSP 004539.

H->A: LOSS OF ACTIVITY, WHEN ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH A-1291.
E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
                                                       MIM, 6030303, -. Gichromosome, telomeric region; IDA.
GO; GO:0000781; Cichromosome, telomeric region; IDA.
GO; GO:0003950; F:NAD ADP-ribosyltransferase activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.
InterPro; IPR002110; ANK.
Fig. PROSSIS ank; 19.
Pfam; PRO5033; ank; 19.
Pfam; PRO5035; ANK; II.
SMART; SM00454; ANK; II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                            PROSITE; PS50088, ANK REPEAT; 15.
PROSITE; PS50297, ANK REP REGION; 1.
PROSITE; PS50105; SAM DOMAIN; 1.
Transferace; Glycosyltransferace; NAD; Golgi stack; Telomere; Nuclear protein; Repeat; ANK repeat; ADP-ribosylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WITH A-1184.
W; E14DE985C710B957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91.5; DB Pred. No. 4.7; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             PARP.
POLY-HIS.
POLY-PRO.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                      EMBL; AF082557; AAC79842.1; -.
EMBL; AF082558; AAC79843.1; -.
EMBL; AF082559; AAC79844.1; -.
HSSP; Q00420; LAWC.
Genew; HGNC:11941; TNKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 VNAK -- DMAGRKSSPLHFAAGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%;
29.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 SETTITIOSG----YGNGADVGQGADNSTIELT--------QNGFRNNATYD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 548 ---TLTLGGANIISANGGTINFQANGGTIKLTSTQNNIVVDCDLAIATDQTGVVDASSLT 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK 65
                                                                      a
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 VLAAGAITLDGSATI-----TGDIGNGGG------GAALQSITLANDATK
-!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a slayer with hexagonal symmetry.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 QLVTRVVTHEMAHAGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 kDa SURFACE-EXPOSED PROTEIN.
32 kDa BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605 NAQTLTISGTIGIIGANNTTLGQFNIGSSKTTLNGGNVAINELVIGNNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 90; DB 1; Length 1656; 23.5%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168097 MW; 3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
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InterPro, IPR006315; Autotransport.
InterPro, IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
TIGRFAMS; TIGR01414; autotrans_barl; 2.
Antigen; S-layer; Cell wall.
I 1338 120 kDa SU
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(Rel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
N100_YEAST
ID N100_YEAST
AC Q02629;
DT 01-UUL-1993
DT 01-UUL-1993
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RESULT 9 OMPB_RICJA

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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 SFGSKPVGSGSLFGQSNNTLGNTTN--NRNGLFGQM-----NSSNQGSSNSGLFGQNS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 GGGGNHNGGGNSSGPDSTLSIY--QYGSANAALALQSDARKSETTITQSGYGN----GA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 10:869-574(1994).

-!- PUNCTION: Essential component of nuclear pore complex.

-!- PUNCTION: Essential component of nuclear pore complex.

Nucleoporins may be involved in both binding and translocation of the proteins during nucleocytoplasmic transport.

-!- SUBCEDLIVIAR LOCATION: Nuclear pore complex.

-!- DOMAIN: Contains G-L-F-G repeats.

-!- SUMILARITY: Belongs to the GLFG family of nucleoporins.
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                                                                                                                                                                                                                                                                                                                           MEDILINE=94378724; PubMed=8091863; Rasmussen S.W.; "Sequence of a 20.7 kb region of yeast chromosome XI includes the "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphare kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to
15-WAR-2004 (Rel. 43, Last annotation update)
Nucleoporin NUP100/NSP100 (Nuclear pore protein NUP100/NSP100).
NUP100 OR NSP100 OR YKL068W OR YKL336.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93054906; PubMed=1385442;
Wente S.R., Rout M.P., Blobel G.;
Manew family of yeast nuclear pore complex proteins.";
J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D3985F9901BBAA51 CRC64;
                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 89; DB 1
25.9%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0001551; NUP100.
GO; GO:0005643; C:nuclear pore; IDA.
InterPro; IPR007330; Nucleoporin2.
InterPro; IPR004325; Nucleoporin_FG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF04096; Nucleoporin2; 1. Pfam; PF03093; Nucleoporin_FG; 25. Nuclear protein; Transport; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          959 AA; 99988 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z15035; CAA78753.1; -. EMBL; X75780; CAA53406.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z28068; CAA81905.1; -. PIR; B44402; B44402. GermOnline; 139824; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 MNSST---QGVFGQN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.6
Best Local Similarity 25.9
Matches 35, Conservative
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                                                                                                                           NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                             MEDDLOW-ZIBEGGGLUGD3450,

RA WOOD V. GWIlliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA WOOD V., GWIlliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA SGOUROS J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA GOTLINS M., Connor R., Cronin A., Davis P., Filewell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Muchle B.J., Hunt S., Jagels K.,

RA Mooney P., Moule S., Mingall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Squares R., Squares R., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Stavens K.,

RA Skelton J., Squares R., Squares R., Sharp S.,

RA Skelton J., Squares R., Squares R., Sharp S.,

RA Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Huer S.,

RA Goffeau J., Cadieu E., Drean S., Gloux S., Lelaure V., Mottier S.,

RA Goffeau A., Cadieu E., Drean S., Gloux S., Lelaure V., Mottier S.,

RA Goffeau A., Cadieu E., Drean S., Gloux S., Lelaure V., Mottier S.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Cerrutti I., Lowe T., MocCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RA M. Weller P., Manstreel B., Randren B., Nurse P.,

RA M., Randre B., Randren B., Paulsen I., Potashkin J.,

RA M., Randre B., Randre B., Randre B., Randre B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Potashkin J., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstreel B., Manstree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIATE-1816,722; PubMed=9501991; Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.; Nakai K., Indentification of open reading frames in Schizosaccharomyces pombe
                 090TR4; PT8796; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Nucleoporin nupl89 (Nuclear pore protein nupl89). Nupr89 OR SPAC1486.05. Schizosacharomyces pombe (Fission yeast). Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales
1778 AA
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21848401; PubMed=11859360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 4:363-369(1997).
  STANDARD;
                                                                                                                                                                                                                                         Schizosaccharomyces
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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endopeptidase).
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P23223;
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                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the TWEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457 TIPA--SGGFSFGQNANNA----PKPAFGSTATTAPKPAGTGLFGGLGAGANTNTATNAT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGTMGTGL - - - FGFGANNNTANNTAPTSTFGGNNSSNFSFGANNNAATKPSGFGFGFTT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSALAGVVPQWGGGGNHNGGGNSSGPDSTL----SIYQYGSANAALALQSDARKSETT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=8728391; PubMed=3302276;
MEDLINE=8728391; PubMed=3302276;
Ride I., Drexler K., Eschbach M.L., Henning U.;
NDNA sequence of genes 38 encoding a receptor-recognizing protein of bacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
I. FUNCTION: Vg38 is at the tip of the long tail fibers and serves as the phage recognition site for the cellular receptor.
I. MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTR AS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage T2.
Viruses, dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
R EMBL; D89145; BAA13807.1; -.
R FISSP; T50074; T50074.
R GeneDB SPOWDe; SPAC1486.05; -.
R GO; GO: 0016020; C:nembrane; ISS.
GO; GO: 0005606; P:protein-nucleus import; ISS.
R GO; GO: 0005606; P:protein-nucleus import; ISS.
R InterPro; IPR007230; Nucleoporing;
R InterPro; IPR004325; Nucleoporing; I.
R Ffam; PF04096; Nucleoporing; I.
R M Nuclear protein; Transport; Repair
R M Nuclear protein; Transport; Repair
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R M Nuclear protein; Transport; Repair
R M Nuclear protein; Transport; Repair
                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 88; DB 1; Length 1778; 27.3%; Pred. No. 13; ive 16; Mismatches 65; Indels
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PIR; S00275; S00275.
InterPro; IPR007932; Tail_fibre_GP38.
Pfam: PF05268; GP38; Tecognition.
Short protein; Phage recognition.
SEQUENCE 262 AA; 25801 MW; 0567366918F6C745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07875;
01-AVG-1988 (Rel. 08, Created)
01-AVG-1988 (Rel. 08, Last sequence update)
01-AVG-1990 (Rel. 15, Last annotation update)
Receptor recognizing protein (Protein Gp38).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 GTGGSL-----FGNANTA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 27.3 es 38; Conservative
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VG38_BPT2
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          DR RODER STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STA
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                                                            ä
                                                                                                                      GGGRPFGVGGKIGSDSILS----GSNASL---TDAGTGGTTF-QYGAGNGGNVGAG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                              GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQG
                                                                                                                                                                                                                                                                                                                                                                                GF63. -
Leishmania donovani.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL TaxID-5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92107220; PubMed=1762629; Webb J.R., Button L.L., McMaster R.W.; "Heterogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani."; Mol. Biochem. Parasitol. 48:173-184(1991)
                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3 4.24 36) (Cell surface protease)
(Major șurface glycoprotein) (GP63 protein) (Promastigote surface
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                      Length 262;
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InterPro; 1PR001577; PeptTdase_M8.
InterPro; 1PR001577; PeptTdase_M8.
InterPro; 1PR001577; PeptTdase_M8.
InterPro; 1PR00152; ISHMANOLYSIN
PRINTS; PR00142; ISHMANOLYSIN
PROSITE; PS00142; ZINC_PROTEASE; 1.
Pydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zymogen, Signal; Cell adhesion; GPI-anchor; Lipoprotein.
SIGNAL
A0 87 ACTIVATION PEPTIDE.
                                                            Indels
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                      DB 1;
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                      Score 86.5; D
Pred. No. 2;
4; Mismatches
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01-NOV-1991 (Rel. 20, Last seq
10-OCT-2003 (Rel. 42, Last anno
                    11.3%;
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STANDARD;
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MEROPS; M08.001;
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EMBL; X52970; CAA37140.1; -.
HSSP; P06620; 1INA.
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A Medina-Acosta E., Karess R.E., Russell D.G.,
Medina-Acosta E., Karess R.E., Russell D.G.,
Medina-Acosta E., Karess R.E., Russell D.G.,
Turcturally distinct genes for the surface protease of Leishmania
T mexicana are developmentally regulated.",
Mol. Biochem. Parasitol. 57:31-46(1993).

I. PUNCTION: Has an integral role during the infection of macrophages
in the mammalian host.

C -!- FUNCTION: Preference for hydrophobic residues at Pl and
Inthe mammalian host.

-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and
C -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and
C -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and
C -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and
C -!- CATALYTIC ACTIVITY: Loc ion per subunit (By similarity).

-!- COFACTOR: Binds I zinc ion per subunit (By similarity).

-!- DEVELOPMENTAL STAGE: Expressed in both the promastigote and the
amastigote forms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       2
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
NCBL_TaxID=5665;
                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leisinanolysin C1 precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                              103 YDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVM-VRQVGFG----NNATA 148
                                                                                                                                                               241 YDQLVTRVVTHEMAHALGFSVVFFRDARILESISNVRHKDFDVPVINSSTA 291
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N-LINKED (GLCNAC. . .) (POTENTIAL)
GPI-anchor amidated asparagine (By
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LEISHMANOLYSIN C1.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                11.3%; Score 86.5; DB 1; Length 590; 47.1%; Pred. No. 4.9;
                                                            similarity).
OFB315D299659F58 CRC64;
                                                                                                                        4; Mismatches
                                                                         62950 MW;
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                                                                                                                        Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=MNYC/BZ/62/M379;
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102
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                                                                         590 AA;
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Best Local Similarity
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MEROPS; M08.001;
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P43150;
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               DISULFID
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GP63_LEIME
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Matches
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Mol. Genet. 223:163-166(1990).
-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercolled water. By similarity).
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUB AND A REGIONAL 48-RESIDUB PRRIODICITY IS SUBERIMPOSED.
-!- MISCELLANGOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
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                       SIMILARITY)
SIMILARITY)
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ZINC (CATALYTIC)
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BY SIMILARITY
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Pred. No. 6
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94.4%;
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445
466
501
646 AA;
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Best Local Similarity
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                                                                                                                                                                                                                34 GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGN-----GADV---- 81
                                                                                                                                    Query Match
Best Local Similarity 26.4%; Pred. No. 18;
Matches 39; Conservative 27; Mismatches 39; Indels 43; Gaps
InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITS: ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
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Database

672 570.5 534 534 380 126 126 111 111,1 105 104.5 104.5

Score

120 118

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Q7X243

RESULT 2 Q7X243

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1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
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MEDLINE-2288234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

"Extensive mosaic structure revealed by the complete genome sequence

of uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U. 3.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Enterobacteriaceae; Enterobacter:
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Last annotation update)
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Best Local Similarity 69.1%; Pred. No. 4.9e-33;
Matches 105; Conservative 17; Mismatches 29
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01-OCT-2003 (TrEMBLr
Curlin-csgA protein.
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SEQUENCE 152 AA
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";

Infect. Immun. 72:4151-4150(2003).

EMBL; AJSIS701; CADS66751.;

SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Fami
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.
Infect. Immun. 72:4151-4186(2003).
EMBL; AJS15700; CAD56772.1; -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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Enterobacteriaceae, Citrobacter.
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Last annotation update)
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74.3%; Score 570.5; DB 2
Best Local Similarity 77.5%; Pred. No. 3.7e-38;
Matches 117; Conservative 14; Mismatches 19
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  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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Citrobacter freundii.
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01-0CT-2003 (TrEMBLr
Curlin-csgA protein.
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SEQUENCE FROM N.A.
STRAIN=Fec4;
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CSGA.
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                                                                                                                                                                  Shewanella oneidensis.";
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 NCBI_TaxID=70863;
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                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                  1 MKFIKVAALAAIVVSGSAMAGMINQ-GGWGHGHGGGGGGPNSTLNIYQNGGGNSALALQ
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                                                                                             Gaps
"Production of Cellulose and Curli Fimbriae by Members of the Fami
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.
Infect. Immun. 72-4151-4158(2003).
EMBL; AJ515702; CAD56(78.1; -.
SEQUENCE 150 AA; 15112 MW; 5D8B82D872DF15F3 CRC64;
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Enterobacteriaceae; Salmonella.
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                                       Length 150;
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Pred. No. 2.7e-23;
0; Mismatches 2; Indels
                                                                    56.7%; Score 435.5; DB 2; Length 60.3%; Pred. No. 2.2e-27; ive 26; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRANT=SB30;
Cox J.M., Felezos S., Woolcock J.B.;
"Virulence of Salmonella enteritidis in chickens correla
colony morphology and expression of SBF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U53207; AAA98671.1;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                               120 LNGALVDQTASNSTVNVTQIGFGNHATAHQY 150
                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                         Created)
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Similarity 97.4%;
74; Conservative C
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                            91; Conservative
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                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           SEF17 fimbrin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis.
                                                                                  Similarity
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01-DEC-2001
                                                                      Query Match
Best Local S
Matches 91
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Q8EIH4;
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Q54069
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TRANSPOSON=Insertion sequence 181;
MRDLINE=99314153; PubMed=1038631;
I.a Ragione R.M., Collighan R.J., Woodward M.J.;
I.a Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078;K80 isolates associated with
IS1 inserti on in csgB and reduced persistence in poultry infection.";
PEMS Microbiol. Lett. 175:247-253(1999).
NON_TER: 29 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 GDNHTGFVYALAGSENDISMEQEGSNNTAYLSMTTGDDNTVDITQDGDSNTVGDSLIADI
MEDLINE 22297686; PubMed=12368813; Meldalberg U.F., Paulson K.E., Gaidos E.J., Nelson W.C., Heidelberg U.F., Paulson K.E., Ward N., Methe B., Clayton R.A., Read T.D., Elsen J.A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Nadupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Muller J., Khouri H., Gill J., Uttersback T.R., McDonald L.A., Reldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Pred. No. 0.0035;
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502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
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Pred. No. 0.048;
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27.0%; Pred. No. 0...
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EMBL, AE01552; AAN53941.1; -.
TIGR, SO0865, -.
Hypothetical protein; Complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete protection of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of
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Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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   DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 AA; 12699 MW; ACFB2D66A48D260F
14.5%; Score 111.5; DE 24.8%; Pred. No. 0.19; iive 24; Mismatches
                                                                                                                                                                                                                                                                                130 AA
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                                                                                   40 MRKLFFASVAVLALSSAAQAA---
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   Query Match
Best Local Similarity 24.8%
Matches 40; Conservative
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SEQUENCE 130 AA
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Q7UCZ1
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RA MEDLINE-2297686; PubWed=12368913;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Togapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA Medyuu R., Peterson J.D., Umyam L.A., White O., Wolf A.M.,
RA Wamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Wamathevan J., Khouri H., Gill J., Otterback T.R., McDonald L.A.,
RA Peldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
RGenome sequence of the dissimilatory metal ion-reducing bacterium
R Shewanella oneidensis.";
RI Nat. Biotechnol. 20:1118-1123(2002).
REMBL; AR015532; AAN53942.1; -.
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
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..., iriguchi M., Kawashima K.,
..., Jeurucka H., Wada T., Yamada ..., Eradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
ENBL; AP005954; BAC50565.1; -.
Complete proteome.
SEQUENCE 177 ...
                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.6%; Score 112; DB 16; Length 139; 28.3%; Pred. No. 0.14; Live 22; Mismatches 45; Indels 14
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                             139 AA; 14811 MW; 41EC1CFA76957920 CRC64;
                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit CsgB, putative.
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Last annotation update)
                  139 AA
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                  PRT;
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NCBI_TaxID=375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.34
Matches 32, Conservative
                    PRELIMINARY;
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                                                                                                                     Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 139 AA;
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CsgA OR BLL53(
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Q89JI3;
                    Q8EIH3
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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Bradyrhizoblum japonicum USDA110.";
DNA Res. 9:189-197(2020)
EMBL; AP005954; BACS0564.1; -.
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                                                                                                                                 43;
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Length 171;
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Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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                                                                                                                                 54; Indels
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Last annotation update)
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Last annotation update)
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98 RNNATYDQLVTRVVTHEMAH---AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).

EMBL, ABUBISII, AAN42658.1; -. Complete proteome.

SEQUENCE 160 AA, 16919 WW, 50269F5268D2A32F CRC64;
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                                                                                                                                                                                                                                              SECUENCE FROM N.A.
STRAIN=201 / Sertotype 2a,
STRAIN=202 / Sertotype 2a,
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang G., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A. (Sao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BacTeria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
NCBI_TaxID=623;
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Melson K.E., Weinel C., Paulsen IT., Dodson R.J., Hilbert H.,
Martins dos Santos V.AP., Fourts D.E., Gill S.R., Pop M., Holmes I
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Brinkac L., Beanan M., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
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Pseudomonadaceae, Pseudomonas.
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1-2003 (TrEMBLrel. 25, Last annotation update)
fiber surface-exposed nucleator CsgB, putative.
                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Minor curlin subunit precursor, similar ro CsgA.
CSGB OR.SF1035.
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29.1%; Pred. No. 0.65;
tive 15; Mismatches
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InterPro; IPR000437; Prok lipoprot S.
BYOSITE; PS00013; PROKAR LIPOPROTEIN; 1.
Complete proteome.
SEQUENCE 157 AA; 16175 MW; C385E98465
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Best Local Similarity 29.18
Matches 34, Conservative
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                                                                                                                                     Shigella flexneri
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
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WEDLINE=22388234; PubMed=12471157;
WEDLINE=22388234; PubMed=12471157;
WEDLINE=22388234; PubMed=12471157;
WEDLINE=22388234; PubMed=12471157;
WEDLINE=22388234; PubMed=12471157;
WEDLINE=22388234; PubMed=12471157;
MADLEV R. D. Buckles E.L., Lious S. R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
MODLEY H.L., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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                                                                                                                         Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 712775-2786(2003).

EMBL, AE016981; AAP16422.1; -- SEQUENCE 151 AA; 15868 MW; 5D5D266B964014A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit precursor.
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29.1%; Pred. No. 0.65;
:ive 15; Mismatches
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                                                           SEQUENCE FROM N.A.
STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
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Enterobacteriaceae; Shigella
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nes 34; Conservative
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